
AbSciCon
2019

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

2
00:00:13,549 --> 00:00:09,190
[Applause]

3
00:00:21,320 --> 00:00:13,559
all right still worth in progress so now

4
00:00:23,300 --> 00:00:21,330
we're at perform DNA repair alright so

5
00:00:27,140 --> 00:00:23,310
here I'm showing you our most everybody

6
00:00:28,310 --> 00:00:27,150
hear me in the back yes okay so here I

7
00:00:31,189 --> 00:00:28,320
am showing you our most current

8
00:00:34,310 --> 00:00:31,199
understanding of the phylogenetic tree

9
00:00:36,439 --> 00:00:34,320
of life with bacteria Eukarya archaea

10
00:00:37,790 --> 00:00:36,449
and I hope I'm not insulting anyone's

11
00:00:40,310 --> 00:00:37,800
intelligence here by just sort of

12
00:00:42,170 --> 00:00:40,320
reminding you how to read a phylogenetic

13
00:00:44,450 --> 00:00:42,180

tree because I will show you another one

14
00:00:46,549 --> 00:00:44,460
in the course of this talk and so you

15
00:00:49,820 --> 00:00:46,559
know the nodes and the phylogenetic tree

16
00:00:51,259 --> 00:00:49,830
places where it branches connect you

17
00:00:53,390 --> 00:00:51,269
know we consider those and burn or

18
00:00:57,969 --> 00:00:53,400
hypothesize ancestors and we can say

19
00:01:00,619 --> 00:00:57,979
that a group is monophyletic if it

20
00:01:01,280 --> 00:01:00,629
shares a unique common ancestor unto

21
00:01:03,950 --> 00:01:01,290
itself

22
00:01:05,780 --> 00:01:03,960
exclusive not including other groups so

23
00:01:08,359 --> 00:01:05,790
here are bacteria forming a monophyletic

24
00:01:09,710 --> 00:01:08,369
group now the inferred ancestor that I

25
00:01:10,940 --> 00:01:09,720
want to talk to you about today and some

26
00:01:12,230 --> 00:01:10,950
people have already brought this up in

27
00:01:14,029 --> 00:01:12,240
their talks I want to talk to you about

28
00:01:15,950 --> 00:01:14,039
the Luca the last Universal common

29
00:01:18,889 --> 00:01:15,960
ancestor of all living on earth and

30
00:01:21,980 --> 00:01:18,899
lived on their Creed's for billion years

31
00:01:22,500 --> 00:01:21,990
ago and this food probably doesn't need

32
00:01:25,290 --> 00:01:22,510
it

33
00:01:28,890 --> 00:01:25,300
put that into a pictographic perspective

34
00:01:31,110 --> 00:01:28,900
if we read this picture from from left

35
00:01:33,210 --> 00:01:31,120
to right we see early Earth on the Left

36
00:01:34,830 --> 00:01:33,220
and modern times including astronomers

37
00:01:38,130 --> 00:01:34,840
people like some of you in this room on

38
00:01:41,990 --> 00:01:38,140

the on the right then of course I'm

39
00:01:46,440 --> 00:01:44,580
okay yes and of course I'm talking about

40
00:01:48,450 --> 00:01:46,450
a time period writing here now I

41
00:01:51,180 --> 00:01:48,460
personally believe you know this is the

42
00:01:55,250 --> 00:01:51,190
the topic of this particular symposium

43
00:01:57,180 --> 00:01:55,260
is you know the Dark Ages and I have I

44
00:01:58,950 --> 00:01:57,190
believe that the look at has great

45
00:02:01,170 --> 00:01:58,960
capacity to teach us about modern

46
00:02:02,670 --> 00:02:01,180
biodiversity and also some capacity to

47
00:02:04,230 --> 00:02:02,680
help us look back further in time

48
00:02:08,010 --> 00:02:04,240
probably not something I need to

49
00:02:11,700 --> 00:02:08,020
convince folks up in this room and so

50
00:02:13,740 --> 00:02:11,710
one way we can understand what we can

51
00:02:17,610 --> 00:02:13,750
understand will Luca is by studying its

52
00:02:18,810 --> 00:02:17,620
genome its genome content and that helps

