AbSciCon
2019

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

2
00:00:12,120 --> 00:00:09,050
[Applause]

3
00:00:15,930 --> 00:00:12,130
you know talk about expansion sequences

4
00:00:19,620 --> 00:00:15,940
in 5s RNA well this this is a very

5
00:00:23,330 --> 00:00:19,630
interesting story to me anyway we've

6
00:00:26,010 --> 00:00:23,340
published this paper back in 1981 and

7
00:00:29,130 --> 00:00:26,020
that means that it was published before

8
00:00:32,490 --> 00:00:29,140
the first 16s RNA complete sequence was

9
00:00:34,830 --> 00:00:32,500
available which means this was the first

10
00:00:37,860 --> 00:00:34,840
insertion sequence discovered and

11
00:00:40,080 --> 00:00:37,870
ribosomal RNA however that turns out not

12
00:00:42,060 --> 00:00:40,090
to be true because was in its infinite

13
00:00:45,930 --> 00:00:42,070

wisdom had done a catalogue of our

14
00:00:48,540 --> 00:00:45,940
ribosomal RNA fragments from 5s RNA from

15
00:00:51,270 --> 00:00:48,550
a clostridium and that actually had an

16
00:00:53,340 --> 00:00:51,280
insert as well so it's kind of

17
00:00:56,729 --> 00:00:53,350
interesting now the way this insert

18
00:00:59,069 --> 00:00:56,739
works is what's happening is you have

19
00:01:01,459 --> 00:00:59,079
extra material right here right and you

20
00:01:04,740 --> 00:01:01,469
come around and what happens if you

21
00:01:07,620 --> 00:01:04,750
cleave this out if you break this off

22
00:01:09,510 --> 00:01:07,630
and throw it away you can just reconnect

23
00:01:11,910 --> 00:01:09,520
this U and G and you have a perfectly

24
00:01:16,080 --> 00:01:11,920
normal secondary structure of the 5s RNA

25
00:01:18,539 --> 00:01:16,090
okay so so that's that's the key thing

26
00:01:21,210 --> 00:01:18,549
that you these insertion sequences of

27
00:01:22,980 --> 00:01:21,220
many of them you you can swittel remove

28
00:01:25,590 --> 00:01:22,990
them and you're right back to where you

29
00:01:28,350 --> 00:01:25,600
were and so they're not causing problems

30
00:01:30,510 --> 00:01:28,360
in particular okay so this is a it's

31
00:01:32,880 --> 00:01:30,520
more or less the secondary structure of

32
00:01:35,429 --> 00:01:32,890
5s RNA there's basically four and a half

33
00:01:37,770 --> 00:01:35,439
helical regions there's the fifth helix

34
00:01:42,679 --> 00:01:37,780
here which involves a non-standard base

35
00:01:47,100 --> 00:01:42,689
pairs okay so let's see how we do here

36
00:01:50,490 --> 00:01:47,110
erased the message managed to push the

37
00:01:53,240 --> 00:01:50,500
wrong button okay so this is what you've

38
00:01:56,340 --> 00:01:53,250

seen already today multiple examples of

39
00:01:58,890 --> 00:01:56,350
our insertion sequences that have been

40
00:02:02,100 --> 00:01:58,900
associated with with the large ribosomal

41
00:02:05,219 --> 00:02:02,110
RNAs and what we see here on the top is

42
00:02:07,230 --> 00:02:05,229
in fact the the thing growing as you go

43
00:02:09,210 --> 00:02:07,240
through a variety of organisms starting

44
00:02:11,699 --> 00:02:09,220
with E coli and ending up with human

45
00:02:14,520 --> 00:02:11,709
this grad graduate gets bigger as you

46
00:02:18,060 --> 00:02:14,530
keep inserting within the insert okay

47
00:02:20,680 --> 00:02:18,070
and so you know so the ribosomal RNA has

48
00:02:23,620 --> 00:02:20,690
grown over time

49
00:02:27,370 --> 00:02:23,630
well so what we wanted to do is to find

50
00:02:29,560 --> 00:02:27,380
out how common this insertion was in 5s

51
00:02:31,900 --> 00:02:29,570
RNA and what were some of the properties

52
00:02:34,030 --> 00:02:31,910
of this insertion so we did something

53
00:02:36,250 --> 00:02:34,040
which in retrospect was sort of stupid

