
AbSciCon
2019

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

2
00:00:11,080 --> 00:00:09,000
[Applause]

3
00:00:13,810 --> 00:00:11,090
good afternoon everyone

4
00:00:18,359 --> 00:00:13,820
so over past hour we've been through

5
00:00:21,430 --> 00:00:18,369
this journey with insertions

6
00:00:23,790 --> 00:00:21,440
duplications by luke insertions by

7
00:00:28,029 --> 00:00:23,800
george fox and the common core by

8
00:00:31,089 --> 00:00:28,039
Jessica and those patterns have been

9
00:00:33,550 --> 00:00:31,099
quite persistent over for billions of

10
00:00:37,870 --> 00:00:33,560
years and we've thought everything is

11
00:00:40,900 --> 00:00:37,880
sort of holes in the same way and in the

12
00:00:43,660 --> 00:00:40,910
next 15 or so minutes I want to invite

13
00:00:46,390 --> 00:00:43,670

you to a journey into a world when all

14
00:00:50,440 --> 00:00:46,400
this is no longer true and this

15
00:00:53,580 --> 00:00:50,450
Wonderland is named mitochondria so I'm

16
00:00:56,410 --> 00:00:53,590
going to be talking about structures of

17
00:00:59,260 --> 00:00:56,420
mitochondrial ribosomes and this work

18
00:01:02,620 --> 00:00:59,270
was done in collaboration with Alexia

19
00:01:04,479 --> 00:01:02,630
moons and Alan brown from skylight flap

20
00:01:06,969 --> 00:01:04,489
and Harvard Medical School in Stockholm

21
00:01:09,940 --> 00:01:06,979
University and all this research was

22
00:01:13,540 --> 00:01:09,950
supported by a Swedish Research Council

23
00:01:20,280 --> 00:01:13,550
and NASA Center for the origins of life

24
00:01:25,870 --> 00:01:20,290
so I think for funding and so as I said

25
00:01:28,590 --> 00:01:25,880
so this emergence of mitochondria was

26
00:01:37,170 --> 00:01:28,600
dated about two billions of years ago

27
00:01:40,690 --> 00:01:37,180
when an alpha proteobacteria basically

28
00:01:46,600 --> 00:01:40,700
gotten incorporated in version 8 it into

29
00:01:48,790 --> 00:01:46,610
a proto eukaryotic cell and now it's

30
00:01:53,620 --> 00:01:48,800
been a hypothesis proposed by lynn

31
00:01:56,320 --> 00:01:53,630
margulis about 50 years ago and this is

32
00:01:58,600 --> 00:01:56,330
now almost unanimously accepted by the

33
00:02:01,149 --> 00:01:58,610
scientific community the fact that the

34
00:02:04,930 --> 00:02:01,159
mitochondria has evolved from an alpha

35
00:02:07,330 --> 00:02:04,940
proteobacteria so and what happened upon

36
00:02:10,119 --> 00:02:07,340
this process there are many many many

37
00:02:13,020 --> 00:02:10,129
complicated different phenomena related

38
00:02:16,479 --> 00:02:13,030

to mutual gene transfer from

39
00:02:18,850 --> 00:02:16,489
mitochondria into a nucleus as well as

40
00:02:23,530 --> 00:02:18,860
protein experts

41
00:02:25,320 --> 00:02:23,540
from cytosol into mitochondria so as a

42
00:02:29,310 --> 00:02:25,330
result of all these processes

43
00:02:32,410 --> 00:02:29,320
mitochondria eventually lost its

44
00:02:38,410 --> 00:02:32,420
independence and it just now became an

45
00:02:42,130 --> 00:02:38,420
organelle and nevertheless the genomic

46
00:02:44,980 --> 00:02:42,140
analyses performed in 90s by Michael

47
00:02:47,020 --> 00:02:44,990
Gray had indicated that there are a

48
00:02:50,670 --> 00:02:47,030
number of genomes that are always

49
00:02:53,530 --> 00:02:50,680
