AbSciCon
2019

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

2
00:00:14,100 --> 00:00:09,110
[Applause]

3
00:00:16,380 --> 00:00:14,110
my name is a nice gentleman I'm a first

4
00:00:18,269 --> 00:00:16,390
year masters student at the University

5
00:00:21,089 --> 00:00:18,279
of Alaska Fairbanks and today I'm

6
00:00:22,980 --> 00:00:21,099
presenting my preliminary results and my

7
00:00:25,740 --> 00:00:22,990
future methods as this is the first year

8
00:00:27,599 --> 00:00:25,750
of my master's in my research titled

9
00:00:30,269 --> 00:00:27,609
predicting optimal growth rates of

10
00:00:34,619 --> 00:00:30,279
marine bacteria using genetic signatures

11
00:00:36,150 --> 00:00:34,629
of cold adaptation so to give kind of a

12
00:00:38,790 --> 00:00:36,160
little bit of background before I kind

13
00:00:40,170 --> 00:00:38,800

of dive into my methods and results I

14
00:00:42,740 --> 00:00:40,180
wanted to give a kind of a broad

15
00:00:45,479 --> 00:00:42,750
definition of the term of sacrifice as

16
00:00:48,149 --> 00:00:45,489
organisms that grow at cold temperatures

17
00:00:50,670 --> 00:00:48,159
ranging from about negative 20 degrees

18
00:00:53,270 --> 00:00:50,680
Celsius to positive 20 degrees Celsius

19
00:00:56,429 --> 00:00:53,280
and the research into these organisms is

20
00:00:58,770 --> 00:00:56,439
really broad and really interesting and

21
00:01:01,740 --> 00:00:58,780
for many different reasons particularly

22
00:01:04,140 --> 00:01:01,750
because ninety percent 90 percent of our

23
00:01:06,390 --> 00:01:04,150
Earth's ocean volume is less than five

24
00:01:08,550 --> 00:01:06,400
degrees Celsius including the Arctic

25
00:01:11,399 --> 00:01:08,560
Ocean which is at risk right now with

26
00:01:13,260 --> 00:01:11,409
increasing atmospheric temperatures but

27
00:01:14,610 --> 00:01:13,270
the primary results and the reason why

28
00:01:17,190 --> 00:01:14,620
we're all here at this conference in

29
00:01:19,470 --> 00:01:17,200
terms of astrobiology is that most of

30
00:01:21,750 --> 00:01:19,480
the water that we find that we will find

31
00:01:25,430 --> 00:01:21,760
we have found in our solar system is

32
00:01:27,930 --> 00:01:25,440
solid ice but an ocean such as on

33
00:01:30,600 --> 00:01:27,940
locations such as Europa are really

34
00:01:33,210 --> 00:01:30,610
likely to be cold so looking at how

35
00:01:39,360 --> 00:01:33,220
these organisms thrive in these really

36
00:01:41,700 --> 00:01:39,370
extreme environments is kind of key so I

37
00:01:45,360 --> 00:01:41,710
wanted to make a quick note before I get

38
00:01:47,219 --> 00:01:45,370

started I wanted to say that most of the

39
00:01:50,820 --> 00:01:47,229
organisms that thrive at sub-zero

40
00:01:52,580 --> 00:01:50,830
temperatures also live and grow at warm

41
00:01:55,110 --> 00:01:52,590
temperatures and these are known as

42
00:01:57,390 --> 00:01:55,120
psycrow tolerance and psycrow trophic

43
00:02:00,690 --> 00:01:57,400
s-- as you can see with these figure

44
00:02:03,270 --> 00:02:00,700
these this figure sorry we have a kind

45
00:02:05,250 --> 00:02:03,280
of a broad range of strains that grow a

46
00:02:07,219 --> 00:02:05,260
lot of different temperatures in

47
00:02:10,440 --> 00:02:07,229
different locations and different

48
00:02:12,089 --> 00:02:10,450
environments and the blue of kind of

49
00:02:14,160 --> 00:02:12,099
square represents minimum temperature

50
00:02:15,900 --> 00:02:14,170
the green circle is the optimal

51
00:02:19,020 --> 00:02:15,910
temperature and the red

52
00:02:20,880 --> 00:02:19,030
is the maximum temperature however when

