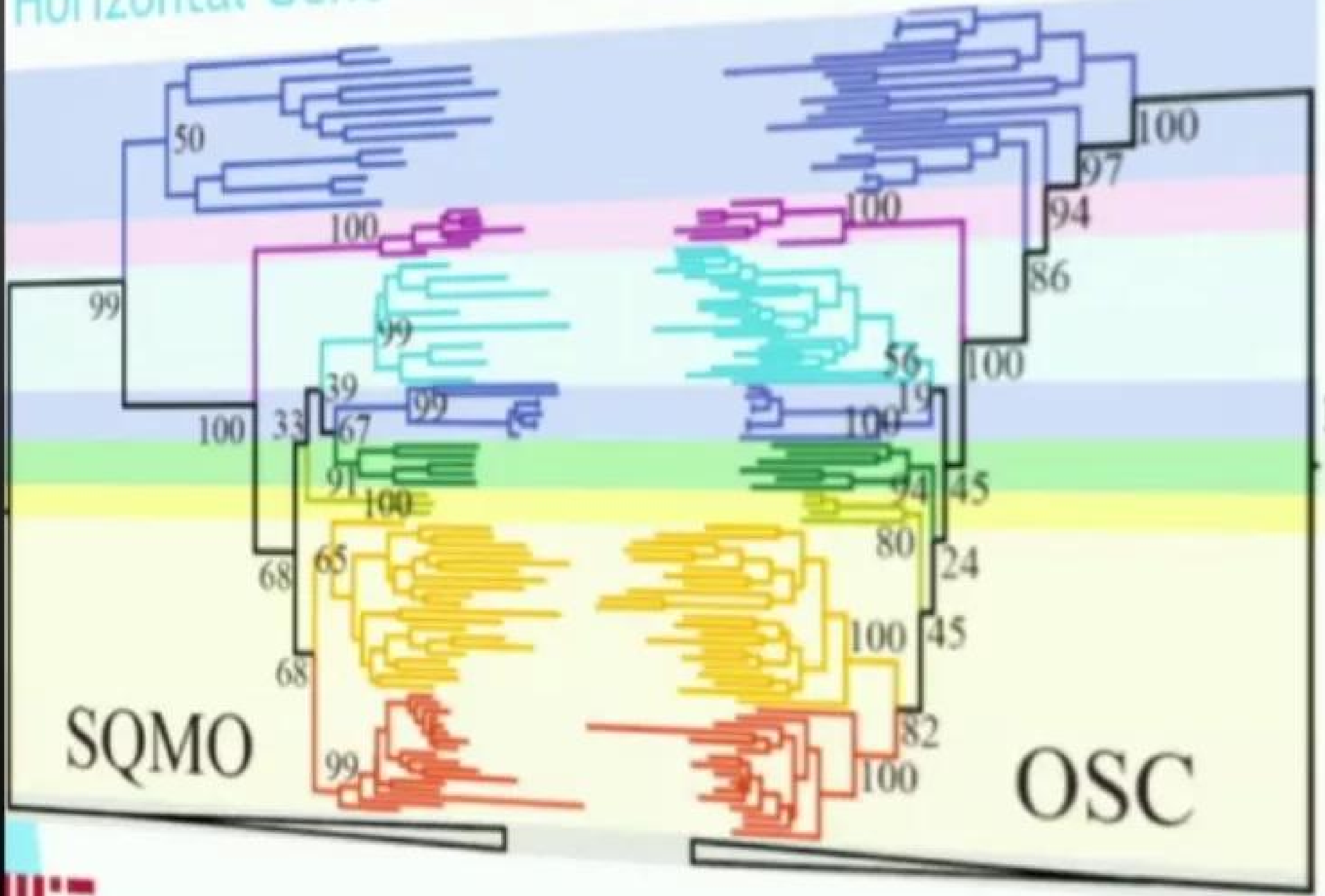
Results

Horizontal Gene Transfers: Together



Bacterial Group I

Excavata

SAR

Bacterial Group II

Archaeplastida

Amoebozoa

Fungi

Holozoa

AbGradCon 2016 - Boulder, CO

1
00:00:10,480 --> 00:00:08,500
hello everyone and good morning I'm

2
00:00:12,549 --> 00:00:10,490
Abigail Karen and I'm going to be

3
00:00:14,709 --> 00:00:12,559
presenting some work I did with David

4
00:00:17,560 --> 00:00:14,719
gold Greg fornia and Roger summons

5
00:00:19,540 --> 00:00:17,570
entitled molecular data suggests sterile

6
00:00:22,060 --> 00:00:19,550
biosynthesis evolved around the great

7
00:00:23,170 --> 00:00:22,070
oxidation event and first I'm going to

8
00:00:24,640 --> 00:00:23,180
give you some backgrounds you can

9
00:00:27,370 --> 00:00:24,650
understand why you should care about

10
00:00:30,490 --> 00:00:27,380
this first thing you need to know is

11
00:00:33,270 --> 00:00:30,500
what is a sterile sterols are some lipid

12
00:00:36,100 --> 00:00:33,280
molecules they're organic they have

13
00:00:38,170 --> 00:00:36,110

these four rings and a sidechain group

14
00:00:40,930 --> 00:00:38,180
that varies depending on what specific

15
00:00:43,959 --> 00:00:40,940
sterile it is this one here ergosterol

16
00:00:47,020 --> 00:00:43,969
is a component of the cell membrane and

17
00:00:51,850 --> 00:00:47,030
fungi sterile you might know is

18
00:00:53,799 --> 00:00:51,860
cholesterol oftenly talked about sterols

19
00:00:55,990 --> 00:00:53,809
in general are created by most eukaryote

20
00:00:59,529 --> 00:00:56,000
lineages and only a very small number of

21
00:01:02,610 --> 00:00:59,539
bacteria as such they're indicative

22
00:01:05,830 --> 00:01:02,620
usually of presence of eukaryotes

23
00:01:08,620 --> 00:01:05,840
furthermore sterols require oxygen to be

24
00:01:10,870 --> 00:01:08,630
synthesized in this first step and also

25
00:01:13,210 --> 00:01:10,880
further downstream depending on what

26
00:01:16,230 --> 00:01:13,220
specific sterile they're going to end up

27
00:01:19,179 --> 00:01:16,240
making so the presence of sterols is

28
00:01:22,149 --> 00:01:19,189
indicative of aerobic metabolism because

29
00:01:23,950 --> 00:01:22,159
it requires oxygen and of eukaryotes so

30
00:01:26,740 --> 00:01:23,960
trying to date when sterile synthesis

31
00:01:29,370 --> 00:01:26,750
first evolved is an interesting has an

32
00:01:33,010 --> 00:01:29,380
interesting implications for early life

33
00:01:35,080 --> 00:01:33,020
so trying to date it so far people can

34
00:01:37,510 --> 00:01:35,090
look at sterols in the rock record their

35
00:01:39,429 --> 00:01:37,520
preserved as staring keeping their

36
00:01:42,429 --> 00:01:39,439
carbon backbone but losing key details

37
00:01:44,830 --> 00:01:42,439
like functional groups however the

38
00:01:48,160 --> 00:01:44,840

record is currently controversial back

39
00:01:50,770 --> 00:01:48,170
in 1999 sterols were reported at 2.7 and

40
00:01:53,080 --> 00:01:50,780
sorry 2.7 billion year old rocks in

41
00:01:54,639 --> 00:01:53,090
australia which was super interesting

42
00:01:57,310 --> 00:01:54,649
because as you might know the great

43
00:01:59,830 --> 00:01:57,320