retained within mitochondria among them

50
00:02:57,730 --> 00:02:53,540
all mitochondria essentially retained

51
00:03:00,910 --> 00:02:57,740
its own translational machinery so the

52
00:03:05,110 --> 00:03:00,920
ribosome is still in there and there are

53
00:03:09,420 --> 00:03:05,120
certain critical components of oxidative

54
00:03:14,710 --> 00:03:09,430
phosphorylation system cycle cytochrome

55
00:03:17,440 --> 00:03:14,720
B cytochrome c k-- subunit 1 and 3 they

56
00:03:20,830 --> 00:03:17,450
still exist in every mitochondrial

57
00:03:26,730 --> 00:03:20,840
genome so mitochondrial ribosomes are

58
00:03:29,320 --> 00:03:26,740
required in order to and mitochondrial

59
00:03:31,960 --> 00:03:29,330
mitochondria from other species contain

60
00:03:35,050 --> 00:03:31,970
some additional variations of those

61
00:03:38,340 --> 00:03:35,060
genomes so my mitochondrial ribosomes

62
00:03:45,700 --> 00:03:38,350
are still required to do the translation

63
00:03:52,030 --> 00:03:45,710

within within mitochondria so and we

64
00:03:54,310 --> 00:03:52,040
have this quite unusual organism it's a

65
00:03:57,910 --> 00:03:54,320
eukaryotic organism called recliner

66
00:04:02,110 --> 00:03:57,920
Manas Americana and it appears that it

67
00:04:04,930 --> 00:04:02,120
contains a genome which is most

68
00:04:07,690 --> 00:04:04,940
bacterial alike genome among all known

69
00:04:12,160 --> 00:04:07,700
you can occur it mitochondrial species

70
00:04:16,240 --> 00:04:12,170
so this genome contains around 70 base

71
00:04:22,240 --> 00:04:16,250
pairs 70 70 kilo base pairs and it

72
00:04:24,820 --> 00:04:22,250
encodes for nearly 67 proteins so

73
00:04:27,240 --> 00:04:24,830
minimum number of proteins encoded by

74
00:04:31,480 --> 00:04:27,250
mitochondrial genome is four or five

75
00:04:37,550 --> 00:04:31,490
these this genome encodes

76
00:04:41,150 --> 00:04:37,560
67 proteins so and it's clearly by these

77
00:04:46,810 --> 00:04:41,160
genomic analysis Michael Gray had

78
00:04:50,240 --> 00:04:46,820
demonstrated back in 90s that the this

79
00:04:55,880 --> 00:04:50,250
mitochondria is closely related to an

80
00:04:58,790 --> 00:04:55,890
alpha Proteobacteria so and there were a

81
00:05:01,910 --> 00:04:58,800
number of genomic analyses done through

82
00:05:06,260 --> 00:05:01,920
a past couple of decades and kill very

83
00:05:08,300 --> 00:05:06,270
recently and this work was motivated and

84
00:05:11,530 --> 00:05:08,310
there gained its attention in the past

85
00:05:14,290 --> 00:05:11,540
few years when crystal structures of

86
00:05:17,720 --> 00:05:14,300
mitochondrial ribosomes became available

87
00:05:21,680 --> 00:05:17,730
from laboratories of Nanban and when

88
00:05:23,510 --> 00:05:21,690

Quinta Ramakrishnan so and through the

89
00:05:27,530 --> 00:05:23,520
rest of my talk I'm going to be talking

90
00:05:31,280 --> 00:05:27,540
about evolutionary processes that

91
00:05:33,650 --> 00:05:31,290
occurred within those mitochondrial my

92
00:05:37,190 --> 00:05:33,660
terrible mo structures and apparently

93
00:05:40,430 --> 00:05:37,200
they're quite different so we have

94
00:05:43,190 --> 00:05:40,440
fungal MITRE episome we have mammalian

95
00:05:46,640 --> 00:05:43,200
mightor episome and we have a parasitic

96
00:05:48,680 --> 00:05:46,650