53
00:02:22,980 --> 00:02:20,890
we kind of reduce this figure down a

54
00:02:24,990 --> 00:02:22,990
little bit we see that the true

55
00:02:27,540 --> 00:02:25,000
sacrifice are those organisms that

56
00:02:30,630 --> 00:02:27,550
thrive in that set range of temperatures

57
00:02:33,900 --> 00:02:30,640
underneath positive 20 degrees Celsius

58
00:02:37,170 --> 00:02:33,910
lie in saline systems and like sea water

59
00:02:40,080 --> 00:02:37,180
and sea ice and marine sediment and this

60
00:02:42,120 --> 00:02:40,090
makes it so that Arctic marine bacteria

61
00:02:44,730 --> 00:02:42,130
are really excellent isolates and

62
00:02:48,120 --> 00:02:44,740
proxies to study these kind of cold

63
00:02:49,680 --> 00:02:48,130

adaptive signatures and probably bio

64
00:02:54,540 --> 00:02:49,690
signatures that we could use and

65
00:02:56,130 --> 00:02:54,550
identify later on however I wanted to

66
00:02:58,170 --> 00:02:56,140
also note that a lot of these strains as

67
00:03:00,930 --> 00:02:58,180
you saw in the previous figure are there

68
00:03:02,880 --> 00:03:00,940
we have very few of them currently and

69
00:03:06,090 --> 00:03:02,890
so in order to address that issue we

70
00:03:08,820 --> 00:03:06,100
have isolated over 600 strains actually

71
00:03:11,280 --> 00:03:08,830
in marine bacteria and sequence 50 of

72
00:03:13,980 --> 00:03:11,290
them so this is a figure by du close ode

73
00:03:15,690 --> 00:03:13,990
that has been unpublished currently but

74
00:03:18,630 --> 00:03:15,700
it kind of shows the broad range of

75
00:03:21,990 --> 00:03:18,640
marine bacteria that we can find in sea

76
00:03:26,400 --> 00:03:24,390
unfortunately psycho Philly is not a

77
00:03:28,949 --> 00:03:26,410
phenotype that is really easily

78
00:03:30,080 --> 00:03:28,959
identifiable which would make my job a

79
00:03:33,120 --> 00:03:30,090
lot easier

80
00:03:35,280 --> 00:03:33,130
but as found in a previous study using

81
00:03:39,360 --> 00:03:35,290
machine learning by Phillip Bauer at L

82
00:03:40,620 --> 00:03:39,370
in 2015 he found that actually that

83
00:03:43,410 --> 00:03:40,630
psycho Philly which is kind of the

84
00:03:46,080 --> 00:03:43,420
orange triangle right there has the

85
00:03:51,320 --> 00:03:46,090
lowest predictability out of all of the

86
00:03:57,600 --> 00:03:55,680
okay so why do we do this and what is

87
00:03:59,940 --> 00:03:57,610
the purpose of this is that if this is

88
00:04:02,160 --> 00:03:59,950

possible if we can use and predict

89
00:04:04,710 --> 00:04:02,170
psycho Philly and use it to predict

90
00:04:07,500 --> 00:04:04,720
growth rates in Arctic marine bacteria

91
00:04:10,979 --> 00:04:07,510
we could use it to make predictions in

92
00:04:13,320 --> 00:04:10,989
other uncultured taxa known only from

93
00:04:17,849 --> 00:04:13,330
meta-genome assembled genomes or max

94
00:04:22,110 --> 00:04:17,859
these two figures are one that are kind

95
00:04:24,600 --> 00:04:22,120
of examples that's know these two

96
00:04:28,140 --> 00:04:24,610
figures are examples of mag's actually

97
00:04:30,330 --> 00:04:28,150
so this is right here

98
00:04:33,510 --> 00:04:30,340
this is known as a mag of a psycho

99
00:04:35,010 --> 00:04:33,520
vector so all of these this broad figure

100
00:04:36,450 --> 00:04:35,020
actually is when you compare a lot of

101
00:04:37,080 --> 00:04:36,460
different strains and compare them to

102
00:04:39,090 --> 00:04:37,090
each other

103
00:04:41,460 --> 00:04:39,100
specifically their context and they're

104
00:04:44,850 --> 00:04:41,470
really closely bunched up together it

105