oxidation event didn't occur until 2.4

44
00:02:03,370 --> 00:01:59,840
billion years ago and that's the first

45
00:02:06,069 --> 00:02:03,380
accumulation of molecular oxygen in the

46
00:02:08,139 --> 00:02:06,079
atmosphere so having me is earlier than

47
00:02:10,330 --> 00:02:08,149
the great oxidation event was a big deal

48
00:02:12,610 --> 00:02:10,340
because oxidative metabolism before we

49
00:02:14,949 --> 00:02:12,620
have appreciable oxygen however that was

50
00:02:17,540 --> 00:02:14,959
recently in the last few years refuted

51
00:02:19,910 --> 00:02:17,550
those rocks don't actually have stair

52
00:02:22,250 --> 00:02:19,920
is preserved in them and the next

53
00:02:24,110 --> 00:02:22,260
closest ones that were sure of in the

54
00:02:28,670 --> 00:02:24,120
rock record are at one point six for

55
00:02:31,340 --> 00:02:28,680
simple 23 to 24 carbon cells and 800

56
00:02:33,560 --> 00:02:31,350
million years ago for complex steering's

57
00:02:35,420 --> 00:02:33,570
with 26 to 30 carbons which are

58
00:02:38,890 --> 00:02:35,430
generally the ones that all modern

59
00:02:41,630 --> 00:02:38,900
eukaryotes create so there's some debate

60
00:02:43,190 --> 00:02:41,640
as to when this pathway evolved and

61
00:02:45,560 --> 00:02:43,200
looking at the rock record isn't

62
00:02:47,540 --> 00:02:45,570
currently helping so we decided to take

63
00:02:49,900 --> 00:02:47,550

an alternative approach and look at the

64
00:02:53,300 --> 00:02:49,910
genes of modern organisms to try and

65
00:02:55,100 --> 00:02:53,310
figure out when this approach when this

66
00:02:57,410 --> 00:02:55,110
adds we evolved just from the genetic

67
00:02:59,990 --> 00:02:57,420
record as such the first thing we had to

68
00:03:02,540 --> 00:03:00,000
do was pick two genes to study and we

69
00:03:05,240 --> 00:03:02,550
decided to pick the first two genes in

70
00:03:06,980 --> 00:03:05,250
the sterile synthesis pathway simply

71
00:03:09,200 --> 00:03:06,990
because these are conserved across all

72
00:03:11,600 --> 00:03:09,210
sterile synthesis pathways and some of

73
00:03:13,340 --> 00:03:11,610
the later genes are not on the first

74
00:03:15,170 --> 00:03:13,350
that I'm going to be talking about as

75
00:03:17,450 --> 00:03:15,180
squalene monooxygenase that converts

76
00:03:18,710 --> 00:03:17,460
squalene to squalene epoxide and the

77
00:03:21,500 --> 00:03:18,720
second gene I'll be talking about is

78
00:03:23,900 --> 00:03:21,510
oxido salt squalene cyclase which turns

79
00:03:28,670 --> 00:03:23,910
this epoxide into a proto sterile such

80
00:03:31,400 --> 00:03:28,680
as cyclo ordinal and now I'm going to

81
00:03:34,010 --> 00:03:31,410
briefly and quickly go through molecular

82
00:03:35,720 --> 00:03:34,020
clocks and how they work just because

83
00:03:37,760 --> 00:03:35,730
I'm not sure how familiar you guys are

84
00:03:40,160 --> 00:03:37,770
with them so the first thing we do is we

85
00:03:44,060 --> 00:03:40,170
acquire amino acid sequences from modern

86
00:03:46,100 --> 00:03:44,070
organisms a whole bunch of them and we

87
00:03:47,960 --> 00:03:46,110
run them through a program that deals

88
00:03:50,030 --> 00:03:47,970

with like insertions and deletions and

89
