2017 Astrobiology Graduate Conference

Charlottesville, VA

1
00:00:00,790 --> 00:00:07,360
[Music]

2
00:00:15,980 --> 00:00:12,860
thanks Mike hi everyone my name is Tony

3
00:00:19,310 --> 00:00:15,990
I'm coming here from LC Earth Life

4
00:00:21,439 --> 00:00:19,320
Science Institute in Tokyo and they

5
00:00:23,929 --> 00:00:21,449
provided some swag outside so I think

6
00:00:26,300 --> 00:00:23,939
it's all gone but there's some Flyers

7
00:00:27,830 --> 00:00:26,310
out there so please take a look and I'm

8
00:00:30,279 --> 00:00:27,840
going to be talking about some

9
00:00:33,620 --> 00:00:30,289
collaborative work I've been doing with

10
00:00:37,100 --> 00:00:33,630
LC city college New York and with

11
00:00:40,910 --> 00:00:37,110
Harvard so one of the major questions

12
00:00:44,030 --> 00:00:40,920
that a lot of people in astrobiology

13
00:00:45,440 --> 00:00:44,040

feel specifically the like when people

14
00:00:48,020 --> 00:00:45,450
are interested in studying the origin of

15
00:00:50,060 --> 00:00:48,030
life are how did the prebiotic building

16
00:00:52,970 --> 00:00:50,070
blocks form and from the warm up talk

17
00:00:54,590 --> 00:00:52,980
earlier we see that yeah it's very

18
00:00:56,779 --> 00:00:54,600
interesting to think about how Mino

19
00:00:59,180 --> 00:00:56,789
acids nucleotides or lipids form and

20
00:01:01,400 --> 00:00:59,190
more specifically how did these building

21
00:01:03,110 --> 00:01:01,410
blocks specifically polymerize or

22
00:01:05,810 --> 00:01:03,120
assemble into something larger and

23
00:01:09,469 --> 00:01:05,820
useful so peptides of proteins nucleic

24
00:01:12,230 --> 00:01:09,479
acids or vesicles and specifically I'm

25
00:01:16,249 --> 00:01:12,240
very interested in amino acids and

26
00:01:18,590 --> 00:01:16,259
peptides and on the early Earth there

27
00:01:21,230 --> 00:01:18,600
have been many or it's been shown that

28
00:01:22,910 --> 00:01:21,240
there are many possibilities for the

29
00:01:26,620 --> 00:01:22,920
emergence of amino acids and peptides

30
00:01:29,420 --> 00:01:26,630
for example extraterrestrial objects or

31
00:01:32,440 --> 00:01:29,430
atmospheric discharge or hydrothermal

32
00:01:35,660 --> 00:01:32,450
vents they can produce amino acids and

33
00:01:37,789 --> 00:01:35,670
volcanic gases or mineral surfaces can

34
00:01:41,240 --> 00:01:37,799
help to catalyze the conjugation of

35
00:01:45,410 --> 00:01:41,250
these amino acids into peptides longer

36
00:01:47,780 --> 00:01:45,420
amino acid containing chains and some

37
00:01:52,130 --> 00:01:47,790
recent work has also suggested that it's

38
00:01:54,350 --> 00:01:52,140

possible that amino acids nucleotides

39
00:01:56,660 --> 00:01:54,360
and lipid precursors could have been

40
00:01:59,420 --> 00:01:56,670
present all together on the early Earth

41
00:02:02,649 --> 00:01:59,430
which suggests that not only should we

42
00:02:06,050 --> 00:02:02,659
study how each of these classes of

43
00:02:09,469 --> 00:02:06,060
molecules emerges and interacts within

44
00:02:11,240 --> 00:02:09,479
their own population but also how these

45
00:02:12,259 --> 00:02:11,250
different polymers interact with each

46
00:02:15,380 --> 00:02:12,269
other

47
00:02:18,430 --> 00:02:15,390
one interesting system that's been

48
00:02:22,089 --> 00:02:18,440
studied previously is the formation of

49
00:02:26,000 --> 00:02:22,099
coacervate switch our face separated

50
00:02:28,430 --> 00:02:26,010
species that form from the interaction