00:04:46,860 --> 00:04:44,860
can be isolated into one strain this is

106
00:04:48,570 --> 00:04:46,870
another figure of a set of the same

107
00:04:50,930 --> 00:04:48,580
psycho factor so the little one in blue

108
00:04:56,189 --> 00:04:50,940
up there of a mag met at a different

109
00:04:59,279 --> 00:04:56,199
Assembly graph so I got started in

110
00:05:01,560 --> 00:04:59,289
formulating my methods by looking at the

111
00:05:04,260 --> 00:05:01,570
mechanisms of cold adaptation had that

112
00:05:07,020 --> 00:05:04,270
had already been determined and these

113
00:05:09,029 --> 00:05:07,030

include Osmo protection through

114
00:05:12,210 --> 00:05:09,039
accumulation of compatible solutes and

115
00:05:15,000 --> 00:05:12,220
osmolytes lipid profile changes for

116
00:05:17,159 --> 00:05:15,010
increased membrane fluidity increased

117
00:05:20,490 --> 00:05:17,169
increased production of EPS or

118
00:05:22,439 --> 00:05:20,500
extracellular polymer a substance called

119
00:05:24,900 --> 00:05:22,449
identification of cold shock proteins

120
00:05:27,900 --> 00:05:24,910
and the identification of cold active

121
00:05:30,629 --> 00:05:27,910
enzymes all of these except for the cold

122
00:05:32,670 --> 00:05:30,639
active enzymes are likely evolutionary

123
00:05:34,860 --> 00:05:32,680
mechanisms that are looked at either

124
00:05:38,010 --> 00:05:34,870
vertically or through horizontal gene

125
00:05:40,320 --> 00:05:38,020
transfer the cold active enzyme has a

126
00:05:43,010 --> 00:05:40,330
vertically inherit change in amino acid

127
00:05:46,469 --> 00:05:43,020
usage which I'll get to a little later

128
00:05:48,689 --> 00:05:46,479
but with how identified all of these

129
00:05:50,790 --> 00:05:48,699
mechanisms led me to kind of the

130
00:05:53,700 --> 00:05:50,800
creation of my goal and these so what

131
00:05:55,980 --> 00:05:53,710
why am I doing this and the goal the end

132
00:05:59,390 --> 00:05:55,990
product of this study if everything goes

133
00:06:02,279 --> 00:05:59,400
well would be to create a phylogenetic

134
00:06:04,589 --> 00:06:02,289
informed predictive model to estimate

135
00:06:06,990 --> 00:06:04,599
growth temperature ranges and optimal

136
00:06:10,350 --> 00:06:07,000
growth rates using only gene content and

137
00:06:12,570 --> 00:06:10,360
amino acid usage and so if this works

138
00:06:14,730 --> 00:06:12,580

and this could help to lay some

139
00:06:17,129 --> 00:06:14,740
groundwork for changes in a microbial

140
00:06:22,860 --> 00:06:17,139
community on structure and function and

141
00:06:25,260 --> 00:06:22,870
a really rapidly warming Arctic okay and

142
00:06:27,980 --> 00:06:25,270
I want also wanted to make a quick thing

143
00:06:30,659 --> 00:06:27,990
clear you'll see in my methods that I

144
00:06:33,960 --> 00:06:30,669
sequenced multiple strains of the same

145
00:06:35,250 --> 00:06:33,970
species and the reason why I did that

146
00:06:36,540 --> 00:06:35,260
and the reason why a lot of people do

147
00:06:38,670 --> 00:06:36,550
that is to look at the difference

148
00:06:40,220 --> 00:06:38,680
between the pan genome and the core

149
00:06:43,070 --> 00:06:40,230
genome most

150
00:06:44,630 --> 00:06:43,080
bacterial species every new strain is

151
00:06:46,850 --> 00:06:44,640
going to have genes that have not been

152
00:06:48,500 --> 00:06:46,860
observed before and the set of all of

153
00:06:51,080 --> 00:06:48,510
those genes is known as the pan genome

154
00:06:53,480 --> 00:06:51,090
so the more strains of the same species

155
00:06:56,360 --> 00:06:53,490
you sequence the more likely you are

156