53
00:02:21,060 --> 00:02:18,820
us to understand what its metabolic

54
00:02:22,620 --> 00:02:21,070
capabilities were what its structures

55
00:02:24,660 --> 00:02:22,630
we're live in there been many studies on

56
00:02:26,670 --> 00:02:24,670
the Luca Gina and I'm showing you some

57
00:02:28,620 --> 00:02:26,680
of those here and the team's inferred to

58
00:02:30,930 --> 00:02:28,630
be present in the Luca based on these

59
00:02:38,070 --> 00:02:30,940
studies have been aggregated into a

60
00:02:39,960 --> 00:02:38,080
database called leukopenia yes so one of

61
00:02:42,330 --> 00:02:39,970
the things that fascinates me is trying

62
00:02:44,220 --> 00:02:42,340
to understand how did the Luca conduct

63
00:02:47,570 --> 00:02:44,230

its DNA processes have a palooka

64
00:02:49,670 --> 00:02:47,580
interact with its own DNA tina and so

65
00:02:52,100 --> 00:02:49,680
these studies of the leuco we know quite

66
00:02:53,720 --> 00:02:52,110
a bit about its ability to do DNA

67
00:02:55,940 --> 00:02:53,730
transcription or at least a little bit

68
00:02:59,030 --> 00:02:55,950
about ability to do DNA transcription

69
00:03:00,770 --> 00:02:59,040
depending on who you ask if it's ability

70
00:03:02,600 --> 00:03:00,780
to do DNA replication then let's

71
00:03:04,400 --> 00:03:02,610
remember that DNA replication is not

72
00:03:07,700 --> 00:03:04,410
just the ability of an organism to make

73
00:03:09,860 --> 00:03:07,710
more DNA DNA replication requires quite

74
00:03:11,810 --> 00:03:09,870
a lot of fidelity in terms of making

75
00:03:13,580 --> 00:03:11,820
that copy and so there's a lot of

76
00:03:16,940 --> 00:03:13,590
excision and repair that goes on during

77
00:03:19,160 --> 00:03:16,950
that process so it's no surprise that

78
00:03:20,900 --> 00:03:19,170
you know at least some of the genes that

79
00:03:22,660 --> 00:03:20,910
we have heard to be present in the Luca

80
00:03:25,580 --> 00:03:22,670
genome were involved in DNA replication

81
00:03:28,760 --> 00:03:25,590
and specifically in excision and

82
00:03:31,250 --> 00:03:28,770
repaired during DNA during DNA

83
00:03:33,350 --> 00:03:31,260
replication and so you know I became

84
00:03:35,390 --> 00:03:33,360
very interested more broadly in DNA

85
00:03:38,180 --> 00:03:35,400
repair enzymes that might have been

86
00:03:41,030 --> 00:03:38,190
present in the luca and so using

87
00:03:45,500 --> 00:03:41,040
Wikipedia and studies in leukopenia that

88
00:03:48,890 --> 00:03:45,510

predicted or rather you think leukopenia

89
00:03:51,800 --> 00:03:48,900
and looking at genes that were predicted

90
00:03:54,080 --> 00:03:51,810
to be present by at least four studies

91
00:03:56,509 --> 00:03:54,090
within leukopenia and considering the

92
00:03:58,460 --> 00:03:56,519
function of these gene families

93
00:04:02,210 --> 00:03:58,470
predicted to be present in my four

94
00:04:04,160 --> 00:04:02,220
studies using a gene ontology resource I

95
00:04:07,310 --> 00:04:04,170
asked them you know how many of these

96
00:04:11,780 --> 00:04:07,320
these genes you know we're involved in

97
00:04:13,670 --> 00:04:11,790
in DNA repair and out of 981 genes

98
00:04:15,130 --> 00:04:13,680
predicted presence in the Luca by at

99
00:04:19,990 --> 00:04:15,140
least four studies we

100
00:04:25,180 --> 00:04:20,000
at 14 of those gene families were

101
00:04:27,460 --> 00:04:25,190
probably involved in DNA repair and so

102
00:04:29,770 --> 00:04:27,470
what were they do it well you know some

103
00:04:31,630 --> 00:04:29,780
again were involved in DNA replication