mite ribosome and they all undergo

97
00:05:50,900 --> 00:05:48,690
substantial changes they accrete

98
00:05:54,020 --> 00:05:50,910
additional components most of them are

99
00:05:56,420 --> 00:05:54,030
proteins such that this is a this

100
00:05:58,850 --> 00:05:56,430
structure came out last year and it's

101
00:06:01,850 --> 00:05:58,860
very surprising because what happened is

102
00:06:04,340 --> 00:06:01,860
my tribe Azam nearly doubled its size

103
00:06:07,250 --> 00:06:04,350
compared to a bacterial ribosome and

104
00:06:13,430 --> 00:06:07,260
most of it it's just the proteins it's

105
00:06:16,580 --> 00:06:13,440
not a ribosome of RNA so and let me sort

106
00:06:20,270 --> 00:06:16,590
of start with maybe touch back on a

107
00:06:24,610 --> 00:06:20,280
question of mic travisano when he asked

108
00:06:27,710 --> 00:06:24,620
about the common core of bacteria it

109
00:06:31,070 --> 00:06:27,720
appears that there are some variations

110
00:06:34,390 --> 00:06:31,080
and some deletions with in bacterial

111
00:06:39,290 --> 00:06:34,400
common core and this is illustrated by

112
00:06:41,090 --> 00:06:39,300
this diagram secondary structure so even

113
00:06:44,110 --> 00:06:41,100

some bacteria do not have certain

114
00:06:46,960 --> 00:06:44,120
components and mostly salsa alpha

115
00:06:50,140 --> 00:06:46,970
alfa Proteobacteria so for example those

116
00:06:52,750 --> 00:06:50,150
regions mark in black here they do not

117
00:06:55,360 --> 00:06:52,760
exist or delete it or shortened even in

118
00:06:58,090 --> 00:06:55,370
alpha Proteobacteria so there is a

119
00:07:01,060 --> 00:06:58,100
remarkable resemblance between what one

120
00:07:03,840 --> 00:07:01,070
can see with ribosomal alpha

121
00:07:07,870 --> 00:07:03,850
Proteobacteria and the ribosome of

122
00:07:10,150 --> 00:07:07,880
requirements Americana which is a mighty

123
00:07:11,460 --> 00:07:10,160
ribosome we have the same deletions we

124
00:07:14,170 --> 00:07:11,470
have the same sequence conservation

125
00:07:16,420 --> 00:07:14,180
conservation essentially all those

126
00:07:26,020 --> 00:07:16,430
diagrams are mapped onto a secondary

127
00:07:30,100 --> 00:07:26,030
structure of E coli so and that was just

128
00:07:34,710 --> 00:07:30,110
the common core but now if we go and try

129
00:07:36,550 --> 00:07:34,720
to explore the entire array of available

130
00:07:39,190 --> 00:07:36,560
ribosome might arrive as almost

131
00:07:41,950 --> 00:07:39,200
structures there is a surprise that

132
00:07:43,810 --> 00:07:41,960
comes and essentially common core

133
00:07:46,510 --> 00:07:43,820
disappears so everything what we've

134
00:07:48,940 --> 00:07:46,520
talked about for for billions of years

135
00:07:51,730 --> 00:07:48,950
reduces down to an area which is

136
00:07:53,980 --> 00:07:51,740
highlighted in grey right here and the

137
00:07:56,350 --> 00:07:53,990
common core it uses down to just the

138
00:08:00,400 --> 00:07:56,360

origin that contains which contains the

139
00:08:03,100 --> 00:08:00,410
PTC a short region of exit tunnel and

140
00:08:06,700 --> 00:08:03,110
the platform of a large unit which

141
00:08:09,040 --> 00:08:06,710
interacts with a small subunit and there

142
00:08:11,350 --> 00:08:09,050
is a couple of other functional regions

143