54
00:02:39,340 --> 00:02:36,260
what we decided to do was to look for

55
00:02:41,140 --> 00:02:39,350
more examples okay and so this is an

56
00:02:43,480 --> 00:02:41,150
interesting thing you should be warned

57
00:02:45,390 --> 00:02:43,490
about if you if you probably know this

58
00:02:48,910 --> 00:02:45,400
but you really ought to be aware of it

59
00:02:53,530 --> 00:02:48,920
these databases are not very helpful if

60
00:02:55,600 --> 00:02:53,540
you want accurate information okay so

61
00:02:57,610 --> 00:02:55,610
there's a database here I'm sorry to

62
00:03:03,070 --> 00:02:57,620
name it specifically but this particular

63
00:03:05,050 --> 00:03:03,080

database is a database of 5s RNA s5s RNA

64
00:03:07,660 --> 00:03:05,060
sequences nothing else it doesn't

65
00:03:09,640 --> 00:03:07,670
contain the hallo caucus 5s RNA with the

66
00:03:12,040 --> 00:03:09,650
insert which is interesting since the

67
00:03:13,870 --> 00:03:12,050
hewa caucus 5s RNA was actually probably

68
00:03:16,300 --> 00:03:13,880
among the first ten that were actually

69
00:03:18,610 --> 00:03:16,310
even sequenced but it's not it's not

70
00:03:21,220 --> 00:03:18,620
even in the database in fact none of no

71
00:03:23,110 --> 00:03:21,230
large 5s RNA is in that particular

72
00:03:25,449 --> 00:03:23,120
database so they just simply have a

73
00:03:28,210 --> 00:03:25,459
prejudice against large they don't like

74
00:03:30,670 --> 00:03:28,220
inserts but we then we went to other

75
00:03:32,199 --> 00:03:30,680
more traditional places like like refseq

76
00:03:35,440 --> 00:03:32,209
and we looked at one hundred and twenty

77
00:03:40,480 --> 00:03:35,450
seven thousand genomes we found 157

78
00:03:43,060 --> 00:03:40,490
candidates for possible 5s rnas wood

79
00:03:44,860 --> 00:03:43,070
inserts and then there were then when

80
00:03:48,640 --> 00:03:44,870
you go through this it turns out that

81
00:03:50,590 --> 00:03:48,650
most of a lot of them are junk and 24

82
00:03:52,540 --> 00:03:50,600
would incorrect gene boundary so when

83
00:03:54,250 --> 00:03:52,550
people annotate these things they have a

84
00:03:56,170 --> 00:03:54,260
hard time finding where it starts and

85
00:03:58,150 --> 00:03:56,180
where it ends and you know that kind of

86
00:04:00,790 --> 00:03:58,160
thing and and there there's some

87
00:04:03,310 --> 00:04:00,800
problems like people have like with

88
00:04:05,260 --> 00:04:03,320

insertions in like it like there were a

89
00:04:07,420 --> 00:04:05,270
lot of 5s RNA is just sort of had a

90
00:04:09,160 --> 00:04:07,430
duplication in the middle of the 5s RNA

91
00:04:11,410 --> 00:04:09,170
and of course there were a lot of them

92
00:04:14,650 --> 00:04:11,420
in which various portions were just an

93
00:04:17,020 --> 00:04:14,660
so so the sequence was not complete so I

94
00:04:19,390 --> 00:04:17,030
can continue forever

95
00:04:21,880 --> 00:04:19,400
but it was so we ended up creating

96
00:04:24,370 --> 00:04:21,890
specialized search tools looking

97
00:04:26,500 --> 00:04:24,380
specifically for the sorts of 5s RNAs

98
00:04:28,990 --> 00:04:26,510
that we thought were interesting so in

99
00:04:30,880 --> 00:04:29,000
the end we found a bunch of them but I

100
00:04:33,760 --> 00:04:30,890
guarantee you we have not found them all

101
00:04:34,119 --> 00:04:33,770
ok but I would just like to say most of

102
00:04:38,079 --> 00:04:34,129
the one

103
00:04:42,399 --> 00:04:38,089
we found they're actually real and so we

104
00:04:45,009 --> 00:04:42,409
found 79 examples with 13 to 108

105
00:04:47,439 --> 00:04:45,019
residues as the insert and so we had put

106
00:04:49,179 --> 00:04:47,449
a boundary I think of 10 the in a

107