51
00:02:29,839 --> 00:02:28,440
of two oppositely charged polymers and

52
00:02:31,100 --> 00:02:29,849
if there's a poster earlier on

53
00:02:33,229 --> 00:02:31,110
codemaster base I think there might be

54
00:02:35,180 --> 00:02:33,239
another one tomorrow so interesting

55
00:02:38,270 --> 00:02:35,190
stuff and essentially one of these

56
00:02:40,789 --> 00:02:38,280
coacervate switch are what this one

57
00:02:43,910 --> 00:02:40,799
specifically is produced from mixing ATP

58
00:02:48,680 --> 00:02:43,920
and poly lysine which is a cationic

59
00:02:51,229 --> 00:02:48,690
peptide forms these segregated globules

60
00:02:56,809 --> 00:02:51,239
that actually segregate and concentrate

61
00:02:59,270 --> 00:02:56,819
RNA so here we see the localization of a

62
00:03:04,100 --> 00:02:59,280
fluorescently labeled RNA into specific

63
00:03:06,589 --> 00:03:04,110

globules in this system but so one of

64
00:03:10,339 --> 00:03:06,599
the things that about the system that is

65
00:03:13,190 --> 00:03:10,349
kind of iffy is the requirement for a

66
00:03:15,770 --> 00:03:13,200
reasonably long peptide chain which on

67
00:03:18,470 --> 00:03:15,780
the prebiotic earth it's you know way

68
00:03:20,420 --> 00:03:18,480
more likely for a smaller polymer to

69
00:03:24,170 --> 00:03:20,430
have existed and conjugated rather than

70
00:03:26,210 --> 00:03:24,180
a longer polymer so this begs the

71
00:03:31,220 --> 00:03:26,220
question now can we utilize smaller

72
00:03:35,809 --> 00:03:31,230
peptides to self-assemble into longer

73
00:03:41,229 --> 00:03:35,819
structures that have similar activities

74
00:03:45,259 --> 00:03:41,239
and similar uses as longer their

75
00:03:46,940 --> 00:03:45,269
original longer peptides so specifically

76
00:03:49,550 --> 00:03:46,950
I'm interested in seeing if we can use

77
00:03:52,729 --> 00:03:49,560
shorter peptides to self-assemble into

78
00:03:56,809 --> 00:03:52,739
perhaps of binding or scaffolding system

79
00:03:59,809 --> 00:03:56,819
for early nucleic acids DNA or RNA the

80
00:04:03,289 --> 00:03:59,819
small peptide self-assembly field was

81
00:04:05,360 --> 00:04:03,299
pioneered maybe fifteen years ago in Tel

82
00:04:08,000 --> 00:04:05,370
Aviv and they actually started from this

83
00:04:10,990 --> 00:04:08,010
peptide which is the beta-amyloid

84
00:04:13,900 --> 00:04:11,000
peptide and

85
00:04:17,229 --> 00:04:13,910
they took two of the amino acids from

86
00:04:20,380 --> 00:04:17,239
this peptide and were able to isolate it

87
00:04:23,890 --> 00:04:20,390
and grow these nano tubular structures

88
00:04:28,270 --> 00:04:23,900

so from just the simple molecule which

89
00:04:30,930 --> 00:04:28,280
is very hydrophobic it forms it's very

90
00:04:32,130 --> 00:04:30,940
favored to form these large

91
00:04:35,920 --> 00:04:32,140
self-assembled

92
00:04:39,460 --> 00:04:35,930
products so what I was interested in

93
00:04:42,670 --> 00:04:39,470
seeing if this could be done was if we

94
00:04:45,880 --> 00:04:42,680
had some mixture of dipeptides

95
00:04:50,680 --> 00:04:45,890
tripeptides and maybe some RNA if these

96
00:04:53,110 --> 00:04:50,690
peptides could by assemble into some

97
00:04:56,110 --> 00:04:53,120
type of fibrillar structure that RNA or

98
00:05:00,720 --> 00:04:56,120
DNA could bind to so in collaboration

99
00:05:02,560 --> 00:05:00,730
with a lab at City College in New York

100
00:05:05,170 --> 00:05:02,570
previously they developed a

101
00:05:08,530 --> 00:05:05,180