00:06:59,990 --> 00:06:56,370
going to have to have that increase I'm

157
00:07:02,870 --> 00:07:00,000
sorry that increase in genes right there

158
00:07:04,610 --> 00:07:02,880
well if you just look at one strain if

159
00:07:06,290 --> 00:07:04,620
you just sequence one strain of the

160
00:07:08,780 --> 00:07:06,300
species you're only going to get a

161
00:07:11,360 --> 00:07:08,790
little bit of those genes and just the

162
00:07:16,460 --> 00:07:11,370
core genome so it's really beneficial to

163
00:07:18,890 --> 00:07:16,470

strain to sequence multiple strains so

164
00:07:22,580 --> 00:07:18,900
no good research is complete without a

165
00:07:24,830 --> 00:07:22,590
prediction and so I predicted so that

166
00:07:26,480 --> 00:07:24,840
the requirement for increased protein

167
00:07:29,000 --> 00:07:26,490
flexibility or the requirement to

168
00:07:31,880 --> 00:07:29,010
predict how psycho philic these bacteria

169
00:07:34,970 --> 00:07:31,890
are would be by looking at amino acid

170
00:07:36,380 --> 00:07:34,980
indices or ratios which are publicly

171
00:07:38,960 --> 00:07:36,390
available through a lot of different

172
00:07:41,870 --> 00:07:38,970
publications currently and so I am

173
00:07:44,270 --> 00:07:41,880
currently using these five amino acid

174
00:07:46,130 --> 00:07:44,280
indices because they were the one that

175
00:07:50,750 --> 00:07:46,140
was most currently on hand at the moment

176
00:07:53,840 --> 00:07:50,760
and the easiest to find but all of these

177
00:07:57,230 --> 00:07:53,850
are really pretty straightforward

178
00:07:59,450 --> 00:07:57,240
and they'll they'll portray kind of a

179
00:08:01,670 --> 00:07:59,460
conventional statistic methods but

180
00:08:04,640 --> 00:08:01,680
unfortunately science is not that easy

181
00:08:07,250 --> 00:08:04,650
and I will also have to take into

182
00:08:09,050 --> 00:08:07,260
account what evolution provides and in

183
00:08:11,000 --> 00:08:09,060
the sense of you're not going to have

184
00:08:13,700 --> 00:08:11,010
just straightforward this is how the

185
00:08:15,110 --> 00:08:13,710
amino indices um index kind of brought

186
00:08:20,030 --> 00:08:15,120
around it's going to come this way and

187
00:08:22,400 --> 00:08:20,040
then it's gonna come that way to start

188
00:08:24,950 --> 00:08:22,410

my methods and so to create this model I

189
00:08:28,100 --> 00:08:24,960
had to identify kind of a core or a

190
00:08:30,770 --> 00:08:28,110
proxy genus to predict the to create the

191
00:08:32,600 --> 00:08:30,780
model and so I chose the genus of Co

192
00:08:35,360 --> 00:08:32,610
alia because this is a bacterial genus

193
00:08:38,150 --> 00:08:35,370
that is found in cold waters around the

194
00:08:40,400 --> 00:08:38,160
world especially in the Arctic but it is

195
00:08:42,830 --> 00:08:40,410
its members are mostly sacra philic and

196
00:08:45,680 --> 00:08:42,840
hallow philic but primarily its genetic

197
00:08:47,690 --> 00:08:45,690
code actually reflects the geological

198
00:08:49,880 --> 00:08:47,700
evolution of polar regions so this would

199
00:08:51,560 --> 00:08:49,890
help take care of my previous problem

200
00:08:56,960 --> 00:08:51,570
looking at the evolution of the

201
00:08:59,090 --> 00:08:56,970
amino acids and so this is kind of step

202
00:09:01,160 --> 00:08:59,100
by sub go through of my methods you

203
00:09:02,840 --> 00:09:01,170
start off with your observations of

204
00:09:06,920 --> 00:09:02,850
course currently we have field

205
00:09:09,499 --> 00:09:06,930
collections from you javac in Barrow 17

206
00:09:13,100 --> 00:09:09,509