00:08:15,339 --> 00:08:11,360
such as L 11 binding domain and the

144
00:08:18,000 --> 00:08:15,349
sarsen erasing loop so and what we did

145
00:08:21,250 --> 00:08:18,010
we reconstructed phylogeny based on

146
00:08:23,890 --> 00:08:21,260
structures of ribosomal RNA and I'm not

147
00:08:26,200 --> 00:08:23,900
going to go into details but just to say

148
00:08:30,100 --> 00:08:26,210
that we will use this phylogeny in order

149
00:08:33,640 --> 00:08:30,110
to time the events of what happens

150
00:08:36,399 --> 00:08:33,650
always mitochondria ribosomes and when

151
00:08:40,149 --> 00:08:36,409
we get this and use this phylogeny and

152
00:08:41,980 --> 00:08:40,159
try to map all different proteins among

153
00:08:42,670 --> 00:08:41,990
different species within different

154
00:08:46,630 --> 00:08:42,680
lineages

155
00:08:50,650 --> 00:08:46,640
so mitochondria retains a number of

156
00:08:53,199 --> 00:08:50,660
bacterial proteins so this mitochondria

157
00:08:55,510 --> 00:08:53,209
of reclaim honest Americana is the most

158
00:08:55,910 --> 00:08:55,520
bacterial like mitochondria it doesn't

159
00:08:58,220 --> 00:08:55,920
gain

160
00:09:00,920 --> 00:08:58,230
any additional proteins are little or no

161
00:09:03,980 --> 00:09:00,930
structural modification to that all the

162
00:09:06,440 --> 00:09:03,990
other ribosomes MITRE absorbs started

163
00:09:08,150 --> 00:09:06,450

creating additional proteins and those

164
00:09:14,000 --> 00:09:08,160
seven right here

165
00:09:16,689 --> 00:09:14,010
ml 41 43 45 46 49 53 and 54 appeared to

166
00:09:19,400 --> 00:09:16,699
be the oldest Oh nearly universal

167
00:09:22,040 --> 00:09:19,410
mitochondrial proteins so when I map

168
00:09:22,939 --> 00:09:22,050
those proteins onto three-dimensional

169
00:09:25,819 --> 00:09:22,949
structures

170
00:09:28,639 --> 00:09:25,829
it appears that those proteins all the

171
00:09:31,490 --> 00:09:28,649
Smita ribosomal proteins they are

172
00:09:33,949 --> 00:09:31,500
clustered centrally into two regions one

173
00:09:37,220 --> 00:09:33,959
is near the ready tunnel the second

174
00:09:40,430 --> 00:09:37,230
group is near central protuberance so

175
00:09:44,930 --> 00:09:40,440
let's start talking about the exit

176
00:09:48,530 --> 00:09:44,940
tunnel so we actually I mentioned

177
00:09:51,110 --> 00:09:48,540
earlier here that the Alpha

178
00:09:54,139 --> 00:09:51,120
proteobacteria ribosome and ribosome of

179
00:09:57,230 --> 00:09:54,149
requirements Americana contains some

180
00:10:01,310 --> 00:09:57,240
pretty heated regions which are marked

181
00:10:06,199 --> 00:10:01,320
in black here so and this but specific

182
00:10:09,680 --> 00:10:06,209
region here it's helix 16 helix 18 right

183
00:10:11,900 --> 00:10:09,690
here and it's shown based on a structure

184
00:10:16,040 --> 00:10:11,910
of e.coli right here of course there is

185
00:10:19,130 --> 00:10:16,050
no deletions but if you look what

186
00:10:21,500 --> 00:10:19,140
happened to or early protimeter ribosome

187
00:10:24,949 --> 00:10:21,510
from our reconstructions it appears that

188
00:10:27,230 --> 00:10:24,959

there are many early protocol and real

189
00:10:30,500 --> 00:10:27,240
proteins are clustered around this

190
00:10:32,960 --> 00:10:30,510
region so we hypothesize that those