computational system to calculate the

102
00:05:12,640 --> 00:05:08,540
aggregation propensity of all 8,000 try

103
00:05:16,990 --> 00:05:12,650
peptides and so there are 20 amino acids

104
00:05:19,090 --> 00:05:17,000
that are present on today's earth that

105
00:05:21,790 --> 00:05:19,100
are created biologically there are

106
00:05:25,570 --> 00:05:21,800
others abiotic ones but we'll just stick

107
00:05:27,250 --> 00:05:25,580
with the 20 biotic amino acids and so

108
00:05:29,890 --> 00:05:27,260
from here basically they're able to

109
00:05:33,970 --> 00:05:29,900
probe all 8,000 tri peptide sequences

110
00:05:37,150 --> 00:05:33,980
and so for example you'd read the first

111
00:05:39,130 --> 00:05:37,160
sequence on the x-axis the second letter

112
00:05:43,180 --> 00:05:39,140
on the y-axis and then within each box

113
00:05:46,570 --> 00:05:43,190

you'd pick the third amino acid and each

114
00:05:49,330 --> 00:05:46,580
box is colored it goes from very light

115
00:05:52,510 --> 00:05:49,340
to very dark and so the darker the spot

116
00:05:56,580 --> 00:05:52,520
the greater propensity for that specific

117
00:06:03,070 --> 00:05:59,469
self-assembled structure from this study

118
00:06:06,100 --> 00:06:03,080
we chose six specific peptides to prou

119
00:06:09,630 --> 00:06:06,110
RNA binding character each of these

120
00:06:13,630 --> 00:06:09,640
peptides contains either two large

121
00:06:16,330 --> 00:06:13,640
hydrophobic groups or smaller aliphatic

122
00:06:18,940 --> 00:06:16,340
groups and each one also specifically

123
00:06:22,000 --> 00:06:18,950
contains a charged amino acid in the

124
00:06:23,879 --> 00:06:22,010
first position so that RNA or DNA which

125
00:06:26,909 --> 00:06:23,889
has a negatively charged backbone

126
00:06:30,110 --> 00:06:26,919
and bind to something that's positively

127
00:06:35,249 --> 00:06:30,120
charged when theoretically these fibers

128
00:06:37,969 --> 00:06:35,259
assemble so we well we took these

129
00:06:41,040 --> 00:06:37,979
structures and first of all studied the

130
00:06:42,689 --> 00:06:41,050
aggregation propensity of these

131
00:06:45,570 --> 00:06:42,699
structures alone and from these

132
00:06:48,119 --> 00:06:45,580
microscope images we can see a kind of

133
00:06:51,360 --> 00:06:48,129
variable character for example two of

134
00:06:53,070 --> 00:06:51,370
these tripeptides don't really form any

135
00:06:57,689 --> 00:06:53,080
fibrillar structure they form some

136
00:06:59,580 --> 00:06:57,699
strange spherical structure the ry f

137
00:07:02,640 --> 00:06:59,590
tripeptide forms these needle-like

138
00:07:07,019 --> 00:07:02,650

structures but specifically we found two

139
00:07:09,059 --> 00:07:07,029
tripeptides kyf and rff that assemble

140
00:07:12,390 --> 00:07:09,069
into these long fibrillar structures

141
00:07:14,100 --> 00:07:12,400
that are fairly dense and we can see

142
00:07:16,679 --> 00:07:14,110
here that some of these structures are

143
00:07:20,159 --> 00:07:16,689
actually fairly thick as well so these

144
00:07:24,300 --> 00:07:20,169
two tripeptides became reasonable

145
00:07:26,879 --> 00:07:24,310
candidates to test for binding of RNA so

146
00:07:30,059 --> 00:07:26,889
the next thing that we tested was we

147
00:07:32,550 --> 00:07:30,069
actually introduced a fluorescent

148
00:07:35,399 --> 00:07:32,560
labeled RNA into one of these assembled

149
00:07:36,779 --> 00:07:35,409
tripeptide systems and so you see on the

150
00:07:40,200 --> 00:07:36,789