00:03:52,460 --> 00:03:50,040
make sure that similar parts are lined

90
00:03:55,370 --> 00:03:52,470
up for each gene just so that they're

91
00:03:57,050 --> 00:03:55,380
comparable we run that through some

92
00:03:59,780 --> 00:03:57,060
other programs to create phylogenetic

93
00:04:02,030 --> 00:03:59,790
trees using asian or maximum likelihood

94
00:04:04,490 --> 00:04:02,040
methods and the trees that are produced

95
00:04:06,560 --> 00:04:04,500
have similar sequences close together

96
00:04:08,570 --> 00:04:06,570
and very different sequences just

97
00:04:10,940 --> 00:04:08,580
further apart in the tree with longer

98
00:04:12,949 --> 00:04:10,950
branch lengths however that still

99
00:04:14,770 --> 00:04:12,959
doesn't give us any dates to add dates

100
00:04:18,289 --> 00:04:14,780
we need to add paleontological beta

101
00:04:20,690 --> 00:04:18,299
fossils to do that you can constrain

102
00:04:23,659 --> 00:04:20,700
specific nodes with specific fossils for

103
00:04:26,090 --> 00:04:23,669
example the mammal reptile split had to

104
00:04:28,670 --> 00:04:26,100
happen before the first solid reptile

105
00:04:31,430 --> 00:04:28,680
fossil so we can calibrate all of these

106
00:04:31,929 --> 00:04:31,440
amniotes with highly nomis and give it a

107
00:04:34,429 --> 00:04:31,939
date

108
00:04:37,420 --> 00:04:34,439
that is earliest and like some

109
00:04:39,589 --> 00:04:37,430
probability for when that node occurred

110
00:04:41,839 --> 00:04:39,599
we do this for a whole bunch of nodes

111
00:04:43,550 --> 00:04:41,849
and it creates a molecular clock which

112
00:04:45,649 --> 00:04:43,560
is basically just a phylogenetic tree

113
00:04:49,189 --> 00:04:45,659

with dates associated with each node and

114
00:04:52,040 --> 00:04:49,199
some probability there so we started

115
00:04:54,920 --> 00:04:52,050
doing this process for sqm oh and 40 SC

116
00:04:59,480 --> 00:04:54,930
and these are two maximum likelihood

117
00:05:01,339 --> 00:04:59,490
trees sqm oh and osc this is a

118
00:05:03,469 --> 00:05:01,349
representative sampling of eukaryotes

119
00:05:06,379 --> 00:05:03,479
and every single bacterial sequence we

120
00:05:10,719 --> 00:05:06,389
could find so the bacteria are this dark

121
00:05:12,980 --> 00:05:10,729
blue we only found 27 different species

122
00:05:15,830 --> 00:05:12,990
across six different phyla so it was

123
00:05:18,439 --> 00:05:15,840
like it's real weird bacteria that had

124
00:05:21,800 --> 00:05:18,449
these jeans and they correlate both in

125
00:05:25,490 --> 00:05:21,810
both Jean trees to these two groups one

126
00:05:29,749 --> 00:05:25,500
basil to eukaryotes and one like inside

127
00:05:32,719 --> 00:05:29,759
the eukaryotes so when you look at this

128
00:05:35,510 --> 00:05:32,729
what I want you to get from this is that

129
00:05:37,640 --> 00:05:35,520
all of these non dark blue things are

130
00:05:39,619 --> 00:05:37,650
eukaryotes and they generally reflect

131
00:05:42,290 --> 00:05:39,629
the species tree so we can say that

132
00:05:44,629 --> 00:05:42,300
these genes were probably present here

133
00:05:46,550 --> 00:05:44,639
in the stem eukaryote and we're just

134
00:05:50,209 --> 00:05:46,560