out of 17 from March 2012 have been

207
00:09:14,809 --> 00:09:13,110
sequenced 1 out of 25 from April 2015

208
00:09:17,900 --> 00:09:14,819
have been sequence that's currently in

209
00:09:20,150 --> 00:09:17,910
progress determining their phenotypic

210
00:09:22,069 --> 00:09:20,160
traits and determining how well they

211
00:09:25,220 --> 00:09:22,079
grow at various temperatures is also in

212
00:09:27,559 --> 00:09:25,230
progress so right now I have about 19

213
00:09:30,170 --> 00:09:27,569

different strange sitting in my fridges

214
00:09:32,329 --> 00:09:30,180
and freezers and I'm looking at the

215
00:09:37,540 --> 00:09:32,339
temperature and how well they're growing

216
00:09:43,699 --> 00:09:40,370
I'm further doing the sequencing of all

217
00:09:46,340 --> 00:09:43,709
of these strains using DNA extraction

218
00:09:51,889 --> 00:09:46,350
library construction and annotation

219
00:09:55,009 --> 00:09:51,899
using the Patric portal in addition to

220
00:09:58,400 --> 00:09:55,019
doing primarily lab laboratory work I'm

221
00:10:00,290 --> 00:09:58,410
also using 44 additional Co alia genomes

222
00:10:03,680 --> 00:10:00,300
that are downloaded from a public

223
00:10:06,170 --> 00:10:03,690
database and with those and with my

224
00:10:08,300 --> 00:10:06,180
laboratory work I was able to create a

225
00:10:11,780 --> 00:10:08,310
phylogenetic tree comparing all of those

226
00:10:14,840 --> 00:10:11,790
I was also able to synthesize cold

227
00:10:16,939 --> 00:10:14,850
adaptation indices all from all of these

228
00:10:18,740 --> 00:10:16,949
genes and put them together and compare

229
00:10:25,400 --> 00:10:18,750
each and these are figures that I will

230
00:10:27,710 --> 00:10:25,410
be showing momentarily so once I have

231
00:10:30,980 --> 00:10:27,720
all of this data the growth rates and

232
00:10:32,750 --> 00:10:30,990
the cold adaptive indices of amino acids

233
00:10:35,480 --> 00:10:32,760
I'm going to take all that data and put

234
00:10:37,790 --> 00:10:35,490
it together into a phylogenetic

235
00:10:41,150 --> 00:10:37,800
generalized least squares regression of

236
00:10:42,949 --> 00:10:41,160
cold adaptation indices to create that

237
00:10:45,139 --> 00:10:42,959
model so that you just give me the

238
00:10:47,600 --> 00:10:45,149

genomes I can tell you what temperature

239
00:10:53,240 --> 00:10:47,610
it'll grow best at and how quickly it'll

240
00:10:55,249 --> 00:10:53,250
grow so this is a heat map of the

241
00:10:57,949 --> 00:10:55,259
preliminary results so at the very top

242
00:11:00,590 --> 00:10:57,959
right here these are the koalas that I'm

243
00:11:03,139 --> 00:11:00,600
currently studying this is a heat map of

244
00:11:05,850 --> 00:11:03,149
all of the strains from a collaborator

245
00:11:07,889 --> 00:11:05,860
of called charles suite which isolated

246
00:11:10,530 --> 00:11:07,899
several hundred strains of bacteria from

247
00:11:12,660 --> 00:11:10,540
Ikea and Chesapeake Bay and right now we

248
00:11:15,150 --> 00:11:12,670
we have sequence only 60 of them and

249
00:11:17,220 --> 00:11:15,160
this is what we are presenting right

250
00:11:19,470 --> 00:11:17,230
here is a phylogenetic tree comparing

251
00:11:21,720 --> 00:11:19,480
all of these sequences and the red

252
00:11:24,960 --> 00:11:21,730
represents how closely related they are

253
00:11:26,819 --> 00:11:24,970
if and the yellow represents if there

254
00:11:33,000 --> 00:11:26,829
was a fluke or if even if they weren't

255
00:11:35,670 --> 00:11:33,010
closely related at all actually this is

256
00:11:37,500 --> 00:11:35,680
the big preliminary results at the end