00:04:51,879 --> 00:04:49,189
minimum insert we would consider to be

108
00:04:54,249 --> 00:04:51,889
interesting was 10 so if so the smallest

109
00:04:55,899 --> 00:04:54,259
was 13 the largest was in fact the halo

110
00:04:58,989 --> 00:04:55,909
caucus one that we started with in the

111
00:05:02,769 --> 00:04:58,999
hundred and eight residues got 79 in the

112
00:05:07,839 --> 00:05:02,779
bacteria and then among the Archy we we

113
00:05:10,659 --> 00:05:07,849

have 10 examples here and 25 bacterial

114
00:05:14,259 --> 00:05:10,669
species so a lot of different organisms

115
00:05:16,749 --> 00:05:14,269
have this insertion of 5s RNA this is

116
00:05:18,850 --> 00:05:16,759
kind of a summary there is one rkl group

117
00:05:21,939 --> 00:05:18,860
which is the halo bacteria Alys which

118
00:05:24,100 --> 00:05:21,949
includes inhale caucus and hey will have

119
00:05:26,589 --> 00:05:24,110
OBM and a bunch of things and then a

120
00:05:29,230 --> 00:05:26,599
bunch of mainly anaerobic organisms in

121
00:05:31,329 --> 00:05:29,240
the Clostridium E's and the hail will

122
00:05:34,059 --> 00:05:31,339
have rallies how we say that the thermal

123
00:05:35,559 --> 00:05:34,069
era of bacteria always and alter

124
00:05:37,600 --> 00:05:35,569
modalities which is actually a

125
00:05:39,730 --> 00:05:37,610
gram-negative group and we were very

126
00:05:41,709 --> 00:05:39,740
upset we hadn't found any gram negatives

127
00:05:44,529 --> 00:05:41,719
until at the very very end of the search

128
00:05:47,829 --> 00:05:44,539
we and we found this guy here and so

129
00:05:51,909 --> 00:05:47,839
there's there's a fair number of these 5

130
00:05:54,249 --> 00:05:51,919
srna's containing insertions so this is

131
00:05:56,499 --> 00:05:54,259
a slide this has been previewed by the

132
00:05:59,889 --> 00:05:56,509
CIA and they don't want you to get

133
00:06:02,350 --> 00:05:59,899
access to this information so so if the

134
00:06:03,730 --> 00:06:02,360
print is very very small so that you

135
00:06:05,769 --> 00:06:03,740
know him if you're not in the first or

136
00:06:08,769 --> 00:06:05,779
second roll you can't read it however

137
00:06:11,230 --> 00:06:08,779
this is a summary this is a summary of

138
00:06:13,119 --> 00:06:11,240

how big the insert is so here's an

139
00:06:14,859 --> 00:06:13,129
organism name over here which you can't

140
00:06:18,639 --> 00:06:14,869
read and you don't care about anyway and

141
00:06:21,339 --> 00:06:18,649
and it has an insert of 61 residues okay

142
00:06:24,669 --> 00:06:21,349
and these down here this guy has 32

143
00:06:27,399 --> 00:06:24,679
residues this one here has 3 inserts

144
00:06:30,939 --> 00:06:27,409
that in the same organism has 3 inserts

145
00:06:34,029 --> 00:06:30,949
one of life 29 one of 39 in one of 85

146
00:06:37,629 --> 00:06:34,039
just sort of interesting and so we have

147
00:06:42,549 --> 00:06:40,449
there's also this is a grouping of the

148
00:06:46,689 --> 00:06:42,559
organisms that have the large inserts

149
00:06:47,620 --> 00:06:46,699
and it's basically what we have is that

150
00:06:48,940 --> 00:06:47,630
we have the

151
00:06:51,430 --> 00:06:48,950
certs I'm not going to show it to you

152
00:06:54,340 --> 00:06:51,440
but we have them categorized into kind

153
00:06:57,190 --> 00:06:54,350
of a structural grouping as to where

154
00:06:58,750 --> 00:06:57,200
they are and this kind of thing and so

155
00:07:01,270 --> 00:06:58,760
this is telling you the structure will

156
00:07:03,970 --> 00:07:01,280
do grouping and we have 17 groups

157
00:07:08,320 --> 00:07:03,980
distinct structural groupings and then

158
00:07:10,420 --> 00:07:08,330
this is showing you where which grouping

159