vertically inherited throughout Eukarya

135
00:05:53,480 --> 00:05:50,219
however the bacteria are weird here like

136
00:05:56,869 --> 00:05:53,490
this group here bacterial group to bec

137
00:05:58,249 --> 00:05:56,879
your ad in nabol from algae so they got

138
00:06:00,740 --> 00:05:58,259

this gene through horizontal gene

139
00:06:05,809 --> 00:06:00,750
transfer probably from some algae at

140
00:06:07,909 --> 00:06:05,819
some point same with this this basal

141
00:06:11,629 --> 00:06:07,919
group there's horizontal gene transfer

142
00:06:13,159 --> 00:06:11,639
here between these bacteria and the stem

143
00:06:14,959 --> 00:06:13,169
eukaryote we can't polarize which

144
00:06:17,929 --> 00:06:14,969
direction it is I can't say oh it

145
00:06:20,300 --> 00:06:17,939
evolved in eukaryotes but there was some

146
00:06:23,450 --> 00:06:20,310
sort of gene sharing here so we can say

147
00:06:27,139 --> 00:06:23,460
by this node we had functional sqm oh

148
00:06:28,700 --> 00:06:27,149
and osc also some of these bacteria been

149
00:06:31,909 --> 00:06:28,710
proven in the lab to actually create

150
00:06:33,589 --> 00:06:31,919
functional sterols so that was like a

151
00:06:34,820 --> 00:06:33,599
lot but basically you just need to know

152
00:06:39,230 --> 00:06:34,830
there's two horizontal gene transfer

153
00:06:40,730 --> 00:06:39,240
into or out of bacteria and we think

154
00:06:41,930 --> 00:06:40,740
since they're this they're in the same

155
00:06:44,300 --> 00:06:41,940
place that they were being transferred

156
00:06:45,060 --> 00:06:44,310
together so we looked at the genome of

157
00:06:48,120 --> 00:06:45,070
all of these

158
00:06:50,670 --> 00:06:48,130
bacteria that have both genes and if you

159
00:06:52,950 --> 00:06:50,680
look OSC is orange eskimos blue and

160
00:06:54,630 --> 00:06:52,960
they're always right about next to each

161
00:06:56,430 --> 00:06:54,640
other on the genome of these bacteria

162
00:06:57,660 --> 00:06:56,440
which is pretty good evidence that the

163
00:06:59,220 --> 00:06:57,670

two genes were being transferred

164
00:07:02,490 --> 00:06:59,230
together in both of these events and

165
00:07:04,140 --> 00:07:02,500
that when we make our clocks if we're

166
00:07:07,080 --> 00:07:04,150
just looking at the transfers we can add

167
00:07:10,620 --> 00:07:07,090
data from sqm o to data from OSC to

168
00:07:14,100 --> 00:07:10,630
constrain those two nodes we ended up

169
00:07:17,460 --> 00:07:14,110
doing ten different analyses looking at

170
00:07:19,650 --> 00:07:17,470
two different topologies simply because

171
00:07:21,480 --> 00:07:19,660
there's some debate if excavates are

172
00:07:24,600 --> 00:07:21,490
basil to the other eukaryotes or if

173
00:07:26,010 --> 00:07:24,610
they're sister to the by cons and just

174
00:07:28,440 --> 00:07:26,020
to cover all our bases we did both

175
00:07:31,380 --> 00:07:28,450
topologies we also looked at five

176
00:07:33,810 --> 00:07:31,390
different datasets the SQ MO and osc

177
00:07:35,180 --> 00:07:33,820
genes concatenated like I just mentioned

178
00:07:38,910 --> 00:07:35,190
because they were being moved together

179
00:07:40,590 --> 00:07:38,920
also as qmo by itself as qmo constrained