257
00:11:41,490 --> 00:11:37,510
of my first year of my Master's so these

258
00:11:43,380 --> 00:11:41,500
this is a histogram of this of all of

259
00:11:46,170 --> 00:11:43,390
the amino acid indices that are labeled

260
00:11:49,199 --> 00:11:46,180
down here I apologize it you cannot read

261
00:11:52,829 --> 00:11:49,209
them right here these are all the Koala

262
00:11:54,569 --> 00:11:52,839
strains these top ones the BRX are the

263
00:11:56,400 --> 00:11:54,579

ones that I'm currently growing while

264
00:11:59,310 --> 00:11:56,410
the rest of these are from public date

265
00:12:01,139 --> 00:11:59,320
available databases but you can see that

266
00:12:04,579 --> 00:12:01,149
these kind of histograms and curves are

267
00:12:06,810 --> 00:12:04,589
really closely related and so the minor

268
00:12:09,900 --> 00:12:06,820
differences of the distribution of these

269
00:12:12,810 --> 00:12:09,910
amino acids were sequence the only real

270
00:12:14,819 --> 00:12:12,820
one is this one right here which is kind

271
00:12:18,870 --> 00:12:14,829
of new and I haven't quite defined why

272
00:12:21,269 --> 00:12:18,880
that is so that's yet to come but this

273
00:12:23,970 --> 00:12:21,279
really suggests that phylogeny in

274
00:12:26,160 --> 00:12:23,980
general so large phylogeny plays a more

275
00:12:28,920 --> 00:12:26,170
important role in determining these

276
00:12:31,139 --> 00:12:28,930
amino acid compositions then the then

277
00:12:35,600 --> 00:12:31,149
does the adaptation to local conditions

278
00:12:39,180 --> 00:12:35,610
because these oh my god I'm sorry yeah

279
00:12:41,009 --> 00:12:39,190
these are taken from Chesapeake Bay but

280
00:12:42,780 --> 00:12:41,019
these are from public available

281
00:12:44,939 --> 00:12:42,790
databases so these are taken from really

282
00:12:47,189 --> 00:12:44,949
a wide variety of environments and

283
00:12:49,380 --> 00:12:47,199
locations and they still managed to have

284
00:12:52,860 --> 00:12:49,390
kind of the same structure which is kind

285
00:12:54,660 --> 00:12:52,870
of incredible in my opinion so the next

286
00:12:58,110 --> 00:12:54,670
step since this study is really in its

287
00:12:59,670 --> 00:12:58,120
infancy is to complete the growth rates

288
00:13:02,280 --> 00:12:59,680

measurements of all the ones that I have

289
00:13:05,370 --> 00:13:02,290
sitting in my fridges and freezers and

290
00:13:07,769 --> 00:13:05,380
sequence all of those strains to catalog

291
00:13:10,680 --> 00:13:07,779
all these cold adaptation related genes

292
00:13:12,720 --> 00:13:10,690
within each of the genomes test for

293
00:13:15,840 --> 00:13:12,730
differences in adaption indices of

294
00:13:17,970 --> 00:13:15,850
individual gene families examine other

295
00:13:19,420 --> 00:13:17,980
genre that have more phenotypic or

296
00:13:21,520 --> 00:13:19,430
genotypic diversity Prem

297
00:13:23,500 --> 00:13:21,530
all of these are so similar to each

298
00:13:25,600 --> 00:13:23,510
other it's going to become beneficial to

299
00:13:27,250 --> 00:13:25,610
use a different and apply different

300
00:13:29,290 --> 00:13:27,260
genus and right now the one that I have

301
00:13:32,620 --> 00:13:29,300
on hand is most likely to be used is

302
00:13:34,870 --> 00:13:32,630
psycho vector and finally incorporate

303
00:13:39,670 --> 00:13:34,880
all of this data into a predictive model

304
00:13:42,220 --> 00:13:39,680
and with that I'd like to acknowledge my

305
00:13:44,650 --> 00:13:42,230
committee my advisor dr. Eric Collins

306
00:13:46,510 --> 00:13:44,660
dr. Charles sweets and Lee's Duclos oh

307