00:07:12,850 --> 00:07:10,430
it is in the well this is showing you

160
00:07:16,930 --> 00:07:12,860
the position I think okay the other

161
00:07:19,990 --> 00:07:16,940
thing anyway so there's turns out to be

162
00:07:24,310 --> 00:07:20,000
then 16 locations in which you find 5s

163
00:07:27,820 --> 00:07:24,320

RNA insertions and interesting thing

164
00:07:30,420 --> 00:07:27,830
here is if you go start here at the 5

165
00:07:33,310 --> 00:07:30,430
prime end and you walk around the 5s RNA

166
00:07:36,220 --> 00:07:33,320
when you come to these he oversees the

167
00:07:38,740 --> 00:07:36,230
insertion is always on the 3 prime stand

168
00:07:40,690 --> 00:07:38,750
always on the second half of the helix

169
00:07:43,210 --> 00:07:40,700
you know coming around 5 prime to 3

170
00:07:44,710 --> 00:07:43,220
prime is e to the to the second half of

171
00:07:47,020 --> 00:07:44,720
the helix that's where you get your

172
00:07:49,300 --> 00:07:47,030
insertions and the only exception to

173
00:07:51,010 --> 00:07:49,310
that is is right here I don't know if

174
00:07:54,250 --> 00:07:51,020
that means anything but it's kind of

175
00:07:57,040 --> 00:07:54,260
kind of strange and interesting now some

176
00:07:59,680 --> 00:07:57,050
of these insertions occur with greater

177
00:08:02,080 --> 00:07:59,690
frequency so there seems to be hotspots

178
00:08:03,580 --> 00:08:02,090
for insertion in different things so

179
00:08:08,590 --> 00:08:03,590
this is a subset of what was on the

180
00:08:11,700 --> 00:08:08,600
previous slide now we we have hot spots

181
00:08:15,010 --> 00:08:11,710
for insertion yes ok and some of these

182
00:08:17,290 --> 00:08:15,020
hot spots I mean we've been looking at

183
00:08:19,480 --> 00:08:17,300
the structure of the 5s RNA in this area

184
00:08:21,520 --> 00:08:19,490
right here is one of the most conserved

185
00:08:23,680 --> 00:08:21,530
parts of the 5s RNA so I'm kind of

186
00:08:26,080 --> 00:08:23,690
shocked to see you know insertions

187
00:08:28,780 --> 00:08:26,090
occurring here we had expected them over

188
00:08:33,520 --> 00:08:28,790

here from some prior mutation or work

189
00:08:37,300 --> 00:08:33,530
that we've done well I should tell you

190
00:08:39,959 --> 00:08:37,310
about 5s RNA and in particular 5s RNA is

191
00:08:43,630 --> 00:08:39,969
typically part of an operand 5s 16s

192
00:08:47,020 --> 00:08:43,640
2016's 23 s 5s is a common operon in

193
00:08:49,000 --> 00:08:47,030
Blunk bacteria and archaea and when

194
00:08:51,340 --> 00:08:49,010
they're frequently in many organisms

195
00:08:54,280 --> 00:08:51,350
there's multiple copies of the operon so

196
00:08:56,140 --> 00:08:54,290
e---coli has something like seven up

197
00:08:59,350 --> 00:08:56,150
seven or six or seven copies of the

198
00:09:01,330 --> 00:08:59,360
operon each of which has a 5s RNA and so

199
00:09:04,990 --> 00:09:01,340
in some of the cases

200
00:09:08,380 --> 00:09:05,000
these operons some of the organisms we

201
00:09:10,420 --> 00:09:08,390
looked at have in fact insertions and

202
00:09:11,830 --> 00:09:10,430
more than more than one copy of the

203
00:09:13,570 --> 00:09:11,840
insertion and one of the more

204
00:09:16,300 --> 00:09:13,580
interesting ones there's an organism

205
00:09:18,730 --> 00:09:16,310
which has six copies of the 5s RNA gene

206
00:09:22,990 --> 00:09:18,740
3 with the insertion and 3 without the

207
00:09:25,300 --> 00:09:23,000
insertion ok now if you only have one

208
00:09:28,030 --> 00:09:25,310
copy of the 5s RNA we assume it's

209
00:09:30,730 --> 00:09:28,040
functional if you have 6 copies of the

210
00:09:33,130 --> 00:09:30,740
identical 5s RNA it's probably also

211
00:09:34,960 --> 00:09:33,140