104
00:04:34,750 --> 00:04:31,640
but some are probably acting outside of

105
00:04:37,440 --> 00:04:34,760
that DNA replication system some

106
00:04:43,450 --> 00:04:37,450
operating in meiosis and doing various

107
00:04:47,409 --> 00:04:43,460
excision repair so we decided to look in

108
00:04:50,110 --> 00:04:47,419
depth at a protein family called MGMT

109
00:04:52,210 --> 00:04:50,120
that's ubiquitous across the Tree of

110
00:04:54,460 --> 00:04:52,220
Life and therefore we assumed probably

111
00:04:57,460 --> 00:04:54,470
present in the Luca so here I'm showing

112
00:05:01,930 --> 00:04:57,470
you a representative in GMT protein now

113
00:05:05,190 --> 00:05:01,940

in e.coli MGMT has three parallels and

114
00:05:08,020 --> 00:05:05,200
they are og ta da and ato

115
00:05:11,080 --> 00:05:08,030
the og T and a da paralogs

116
00:05:14,409 --> 00:05:11,090
are pretty similar to one another they

117
00:05:16,360 --> 00:05:14,419
have an in terminal domain that does D

118
00:05:18,550 --> 00:05:16,370
alkylation of DNA phosphate so

119
00:05:20,710 --> 00:05:18,560
essentially removing methyl groups from

120
00:05:23,620 --> 00:05:20,720
DNA phosphates a form of DNA damage

121
00:05:25,719 --> 00:05:23,630
repairing that and a c-terminal domain

122
00:05:28,840 --> 00:05:25,729
so these are by functional a c-terminal

123
00:05:34,659 --> 00:05:28,850
domain that D methylates or de-escalates

124
00:05:37,360 --> 00:05:34,669
oh six wonnie or of work finding OG

125
00:05:39,909 --> 00:05:37,370
ta-daa act as monomers that is they

126
00:05:41,770 --> 00:05:39,919
don't recruit other proteins to be part

127
00:05:43,820 --> 00:05:41,780
of a complex to do these DNA repairs

128
00:05:46,220 --> 00:05:43,830
they act on their bow and

129
00:05:48,230 --> 00:05:46,230
they're sudo enzymes why I like sudo

130
00:05:49,850 --> 00:05:48,240
enzymes well after they do their job

131
00:05:53,840 --> 00:05:49,860
they D methylate or de-escalate

132
00:05:57,760 --> 00:05:53,850
something they're defunct and now they

133
00:06:00,410 --> 00:05:57,770
differ in terms of OTT is Institute

134
00:06:03,770 --> 00:06:00,420
constituents if we produce so it's

135
00:06:05,480 --> 00:06:03,780
always on where a DA is auto induced and

136
00:06:09,770 --> 00:06:05,490
in fact it becomes its own transcription

137
00:06:12,080 --> 00:06:09,780
factor now ATM is a little bit different

138
00:06:14,510 --> 00:06:12,090

it lacks this in terminal domain

139
00:06:16,430 --> 00:06:14,520
function and it has the c-terminal

140
00:06:18,680 --> 00:06:16,440
domain function it is able to bind DNA

141
00:06:22,040 --> 00:06:18,690
but it doesn't actually do demethylation

142
00:06:25,130 --> 00:06:22,050
or duty appellation instead it recruits

143
00:06:27,290 --> 00:06:25,140
other DNA repair enzymes that are not

144
00:06:29,180 --> 00:06:27,300
part of this protein family so if I'm

145
00:06:31,580 --> 00:06:29,190
related to this protein family to

146
00:06:34,580 --> 00:06:31,590
actually do the DNA repair and this new

147
00:06:36,410 --> 00:06:34,590
believe is at root in time meaning it

148
00:06:37,880 --> 00:06:36,420
can be reused and in terms of its

149
00:06:43,880 --> 00:06:37,890
production we don't know if it's always

150
00:06:46,640 --> 00:06:43,890
on or if it's an induced so why do we

151
00:06:49,070 --> 00:06:46,650
care so much about the alkylation or

152
00:06:50,390 --> 00:06:49,080
demethylation the evolution of DNA and

153
00:06:54,070 --> 00:06:50,400
one might early

154
00:06:59,230 --> 00:06:54,080
healthcare so