191
00:10:36,470 --> 00:10:32,970
proteins are responsible for the build

192
00:10:39,620 --> 00:10:36,480
stabilization of this region and then in

193
00:10:45,470 --> 00:10:39,630
some later MITRE episome so if you go to

194
00:10:48,079 --> 00:10:45,480
a pista quante creates a fungi or

195
00:10:50,540 --> 00:10:48,089
mammalian ribosomes is helix completely

196
00:10:52,790 --> 00:10:50,550
disappears so that suggests that the

197
00:10:55,430 --> 00:10:52,800
existent secretion of those proteins

198
00:10:58,009 --> 00:10:55,440
just does a good job by itself

199
00:11:00,710 --> 00:10:58,019
RNA is no longer needed so basically

200
00:11:05,770 --> 00:11:00,720
we're just talking about a complete

201
00:11:11,490 --> 00:11:05,780
replacement and of of this region

202
00:11:14,710 --> 00:11:11,500
so now let's talk about the exit tunnel

203
00:11:18,000 --> 00:11:14,720
the tunnel also gets remodeled and it

204
00:11:20,710 --> 00:11:18,010
gets remodeled in two separate ways as

205
00:11:23,730 --> 00:11:20,720
especially when I'm talking about more

206
00:11:27,220 --> 00:11:23,740
advanced mitochondrial species I imply

207
00:11:28,780 --> 00:11:27,230
funda and a pistol quanta fungi and

208
00:11:35,110 --> 00:11:28,790
mammalian ribosomes this is what

209
00:11:38,320 --> 00:11:35,120
analysis was done and so mammalian

210
00:11:41,140 --> 00:11:38,330
ribosomes undergo into a mode of

211
00:11:43,150 --> 00:11:41,150
deletion so RNA gets shorter shorter and

212
00:11:46,300 --> 00:11:43,160
shorter and apparently we are getting

213
00:11:50,170 --> 00:11:46,310

more additional proteins in fungi

214
00:11:54,250 --> 00:11:50,180
ribosome the RNA doesn't get shorter but

215
00:11:57,150 --> 00:11:54,260
additional proteins get and stabilize

216
00:12:01,330 --> 00:11:57,160
this such that RNA itself undergoes

217
00:12:02,710 --> 00:12:01,340
refolding and it causes the change in

218
00:12:05,970 --> 00:12:02,720
the AG tunnel path

219
00:12:08,980 --> 00:12:05,980
so there is a new exit tunnel pass in

220
00:12:11,950 --> 00:12:08,990
East mitochondrial ribosome and it's

221
00:12:15,460 --> 00:12:11,960
diverted from its original path vertical

222
00:12:17,200 --> 00:12:15,470
path which exists in all other episodes

223
00:12:25,300 --> 00:12:17,210
including mitochondrial ribosomes

224
00:12:29,400 --> 00:12:25,310
bacterial ribosomes etc so and good so

225
00:12:32,170 --> 00:12:29,410
then a similar events occur within

226
00:12:38,230 --> 00:12:32,180
another region called central court

227
00:12:41,440 --> 00:12:38,240
appearance so we have accretion of those

228
00:12:46,360 --> 00:12:41,450
additional all these proteins ml 46 and

229
00:12:50,829 --> 00:12:46,370
ml 40 and even if George likes to talk

230
00:12:52,870 --> 00:12:50,839
about 5s RNA it is being lost upon

231
00:12:57,450 --> 00:12:52,880
accretion of those proteins probably

232
00:13:00,130 --> 00:12:57,460
because of their aesthetic issues and

233
00:13:04,630 --> 00:13:00,140
this coincides with the creation of

234
00:13:07,600 --> 00:13:04,640
protein BL 25 but then mitochondria gets

235
00:13:10,210 --> 00:13:07,610
protein ml 38 crediting into the

236
00:13:13,060 --> 00:13:10,220
basement of this central protuberance

237
00:13:17,410 --> 00:13:13,070
region and this is the reconstruction

238