still functional but you know if there's

212
00:09:36,580 --> 00:09:34,970
only one copy we're pretty confident

213
00:09:40,000 --> 00:09:36,590

it's going to be functional because 5s

214
00:09:42,160 --> 00:09:40,010
RNA is kind of important in most

215
00:09:47,920 --> 00:09:42,170
organisms Anton will disagree with that

216
00:09:49,870 --> 00:09:47,930
note that ok so sometimes multiple genes

217
00:09:51,910 --> 00:09:49,880
exist but not all have the inserts so

218
00:09:54,310 --> 00:09:51,920
this is in the same organism you see

219
00:09:57,850 --> 00:09:54,320
you've got the insert here in this case

220
00:09:59,380 --> 00:09:57,860
and you it's not present here ok and so

221
00:10:01,780 --> 00:09:59,390
then that raises the question when

222
00:10:04,270 --> 00:10:01,790
there's more than one copy is this

223
00:10:06,130 --> 00:10:04,280
really functional we suspect so but we

224
00:10:10,840 --> 00:10:06,140
haven't done any experiments to indicate

225
00:10:13,300 --> 00:10:10,850
that so here's another case sometimes

226
00:10:17,440 --> 00:10:13,310
there's more than one example of the

227
00:10:19,990 --> 00:10:17,450
intron and so here's a case where we

228
00:10:23,410 --> 00:10:20,000
have in the same organism write it with

229
00:10:27,640 --> 00:10:23,420
two different versions of the 5s RNA one

230
00:10:30,310 --> 00:10:27,650
one of which has the well it has the

231
00:10:32,350 --> 00:10:30,320
insertion here right and this other one

232
00:10:34,960 --> 00:10:32,360
has the insertion in the same place as

233
00:10:38,560 --> 00:10:34,970
over here but it has an extra insertion

234
00:10:41,290 --> 00:10:38,570
out here small insertion here so that

235
00:10:44,320 --> 00:10:41,300
that's sort of there's lots of strange

236
00:10:47,110 --> 00:10:44,330
things that show up I should mention to

237
00:10:49,120 --> 00:10:47,120
you I suppose you know how is the

238
00:10:51,210 --> 00:10:49,130

insertion accommodated in the ribosome

239
00:10:55,030 --> 00:10:51,220
that's sort of a fundamental question

240
00:10:57,450 --> 00:10:55,040
and this is the predicted secondary

241
00:11:01,750 --> 00:10:57,460
structure of the hewa caucus insert and

242
00:11:04,360 --> 00:11:01,760
we have up here the 5 prime end of this

243
00:11:06,460 --> 00:11:04,370
thing ok and and the 3 goes all the way

244
00:11:08,500 --> 00:11:06,470
around back to the 3 prime end and so

245
00:11:11,140 --> 00:11:08,510
what we have are two major HeLa C's we

246
00:11:13,600 --> 00:11:11,150
have a helix here above the insert and

247
00:11:14,680 --> 00:11:13,610
we have this huge helix here below the

248
00:11:16,900 --> 00:11:14,690
insert and

249
00:11:18,580 --> 00:11:16,910
have predicted the predicted structure

250
00:11:21,130 --> 00:11:18,590
but it's probably pretty good because

251
00:11:23,560 --> 00:11:21,140
you got lots of base pairs and now

252
00:11:25,420 --> 00:11:23,570
there's we had a poster downstairs some

253
00:11:27,550 --> 00:11:25,430
of you may have noticed it and which we

254
00:11:30,670 --> 00:11:27,560
actually have been doing some cryo-em

255
00:11:33,850 --> 00:11:30,680
work with collaborators to understand

256
00:11:35,860 --> 00:11:33,860
the structure of the 5s RNA and we have

257
00:11:37,570 --> 00:11:35,870
how the inserts accommodated and it

258
00:11:39,160 --> 00:11:37,580
turns out that there's a little when you

259
00:11:41,500 --> 00:11:39,170
we have like a seven angstrom resolution

260
00:11:43,450 --> 00:11:41,510
structure and when you look at it

261
00:11:45,640 --> 00:11:43,460
there's two bulges there's a little very

262
00:11:47,560 --> 00:11:45,650
small bulge which apparently corresponds

263
00:11:49,600 --> 00:11:47,570