155
00:07:01,089 --> 00:06:59,240
thinking in terms of MGMT so remembering

156
00:07:03,790 --> 00:07:01,099
that it is going to one of its functions

157
00:07:06,360 --> 00:07:03,800
is to deep methylated des played a

158
00:07:09,279 --> 00:07:06,370
thymine or a guanine

159
00:07:12,850 --> 00:07:09,289
so these spaces become methylated or a

160
00:07:13,930 --> 00:07:12,860
belated and in fact that causes oh they

161
00:07:16,390 --> 00:07:13,940
were supposed to be a little animation

162
00:07:18,430 --> 00:07:16,400
there I apologize for its absence but in

163
00:07:20,920 --> 00:07:18,440

fact what that causes is mismatched

164
00:07:22,960 --> 00:07:20,930
pairing so T normally binds with a

165
00:07:24,610 --> 00:07:22,970
that's not news to anybody here but in

166
00:07:27,309 --> 00:07:24,620
fact when this is methylated it bonds

167
00:07:29,260 --> 00:07:27,319
with G similarly when G is methylated it

168
00:07:31,450 --> 00:07:29,270
bonds with T and these point mutations

169
00:07:33,999 --> 00:07:31,460
in DNA caused by this methylation in RF

170
00:07:37,450 --> 00:07:34,009
elation can lead to this can be computed

171
00:07:41,110 --> 00:07:37,460
through DNA replication or through

172
00:07:42,999 --> 00:07:41,120
transcription so what are the sources of

173
00:07:45,670 --> 00:07:43,009
the methyl group the methyl groups that

174
00:07:48,159 --> 00:07:45,680
cause damage to DNA well they can be

175
00:07:50,230 --> 00:07:48,169
endogenous or exogenous most most often

176
00:07:52,690 --> 00:07:50,240
in modern life their exogenous sources

177
00:07:55,540 --> 00:07:52,700
coming from the environment

178
00:07:58,060 --> 00:07:55,550
endogenous sources can include this demo

179
00:07:59,710 --> 00:07:58,070
online and so those of you that are

180
00:08:01,150 --> 00:07:59,720
familiar with this molecule know that we

181
00:08:02,530 --> 00:08:01,160
really need it it's a really important

182
00:08:06,070 --> 00:08:02,540
molecule and it does a lot of good work

183
00:08:07,960 --> 00:08:06,080
in the body however it turns out that

184
00:08:09,880 --> 00:08:07,970
this can in fact randomly methylate

185
00:08:11,890 --> 00:08:09,890
parts of the DNA transfer a methyl group

186
00:08:12,640 --> 00:08:11,900
to parts of the DNA but we don't want it

187
00:08:15,990 --> 00:08:12,650
to do that too

188
00:08:23,260 --> 00:08:16,000

and so actually causing damage and so

189
00:08:26,050 --> 00:08:23,270
one possibility is that as there was

190
00:08:28,030 --> 00:08:26,060
more methane present in the early

191
00:08:30,970 --> 00:08:28,040
atmosphere so here showing you early

192
00:08:33,550 --> 00:08:30,980
atmosphere of Earth more methane present

193
00:08:35,770 --> 00:08:33,560
and possibly membranes of early

194
00:08:38,380 --> 00:08:35,780
organisms were a bit leaky we know that

195
00:08:40,300 --> 00:08:38,390
this is a very old molecule predating

196
00:08:41,890 --> 00:08:40,310
the Luca so it's possible that there was

197
00:08:44,500 --> 00:08:41,900
more of this floating around at living

198
00:08:47,560 --> 00:08:44,510
systems anyway methylating DNA of course

199
00:08:50,500 --> 00:08:47,570
it's also possible that there were other

200
00:08:52,480 --> 00:08:50,510
sources for more fur methylation as well

201
00:08:54,250 --> 00:08:52,490
and again you know these are repair

202
00:08:55,510 --> 00:08:54,260
enzymes that we need in our systems and

203
00:09:00,660 --> 00:08:55,520
of course we're not exposed to this

204
00:09:02,750 --> 00:09:00,670
level of methane all right

205