00:13:19,430 --> 00:13:17,420

which corresponds to nearly loca last a

239
00:13:22,640 --> 00:13:19,440
pista quantum common ancestor of my

240
00:13:24,910 --> 00:13:22,650
the Condor ribosome and from this point

241
00:13:28,760 --> 00:13:24,920
the events took again two different

242
00:13:32,390 --> 00:13:28,770
approaches in mammalian ribosomes we the

243
00:13:36,160 --> 00:13:32,400
Galician continues on such that there is

244
00:13:39,170 --> 00:13:36,170
a deterioration of our RNA and

245
00:13:42,950 --> 00:13:39,180
mitochondria had to do a trick so it

246
00:13:46,370 --> 00:13:42,960
lacks its own RNA and it has to steal a

247
00:13:50,230 --> 00:13:46,380
tRNA molecule and just incorporate it

248
00:13:52,790 --> 00:13:50,240
into a central protuberance whereas in

249
00:13:56,120 --> 00:13:52,800
East mitochondria there are some

250
00:13:59,360 --> 00:13:56,130
additional Acree accretions expansions

251
00:14:01,670 --> 00:13:59,370
that associate with additional mighty

252
00:14:04,160 --> 00:14:01,680
ribosomal proteins and stabilize this

253
00:14:06,410 --> 00:14:04,170
region so again there are two different

254
00:14:11,570 --> 00:14:06,420
regimes in which those two mitochondria

255
00:14:15,020 --> 00:14:11,580
ribosomes can evolve so in order to

256
00:14:17,270 --> 00:14:15,030
conclude we we've shown that genetic

257
00:14:20,950 --> 00:14:17,280
corrosion has considerable effects on my

258
00:14:24,740 --> 00:14:20,960
mitre episomal structure and function

259
00:14:27,170 --> 00:14:24,750
loss of mitochondrial RNA stabilizes my

260
00:14:29,390 --> 00:14:27,180
tribus ohm and the structural fragility

261
00:14:32,440 --> 00:14:29,400
of metastable intermediates makes a more

262
00:14:35,570 --> 00:14:32,450
receptive to accommodating new elements

263
00:14:38,060 --> 00:14:35,580

patching occurs in an onion like fashion

264
00:14:41,240 --> 00:14:38,070
where new elements are created on to

265
00:14:44,720 --> 00:14:41,250
preexisting core and these structural

266
00:14:46,810 --> 00:14:44,730
patches are the addition of species

267
00:14:50,330 --> 00:14:46,820
specific pre-existing non-ribosomal

268
00:14:54,140 --> 00:14:50,340
macromolecules so all those new proteins

269
00:14:54,800 --> 00:14:54,150
they were available so now if I have a

270
00:14:57,830 --> 00:14:54,810
minute

271
00:15:00,410 --> 00:14:57,840
why all this is related to the origins

272
00:15:03,530 --> 00:15:00,420
of life we are talking about

273
00:15:05,900 --> 00:15:03,540
mitochondria here and I'm going back to

274
00:15:08,150 --> 00:15:05,910
the idea of the common core so the

275
00:15:12,230 --> 00:15:08,160
nature has managed to retain the common

276
00:15:14,810 --> 00:15:12,240
core over for billions of years the

277
00:15:18,680 --> 00:15:14,820
nature managed to contains a common core

278
00:15:22,400 --> 00:15:18,690
at the moment of at the moment of Luca

279
00:15:26,500 --> 00:15:22,410
when archaea split from bacteria and yet

280
00:15:31,350 --> 00:15:26,510
it just completely gave up on

281
00:15:37,590 --> 00:15:34,800
alpha product Iria got incorporated in a

282
00:15:40,079 --> 00:15:37,600
eukaryotic cell and it just under went

283
00:15:43,530 --> 00:15:40,089
through all this remodeling so what it

284
00:15:46,230 --> 00:15:43,540
suggests that there are very different