00:13:49,270 --> 00:13:46,520
and Jody Deming and Shelley carpenter

308
00:13:51,580 --> 00:13:49,280
for sample collection and helping me and

309
00:13:58,390 --> 00:13:51,590
as well as my funding sources and with

310
00:14:00,490 --> 00:13:58,400
that I'll take questions thanks to

311
00:14:01,840 --> 00:14:00,500
having any questions for a nice if you

312
00:14:03,850 --> 00:14:01,850
could come up to the microphone in the

313
00:14:23,470 --> 00:14:03,860

center and say where you're from and

314
00:14:43,810 --> 00:14:23,480
your name the stage one oh yeah yeah

315
00:14:49,980 --> 00:14:43,820
that would be why thank you yes so it's

316
00:14:52,750 --> 00:14:49,990
an interesting observation so it is know

317
00:14:56,170 --> 00:14:52,760
we've done this data analysis multiple

318
00:14:57,640 --> 00:14:56,180
times that things that reside or

319
00:14:59,470 --> 00:14:57,650
bacteria that resides in cold

320
00:15:03,040 --> 00:14:59,480
temperatures or hot temperatures tend to

321
00:15:04,780 --> 00:15:03,050
share amino acid composition across the

322
00:15:08,200 --> 00:15:04,790
genes that are relevant for activity in

323
00:15:10,780 --> 00:15:08,210
these types of environments the fact

324
00:15:14,440 --> 00:15:10,790
that their evolutionary similar bacteria

325
00:15:17,710 --> 00:15:14,450
tend to not have the same composition

326
00:15:19,450 --> 00:15:17,720
across everything great it's actually

327
00:15:21,370 --> 00:15:19,460
expected so there is a lot of horizontal

328
00:15:25,530 --> 00:15:21,380
gene transfer and implementation which

329
00:15:28,140 --> 00:15:25,540
is also driven by so I'm kind of curious

330
00:15:31,970 --> 00:15:28,150
what is the big

331
00:15:34,830 --> 00:15:31,980
ooomph right of these genes that are

332
00:15:37,140 --> 00:15:34,840
looking not like their genome but

333
00:15:39,600 --> 00:15:37,150
similar across even though the genomes

334
00:15:41,550 --> 00:15:39,610
are similar you know I'm not quite

335
00:15:45,060 --> 00:15:41,560
understanding your question so yes we

336
00:15:48,150 --> 00:15:45,070
know about the adaptation so what is the

337
00:15:55,710 --> 00:15:48,160
the big deal about them being different

338
00:15:58,080 --> 00:15:55,720

from the genome similarities so how

339
00:16:00,180 --> 00:15:58,090
important is it that the genes that are

340
00:16:01,770 --> 00:16:00,190
useful for adaptations or particular

341
00:16:05,760 --> 00:16:01,780
environment are different from the

342
00:16:08,520 --> 00:16:05,770
genomes that they come it's important in

343
00:16:12,450 --> 00:16:08,530
the sense that they they use different

344
00:16:14,430 --> 00:16:12,460
factions I'm also admittedly new to the

345
00:16:16,140 --> 00:16:14,440
field so these is probably something

346
00:16:19,560 --> 00:16:16,150
I'll take a closer look at and identify

347
00:16:22,320 --> 00:16:19,570
later on in my research oh I'm sorry

348
00:16:23,730 --> 00:16:22,330
yes so it'll be something that I take a

349
00:16:25,560 --> 00:16:23,740
closer look like I'd love to chat with

350
00:16:26,790 --> 00:16:25,570
you actually later on if you have a

351
00:16:30,870 --> 00:16:26,800
moment to talk about that yeah

352
00:16:32,940 --> 00:16:30,880
absolutely yeah so so the big deal kind

353
00:16:38,640 --> 00:16:32,950
of looking forward to if you identify

354
00:16:43,320 --> 00:16:38,650
the genes that are similar you can

355
00:16:47,310 --> 00:16:43,330
identify new yes so I think that that

356
00:16:48,000 --> 00:16:47,320
would be really cool so I think that's

357
00:16:50,240 --> 00:16:48,010
all the time we have for questions