to this top part here and then there's a

264
00:11:51,340 --> 00:11:49,610
larger bulge which appears the core

265
00:11:54,160 --> 00:11:51,350
which is probably corresponds to this

266
00:11:56,680 --> 00:11:54,170
but what's likely happening is sort of

267
00:11:58,990 --> 00:11:56,690
speculative we're just saying this has a

268
00:12:01,420 --> 00:11:59,000
very extensive secondary structure so

269
00:12:03,910 --> 00:12:01,430
it's pretty much a rod and so what you

270
00:12:07,270 --> 00:12:03,920
can do is if you put that rod in the

271
00:12:08,740 --> 00:12:07,280
right place in the ribosome it'll just

272
00:12:10,840 --> 00:12:08,750
go out in the middle of nowhere and

273
00:12:13,660 --> 00:12:10,850
cause no problem so I suspect that's how

274
00:12:15,970 --> 00:12:13,670
they get accommodated by just a little

275
00:12:17,950 --> 00:12:15,980
bit of these asymmetrical loops along

276
00:12:19,600 --> 00:12:17,960
the way there's all these logical roofs

277
00:12:21,280 --> 00:12:19,610
that allow it to instead of being a

278
00:12:23,800 --> 00:12:21,290
totally straight thing it's probably

279
00:12:26,470 --> 00:12:23,810
bending a little bit and then it ends up

280
00:12:29,530 --> 00:12:26,480
going off in a direction which is not

281
00:12:35,340 --> 00:12:29,540
getting anybody's way and so that's sort

282
00:12:38,650 --> 00:12:35,350
of okay now before I talk about this

283
00:12:41,670 --> 00:12:38,660
there there's as they're gonna say I

284
00:12:44,650 --> 00:12:41,680
forgot so I won't talk about that

285
00:12:46,630 --> 00:12:44,660
these 5s RNA expansions are actually

286
00:12:48,880 --> 00:12:46,640
rare so I mean we found a lot right now

287
00:12:51,370 --> 00:12:48,890
so we finally 75 of them but the reality

288
00:12:54,850 --> 00:12:51,380

is that 75 out of hundred thousand

289
00:12:56,800 --> 00:12:54,860
genomes I mean it's they're pretty rare

290
00:12:59,740 --> 00:12:56,810
actually and only occurring in four

291
00:13:02,740 --> 00:12:59,750
general okay I don't know if it means

292
00:13:06,430 --> 00:13:02,750
anything but even the bacterial example

293
00:13:09,520 --> 00:13:06,440
sent me I mean the are actually the are

294
00:13:10,870 --> 00:13:09,530
actually hallo Felix so not all of them

295
00:13:12,820 --> 00:13:10,880
are hail effect but a lot of the

296
00:13:15,550 --> 00:13:12,830
organisms that have this insert or halo

297
00:13:17,680 --> 00:13:15,560
philic there appear to be for short

298
00:13:20,770 --> 00:13:17,690
locations which is not in the hot spots

299
00:13:23,380 --> 00:13:20,780
okay and frequently or sometimes

300
00:13:25,390 --> 00:13:23,390
multiple copies exists and we suspect

301
00:13:26,770 --> 00:13:25,400
most of them are actually functional

302
00:13:28,990 --> 00:13:26,780
okay and

303
00:13:31,720 --> 00:13:29,000
there's a question which comes up which

304
00:13:33,880 --> 00:13:31,730
is kind of the origins question why are

305
00:13:36,900 --> 00:13:33,890
they mostly recent now when you take

306
00:13:40,390 --> 00:13:36,910
when you have examples from the same

307
00:13:42,220 --> 00:13:40,400
organism from different species of the

308
00:13:44,020 --> 00:13:42,230
same organism so you get the genus and

309
00:13:46,540 --> 00:13:44,030
different species it's the same organism

310
00:13:48,760 --> 00:13:46,550
they have the 5s RNA and you compare the

311
00:13:50,770 --> 00:13:48,770
sequences what you find out is there are

312
00:13:53,770 --> 00:13:50,780
some sequence differences and those

313
00:13:56,620 --> 00:13:53,780

sequence differences do you know they

314
00:13:59,200 --> 00:13:56,630
take care of the structure okay they

315
00:14:03,250 --> 00:13:59,210