285
00:15:48,620 --> 00:15:46,240
types of evolutionary pressures that got

286
00:15:51,420 --> 00:15:48,630
applied onto this system of

287
00:15:53,400 --> 00:15:51,430
mitochondrial ribosomes and it just

288
00:15:56,189 --> 00:15:53,410

simply recorded all differences in

289
00:15:58,620 --> 00:15:56,199
evolutionary pressure and to me the

290
00:16:01,559 --> 00:15:58,630
critical difference is the difference in

291
00:16:06,420 --> 00:16:01,569
complexity the complexity of eukaryotic

292
00:16:09,629 --> 00:16:06,430
cell compared to complexity of bacteria

293
00:16:12,329 --> 00:16:09,639
when there is such a difference and it

294
00:16:14,730 --> 00:16:12,339
occurred over a short time it promoted

295
00:16:18,749 --> 00:16:14,740
such a severe changes in the structure

296
00:16:22,550 --> 00:16:18,759
of ribosome which suggests that when we

297
00:16:27,420 --> 00:16:22,560
got all different environmental changes

298
00:16:32,370 --> 00:16:27,430
changes in metabolism changes in cell

299
00:16:34,920 --> 00:16:32,380
composition upon split of Luca there

300
00:16:37,379 --> 00:16:34,930
were all of them we are not critical to

301
00:16:40,199 --> 00:16:37,389
the structure of the ribosome so it

302
00:16:46,240 --> 00:16:40,209
survived and maintained its own common

303
00:16:54,890 --> 00:16:51,260
very quick question you know I just have

304
00:16:58,100 --> 00:16:54,900
I have a question on a comment maybe the

305
00:17:03,650 --> 00:16:58,110
formulation of the question it would be

306
00:17:07,160 --> 00:17:03,660
to to ask truly why the ribosomal RNA in

307
00:17:10,370 --> 00:17:07,170
a carrots on in bacteria is so conserved

308
00:17:12,770 --> 00:17:10,380
in a sense because rather than looking

309
00:17:15,800 --> 00:17:12,780
at what's happening in the my to

310
00:17:18,079 --> 00:17:15,810
ribosome in fact I would say that it's

311
00:17:21,560 --> 00:17:18,089
really illustrating that the ribosomal

312
00:17:23,780 --> 00:17:21,570
RNA as you said indeed is under multiple

313
00:17:26,000 --> 00:17:23,790

order pressure but one that is becoming

314
00:17:27,949 --> 00:17:26,010
very apparent when you're looking at

315
00:17:31,100 --> 00:17:27,959
bacteria on a coyote is that it's

316
00:17:33,290 --> 00:17:31,110
completely remodeled the process of

317
00:17:36,200 --> 00:17:33,300
folding is completely controlled there's

318
00:17:38,600 --> 00:17:36,210
a huge amount of modification that takes

319
00:17:42,440 --> 00:17:38,610
place in a sequential fashion and in

320
00:17:45,890 --> 00:17:42,450
fact the ribosome sequence is conserved

321
00:17:48,590 --> 00:17:45,900
also because he has to switch well so I

322
00:17:50,900 --> 00:17:48,600
guess the short answer to your question

323
00:17:54,140 --> 00:17:50,910
would be when you need the car do you

324
00:17:59,030 --> 00:17:54,150
really care whether it's a Honda or camp

325
00:18:01,220 --> 00:17:59,040
or Toyota you don't but they're nearly

326
00:18:02,810 --> 00:18:01,230
identical they do the same functions and

327
00:18:06,440 --> 00:18:02,820
all the differences are just tiny

328
00:18:07,430 --> 00:18:06,450
details right right I'm sorry we're

329
00:18:08,630 --> 00:18:07,440
gonna have to interrupt this

330
00:18:11,890 --> 00:18:08,640
conversation we have another session