180
00:07:43,410 --> 00:07:40,600
by an out group of genes from the Oba

181
00:07:45,840 --> 00:07:43,420
quinone biosynthesis pathway OSC by

182
00:07:48,090 --> 00:07:45,850
itself and osc constrained by an out

183
00:07:51,750 --> 00:07:48,100
group of squalene hoping cyclase it's

184
00:07:53,430 --> 00:07:51,760
sort of bacterial analogue each analysis

185
00:07:56,910 --> 00:07:53,440
had between 14 and 18 fossil

186
00:07:59,430 --> 00:07:56,920
calibrations added and I have to mention

187
00:08:01,470 --> 00:07:59,440
that we did exclude the SQ mo alone data

188
00:08:03,930 --> 00:08:01,480

set from our numerical analyses that

189
00:08:06,690 --> 00:08:03,940
we'll get into later simply because it

190
00:08:08,880 --> 00:08:06,700
was broadly inconsistent with our other

191
00:08:12,690 --> 00:08:08,890
analyses broadly and consistent with

192
00:08:16,230 --> 00:08:12,700
previous molecular clock work and very

193
00:08:17,850 --> 00:08:16,240
very old but when we added a

194
00:08:22,230 --> 00:08:17,860
constraining out group or the data from

195
00:08:23,670 --> 00:08:22,240
OSC it fixed the problem so here's an

196
00:08:25,500 --> 00:08:23,680
example of one of our molecular clocks

197
00:08:26,940 --> 00:08:25,510
this is the concatenated one so that I

198
00:08:29,640 --> 00:08:26,950
could particularly look at the two

199
00:08:32,630 --> 00:08:29,650
bacterial transfers first I want to talk

200
00:08:35,280 --> 00:08:32,640
about this green star that's

201
00:08:39,300 --> 00:08:35,290
representing crown Eukarya all of the

202
00:08:41,610 --> 00:08:39,310
eukaryotes here do make modern at least

203
00:08:44,820 --> 00:08:41,620
the modern versions create 26 to 30

204
00:08:48,390 --> 00:08:44,830
sterols 30 carbon sterols as such we can

205
00:08:50,910 --> 00:08:48,400
infer that way back here we had the

206
00:08:53,220 --> 00:08:50,920
genetic machinery to do so so we would

207
00:08:56,340 --> 00:08:53,230
expect to see 26 to 30 carbon sterols in

208
00:08:57,960 --> 00:08:56,350
the rock record around here but the

209
00:08:58,470 --> 00:08:57,970
average date we get for that node is one

210
00:09:00,720 --> 00:08:58,480
point

211
00:09:02,400 --> 00:09:00,730
six billion years ago which is much

212
00:09:06,150 --> 00:09:02,410
earlier than that 800 million i

213
00:09:07,949 --> 00:09:06,160

mentioned earlier furthermore if you

214
00:09:10,230 --> 00:09:07,959
look at this red node that represents

215
00:09:12,540 --> 00:09:10,240
the first transfer between the bacteria

216
00:09:15,329 --> 00:09:12,550
and the stem eukaryote so the pathway

217
00:09:18,110 --> 00:09:15,339
existed by then and we should expect to

218
00:09:20,910 --> 00:09:18,120
see at least proto sterols by this node

219
00:09:22,500 --> 00:09:20,920
as you can probably tell this

220
00:09:25,319 --> 00:09:22,510
ninety-five percent confidence interval

221
00:09:29,189 --> 00:09:25,329
is really big it's like 800 million

222
00:09:31,259 --> 00:09:29,199
years so I can't really say that much

223
00:09:32,730 --> 00:09:31,269
about when this occurred but the

224
00:09:35,579 --> 00:09:32,740
confidence interval in none of our

225
00:09:37,199 --> 00:09:35,589
analyses enters me so proterozoic so we