keep the structure valid and so the

316
00:14:05,530 --> 00:14:03,260
question we have is since then some of

317
00:14:06,970 --> 00:14:05,540
the some of them are old in the sense of

318
00:14:08,770 --> 00:14:06,980
you know a hundred thousand years but

319
00:14:10,540 --> 00:14:08,780
none of them are old in the sense of the

320
00:14:13,150 --> 00:14:10,550
four million years that we would like

321
00:14:15,850 --> 00:14:13,160
okay and some of the earlier talks and

322
00:14:19,020 --> 00:14:15,860
so I don't know why you don't have any

323
00:14:21,700 --> 00:14:19,030
old 5s RNA expansions but we don't and

324
00:14:29,190 --> 00:14:21,710
Jessica you she wants me to answer

325
00:14:36,990 --> 00:14:35,490
do we have any questions I was just

326
00:14:38,610 --> 00:14:37,000
wondering if there's been any rt-pcr

327
00:14:40,530 --> 00:14:38,620
work that demonstrates whether these

328
00:14:43,410 --> 00:14:40,540
insertions are actually edited out of

329
00:14:46,800 --> 00:14:43,420
the the ribosomal RNA are they edited

330
00:14:48,780 --> 00:14:46,810
out there they're simply immature cells

331
00:14:51,300 --> 00:14:48,790
they're not added at all I mean we

332
00:14:54,900 --> 00:14:51,310
haven't we have an ongoing experiment

333
00:14:57,420 --> 00:14:54,910
where we tried trying to insert them

334
00:14:59,550 --> 00:14:57,430
into the 23 s RNA institution so they

335
00:15:01,949 --> 00:14:59,560
interact with the 23 s RNA and we're a

336
00:15:04,439 --> 00:15:01,959
characteristic place and we want to we

337
00:15:07,590 --> 00:15:04,449
want to lock it in and see if the 5s RNA

338
00:15:11,009 --> 00:15:07,600

has to be separate from the 23 s RNA and

339
00:15:17,819 --> 00:15:11,019
that experiment has kind of ongoing for

340
00:15:19,110 --> 00:15:17,829
the last five years yeah I was just

341
00:15:23,150 --> 00:15:19,120
wondering whether there are any cases in

342
00:15:27,960 --> 00:15:23,160
which these sequences of RNA are ever

343
00:15:30,840 --> 00:15:27,970
translated I'm not sorry translated into

344
00:15:32,250 --> 00:15:30,850
proteins we're not supposed to be I

345
00:15:34,319 --> 00:15:32,260
guess but you know they're not supposed

346
00:15:37,259 --> 00:15:34,329
to be we haven't specifically

347
00:15:39,319 --> 00:15:37,269
specifically looked in the case of 5s

348
00:15:42,360 --> 00:15:39,329
RNA people have looked in the case of

349
00:15:44,819 --> 00:15:42,370
the large ribosomal RNAs and there's one

350
00:15:46,590 --> 00:15:44,829
area in the 23 s RNA that some people

351
00:15:48,630 --> 00:15:46,600
are convinced is coding

352
00:15:50,579 --> 00:15:48,640
even though it's in the 23 snrna gene

353
00:15:51,750 --> 00:15:50,589
and think might be coding something so

354
00:15:55,050 --> 00:15:51,760
they're happening but there hasn't been

355
00:15:57,150 --> 00:15:55,060
anything like that found for 5s RNA yeah

356
00:15:59,670 --> 00:15:57,160
yeah the other thing one thing I didn't

357
00:16:01,740 --> 00:15:59,680
mention is I showed you the way the

358
00:16:03,990 --> 00:16:01,750
insertion occurs you you cut it out and

359
00:16:06,780 --> 00:16:04,000
every goes away and there's no problem

360
00:16:08,400 --> 00:16:06,790
but occasionally some of them actually

361
00:16:09,990 --> 00:16:08,410
you can't just cut it out and put it

362
00:16:12,059 --> 00:16:10,000
back together you have to do some kind

363
00:16:12,569 --> 00:16:12,069

of insertion or deletion event along

364
00:16:14,250 --> 00:16:12,579
with it

365
00:16:16,590 --> 00:16:14,260
but the vast majority I mean it's a

366
00:16:20,280 --> 00:16:16,600
simple cut and it goes away and you just

367
00:16:28,620 --> 00:16:20,290
seal it back up thank you I allowed