00:09:06,420 --> 00:09:02,760
so anyway to convince ourselves that

206
00:09:08,550 --> 00:09:06,430
this in GMT protein family was president

207
00:09:11,100 --> 00:09:08,560
in the last Universal common ancestor we

208
00:09:13,230 --> 00:09:11,110
reconstructed a phylogeny using sampling

209
00:09:15,560 --> 00:09:13,240
from across the Tree of Life and rather

210
00:09:17,280 --> 00:09:15,570
from across the prokaryotic tree of life

211
00:09:18,480 --> 00:09:17,290
eukaryotes probably would not have

212
00:09:19,980 --> 00:09:18,490
contributed very much to our

213
00:09:22,320 --> 00:09:19,990

understanding here I'm sorry to say

214
00:09:25,260 --> 00:09:22,330
because I studied eukaryote before this

215
00:09:28,170 --> 00:09:25,270
and so um nevertheless

216
00:09:28,740 --> 00:09:28,180
uh we using all three of the the

217
00:09:31,950 --> 00:09:28,750
parralox

218
00:09:37,140 --> 00:09:31,960
OG t AP a and a TL and so what we

219
00:09:39,330 --> 00:09:37,150
determined is that in fact this protein

220
00:09:41,010 --> 00:09:39,340
family of G of T was present in the last

221
00:09:44,210 --> 00:09:41,020
Universal common ancestor this node here

222
00:09:50,130 --> 00:09:44,220
representing the Luca and following the

223
00:09:51,750 --> 00:09:50,140
it diversified into an RKO and bacterial

224
00:09:52,980 --> 00:09:51,760
lineage following the species Tree of

225
00:09:55,980 --> 00:09:52,990
Life are consistent with the species

226
00:09:59,280 --> 00:09:55,990
Tree of Life and it turns out that the

227
00:10:00,750 --> 00:09:59,290
og t-type enzyme was probably ancestral

228
00:10:02,550 --> 00:10:00,760
here so remember that's the one that's

229
00:10:06,930 --> 00:10:02,560
constitutively produced and by

230
00:10:09,300 --> 00:10:06,940
functional so then we have the origin of

231
00:10:10,950 --> 00:10:09,310
ABA so again that one zips operate since

232
00:10:14,370 --> 00:10:10,960
its own transcription factor arrives

233
00:10:16,740 --> 00:10:14,380
later within the bacterial lineage and a

234
00:10:19,620 --> 00:10:16,750
TL which again is recruiting other

235
00:10:23,520 --> 00:10:19,630
proteins from other prepare protein or

236
00:10:25,100 --> 00:10:23,530
rather of DNA to prepare families arise

237
00:10:28,069 --> 00:10:25,110
here later

238
00:10:30,440 --> 00:10:28,079

I should point out that this is

239
00:10:32,300 --> 00:10:30,450
primarily this ATL is primarily found in

240
00:10:37,430 --> 00:10:32,310
bacteria so probably arising due to our

241
00:10:40,040 --> 00:10:37,440
horizontal gene transfer from archaea so

242
00:10:41,840 --> 00:10:40,050
what do these things look like well so

243
00:10:43,040 --> 00:10:41,850
these images that I'm showing you here

244
00:10:43,790 --> 00:10:43,050
and I'll start these movies up here in

245
00:10:47,050 --> 00:10:43,800
just a second

246
00:10:49,130 --> 00:10:47,060
these are the MGMT paralogs

247
00:10:51,829 --> 00:10:49,140
based on crystalline structure as shown

248
00:10:54,470 --> 00:10:51,839
here from a cola and you can see I'm

249
00:10:56,360 --> 00:10:54,480
showing you here in light colors these

250
00:10:58,040 --> 00:10:56,370
are the in terminal domains that are

251
00:11:02,300 --> 00:10:58,050
doing the demethylation

252
00:11:05,620 --> 00:11:02,310
of data the phosphate in DNA and these

253
00:11:07,970 --> 00:11:05,630
darker colors here these are the

254
00:11:10,269 --> 00:11:07,980
c-terminal domains that our response

255
00:11:13,940 --> 00:11:10,279
will afford d methylating or deflating

256
00:11:17,780 --> 00:11:15,790
[Music]