226
00:09:40,259 --> 00:09:37,209
can at least conclude that from this

227
00:09:42,720 --> 00:09:40,269
work these two genes should exist before

228
00:09:46,439 --> 00:09:42,730
the mesoproterozoic and if we look more

229
00:09:48,509 --> 00:09:46,449
closely at that node which is here the

230
00:09:50,970 --> 00:09:48,519
maximum probability in all of the

231
00:09:54,420 --> 00:09:50,980
analyses excluding that s qm o alone one

232
00:09:56,189 --> 00:09:54,430
the light blue occur like right during

233
00:09:58,740 --> 00:09:56,199
or right after the great oxidation event

234
00:10:01,980 --> 00:09:58,750
which is reasonable because the pathway

235
00:10:07,220 --> 00:10:01,990
requires oxygen so sharing it right

236
00:10:10,879 --> 00:10:07,230
about then would be useful I guess so

237
00:10:13,319 --> 00:10:10,889
that's about it in conclusion the

238
00:10:16,769 --> 00:10:13,329

pathway the the sterile synthesis

239
00:10:19,680 --> 00:10:16,779
pathway seems to have evolved much

240
00:10:21,360 --> 00:10:19,690
earlier than the rock record suggests if

241
00:10:23,550 --> 00:10:21,370
you look at this little chart the

242
00:10:26,280 --> 00:10:23,560
horizontal lines are our predictions and

243
00:10:29,850 --> 00:10:26,290
the vertical lines are the first thing

244
00:10:32,009 --> 00:10:29,860
we found in the rock record other things

245
00:10:33,750 --> 00:10:32,019
of note the evolution of the pathway

246
00:10:36,000 --> 00:10:33,760
correlates with the great oxidation

247
00:10:39,569 --> 00:10:36,010
event so as soon as we have oxygen we're

248
00:10:41,400 --> 00:10:39,579
making these sterols and a sterile

249
00:10:43,530 --> 00:10:41,410
biosynthesis predates the evolution of

250
00:10:45,420 --> 00:10:43,540
crown group Eukarya and might have been

251
00:10:49,040 --> 00:10:45,430
an important pre adaptation for

252
00:10:51,920 --> 00:10:49,050
subsequent you carry already ation and

253
00:10:53,850 --> 00:10:51,930
that's about it I'd like to acknowledge

254
00:10:55,949 --> 00:10:53,860
specifically David gold who was my

255
00:11:04,420 --> 00:10:55,959
mentor on this project and the summons

256
00:11:14,330 --> 00:11:12,110
questions for Abigail great talk so it

257
00:11:16,220 --> 00:11:14,340
seems reasonable that the you know by

258
00:11:18,590 --> 00:11:16,230
Owens biosynthetic pathway involving

259
00:11:22,730 --> 00:11:18,600
oxygen kind of came about around the

260
00:11:24,200 --> 00:11:22,740
great oxidation event but do you think

261
00:11:27,320 --> 00:11:24,210
there might have been like a different

262
00:11:30,440 --> 00:11:27,330
pathway that was still making you know

263
00:11:33,980 --> 00:11:30,450

sterols prior to oxidation that would

264
00:11:36,380 --> 00:11:33,990
not necessarily look very similar um I'm

265
00:11:38,930 --> 00:11:36,390
not entirely sure I sort of doubt it

266
00:11:42,020 --> 00:11:38,940
because at least the the cyclase

267
00:11:45,740 --> 00:11:42,030
involved is very similar to squalene

268
00:11:47,570 --> 00:11:45,750
Hopi and cyclase and hoping Tsar serve a

269
00:11:50,360 --> 00:11:47,580
very similar function but in bacteria

270
00:11:53,240 --> 00:11:50,370
and so at least when I do the trees it

271
00:11:55,250 --> 00:11:53,250
looks pretty clear that that gene sort

272
00:11:58,280 --> 00:11:55,260
of branched off around then from this

273
00:12:00,200 --> 00:11:58,290
hoping gene I guess there could have

274
00:12:03,110 --> 00:12:00,210
been an entirely different pathway but I

275
00:12:05,030 --> 00:12:03,120
have no way to tell yeah its retail with

276
00:12:06,980 --> 00:12:05,040
this method I guess I don't think it's

277
00:12:20,020 --> 00:12:06,990
very likely that some other pathway also

278
00:12:25,400 --> 00:12:23,360
um so being unfamiliar with the

279
00:12:28,490 --> 00:12:25,410
molecular clock method what's the

280
00:12:30,710 --> 00:12:28,500
uncertainty in this sort of analysis in

281
00:12:32,930 --> 00:12:30,720
this analysis I mean so we have a

282
00:12:35,420 --> 00:12:32,940
different amount of uncertainty on each

283
00:12:42,079 --> 00:12:35,430
of the nodes which are these it's kind

284
00:12:44,480 --> 00:12:42,089
of hard to see but like these bars so we

285
00:12:46,160 --> 00:12:44,490
have particularly large uncertainties

286
00:12:48,440 --> 00:12:46,170
because this clock is only being run

287
00:12:50,390 --> 00:12:48,450
with one gene or in this case two genes

288
00:12:51,770 --> 00:12:50,400

of information and like most published

289
00:12:55,220 --> 00:12:51,780
clocks that are just trying to determine

290
00:12:57,500 --> 00:12:55,230
the species tree are run with like tens

291
00:13:00,260 --> 00:12:57,510
of jeans all concatenated together so we

292
00:13:01,940 --> 00:13:00,270
do have more uncertainty than a clock

293
00:13:05,380 --> 00:13:01,950
that was just looking at the species

294
00:13:08,990 --> 00:13:05,390
tree but like I said our conclusions are

295
00:13:11,329 --> 00:13:09,000
so broad that I think it's fine like

296
00:13:12,650 --> 00:13:11,339
we're not saying this definitely

297
00:13:16,129 --> 00:13:12,660
occurred at this date

298
00:13:18,590 --> 00:13:16,139
our conclusion is like this occurred you

299
00:13:21,079 --> 00:13:18,600
know 600 million years earlier than the

300
00:13:22,400 --> 00:13:21,089
rocks so I think our conclusions are

301
00:13:24,710 --> 00:13:22,410
solid but there's still a lot of

302
00:13:29,509 --> 00:13:24,720
uncertainty in the exact dates okay

303
00:13:34,389 --> 00:13:29,519
thanks does that answer it okay I think

304
00:13:38,389 --> 00:13:34,399
we have time for one more quick question

305
00:13:39,710 --> 00:13:38,399
how conserved are these genes so how

306
00:13:43,639 --> 00:13:39,720
many mutations are you trying to make

307
00:13:46,639 --> 00:13:43,649
this molecular clock with they're fairly

308
00:13:48,319 --> 00:13:46,649
well conserved um i don't think i have

309
00:13:51,319 --> 00:13:48,329
like a good quantitative answer for you

310
00:13:54,290 --> 00:13:51,329
ah looking for eugene the tree in

311
00:13:56,509 --> 00:13:54,300
general hasn't like the genes have

312
00:13:59,210 --> 00:13:56,519
enough variety that we do just get the

313
00:14:02,360 --> 00:13:59,220

eukaryote species tree pretty reliably

314
00:14:04,429 --> 00:14:02,370
so I think we can be fairly confident

315
00:14:11,150 --> 00:14:04,439
that what we're seeing is real but they