257
00:11:19,910 --> 00:11:17,790
started for you so you can see the

258
00:11:22,370 --> 00:11:19,920
structure and to point out here in this

259
00:11:24,380 --> 00:11:22,380
ATL at the end of our set we see only

260
00:11:27,470 --> 00:11:24,390
this dark colored structure this is the

261
00:11:29,930 --> 00:11:27,480
homologous would be the c-terminal

262
00:11:36,620 --> 00:11:29,940
domain over here so only you know that

263
00:11:41,329 --> 00:11:36,630

function that the bonds DNA and recruits

264
00:11:42,950 --> 00:11:41,339
other enzymes to to make repairs the

265
00:11:46,970 --> 00:11:42,960
Humvee

266
00:11:46,980 --> 00:11:49,940
Wow

267
00:11:55,250 --> 00:11:52,160
there we go all right so how does the

268
00:11:57,079 --> 00:11:55,260
luca compare so we did some sequence

269
00:11:59,480 --> 00:11:57,089
reconstruction here ancestral sequence

270
00:12:01,280 --> 00:11:59,490
reconstruction as well as 3d modeling

271
00:12:04,550 --> 00:12:01,290
and so here's what we get and what you

272
00:12:07,420 --> 00:12:04,560
can see is that there is the darker

273
00:12:09,829 --> 00:12:07,430
color the darker orange here represents

274
00:12:13,160 --> 00:12:09,839
homologous with the c-terminal domain

275
00:12:15,079 --> 00:12:13,170
that is presumably performing our care

276
00:12:17,090 --> 00:12:15,089
by removing it ethyl group or a methyl

277
00:12:20,930 --> 00:12:17,100
group from wanting and fighting and then

278
00:12:22,519 --> 00:12:20,940
we have kind of a simple interval in

279
00:12:24,500 --> 00:12:22,529
terminal domain here so it's not quite

280
00:12:27,290 --> 00:12:24,510
as complexes what's going over on over

281
00:12:29,300 --> 00:12:27,300
here at OG tier 88 is lacking these beta

282
00:12:33,530 --> 00:12:29,310
sheets but still possibly some

283
00:12:37,879 --> 00:12:33,540
functionality here in the the in

284
00:12:40,310 --> 00:12:37,889
terminal domain alright so where are we

285
00:12:42,650 --> 00:12:40,320
well we came into the study knowing that

286
00:12:44,660 --> 00:12:42,660
Luca possessed enzymes acted on DNA so

287
00:12:47,269 --> 00:12:44,670
it's interacting with its own DNA genome

288
00:12:49,730 --> 00:12:47,279

and we know that these enzymes included

289
00:12:52,699 --> 00:12:49,740
enzymes for DNA repair especially within

290
00:12:56,090 --> 00:12:52,709
replication so we found was that there

291
00:12:57,829 --> 00:12:56,100
are potentially more DNA enzymes present

292
00:12:59,150 --> 00:12:57,839
in the Luca that we realized and not all

293
00:13:03,310 --> 00:12:59,160
of those are acting within the DNA

294
00:13:06,439 --> 00:13:03,320
repair system most likely such as MGMT

295
00:13:10,880 --> 00:13:06,449
in G and T in the Luca appears to have

296
00:13:12,680 --> 00:13:10,890
functions similar to og ta da so you

297
00:13:14,840 --> 00:13:12,690
know having both an n-terminal and a

298
00:13:18,949 --> 00:13:14,850
c-terminal domain possibly again dual

299
00:13:22,069 --> 00:13:18,959
functional like modern MGMT and the MGMT

300
00:13:24,380 --> 00:13:22,079
protein we saw later or present in the

301
00:13:26,090 --> 00:13:24,390
luca later diversified in both archaea

302
00:13:27,790 --> 00:13:26,100
and bacteria to produce some additional

303
00:13:30,680 --> 00:13:27,800
functionality

304
00:13:33,050 --> 00:13:30,690
so I would go on to speculate that these

305
00:13:35,300 --> 00:13:33,060
relics at least relatively simple DNA

306
00:13:36,890 --> 00:13:35,310
repair was probably possible and pre

307
00:13:38,600 --> 00:13:36,900
with the organisms so something that

308
00:13:40,420 --> 00:13:38,610
maybe so if you who are studying such

309
00:13:43,010 --> 00:13:40,430
organisms should be on the lookout for

310
00:13:49,070 --> 00:13:43,020
and that's all I have to say about this

311
00:13:49,080 --> 00:13:57,340
so we have time for one short question

312
00:14:03,110 --> 00:14:00,829
very illuminating have I was interested

313
00:14:05,180 --> 00:14:03,120

in the final hypotheses and one of the

314
00:14:07,670 --> 00:14:05,190
things in the null hypotheses in your

315
00:14:10,250 --> 00:14:07,680
final statement would be that in order

316
00:14:13,970 --> 00:14:10,260
to get Luca or a tall order to get the

317
00:14:16,040 --> 00:14:13,980
last common Universal ancestor or the

318
00:14:18,710 --> 00:14:16,050
unity of biochemistry he might have had

319
00:14:20,900 --> 00:14:18,720
a polymerases that made a lot of

320
00:14:23,180 --> 00:14:20,910
mistakes very similar to what you

321
00:14:25,610 --> 00:14:23,190
actually have in let's say viral DNA

322
00:14:28,850 --> 00:14:25,620
because that that would allow you more

323
00:14:31,490 --> 00:14:28,860
options to arrive finally at the final

324
00:14:41,800 --> 00:14:31,500
unity of biochemistry so it's just a