right here this is a fluorescence

151
00:07:45,209 --> 00:07:40,210
microscope image and it appears that the

152
00:07:49,170 --> 00:07:45,219
fluorescently labeled RNA is assembling

153
00:07:52,170 --> 00:07:49,180
or is localizing to these assembled

154
00:07:55,079 --> 00:07:52,180
fibrillar structures which suggests that

155
00:07:57,540 --> 00:07:55,089
it is interacting with the fibers

156
00:08:01,950 --> 00:07:57,550
themselves preferentially rather than

157
00:08:06,119 --> 00:08:01,960
just staying in the solution similarly

158
00:08:09,600 --> 00:08:06,129
we also observed a slightly a similar

159
00:08:13,409 --> 00:08:09,610
behavior with the rff tripeptide upon

160
00:08:15,510 --> 00:08:13,419
pepti RNA binding it was a little less

161
00:08:18,559 --> 00:08:15,520
apparent and one of the things we

162
00:08:21,570 --> 00:08:18,569
learned about the rff peptide was that

163
00:08:24,570 --> 00:08:21,580

this these structures only formed under

164
00:08:26,700 --> 00:08:24,580
specific conditions in phosphate buffer

165
00:08:29,760 --> 00:08:26,710
which is not very compatible with

166
00:08:32,159 --> 00:08:29,770
magnesium which is used in a lot of RNA

167
00:08:34,170 --> 00:08:32,169
and ribosomal reactions so we went

168
00:08:38,130 --> 00:08:34,180
forward and characterized further the

169
00:08:40,470 --> 00:08:38,140
kyf tripeptide and we also found

170
00:08:43,680 --> 00:08:40,480
that not only does single-stranded RNA

171
00:08:46,020 --> 00:08:43,690
bind to these fibrillar structures but

172
00:08:48,450 --> 00:08:46,030
also double-stranded RNA a different

173
00:08:51,810 --> 00:08:48,460
length of single-stranded RNA as well as

174
00:08:56,570 --> 00:08:51,820
single-stranded DNA and so it can bind

175
00:09:00,390 --> 00:08:56,580
to many different types of nucleic acids

176
00:09:04,500 --> 00:09:00,400
actually might just work here yeah so

177
00:09:08,520 --> 00:09:04,510
here now is something interesting that

178
00:09:11,700 --> 00:09:08,530
came out from this study in that now

179
00:09:15,150 --> 00:09:11,710
that we know that these fluorescently

180
00:09:20,760 --> 00:09:15,160
labeled RNA are apparently binding to

181
00:09:24,570 --> 00:09:20,770
the assembled fibril structures we

182
00:09:27,120 --> 00:09:24,580
thought oh can we use this RNA molecule

183
00:09:30,930 --> 00:09:27,130
this fluorescence now to probe the

184
00:09:33,900 --> 00:09:30,940
dynamics of the fibrils themselves so

185
00:09:36,390 --> 00:09:33,910
here this image or this movie we're

186
00:09:41,790 --> 00:09:36,400
going to be showing it's a time course

187
00:09:44,130 --> 00:09:41,800
of a self-assembling tripeptide fibril

188
00:09:47,760 --> 00:09:44,140

structure with fluorescently labeled RNA

189
00:09:51,720 --> 00:09:47,770
that localizes to these structures so

190
00:09:54,180 --> 00:09:51,730
I'm just going to play this and you can

191
00:09:55,710 --> 00:09:54,190
see over time that there's some dynamic

192
00:09:59,030 --> 00:09:55,720
change going on with these fiber

193
00:10:05,360 --> 00:09:59,040
structures they appear to be growing and

194
00:10:07,620 --> 00:10:05,370
changing over time play that again

195
00:10:11,580 --> 00:10:07,630
of course this raises a bunch of

196
00:10:13,920 --> 00:10:11,590
interesting questions like why is it

197
00:10:17,010 --> 00:10:13,930
growing from one side is the nucleation

198
00:10:18,810 --> 00:10:17,020
site important what about the substrate

199
00:10:21,180 --> 00:10:18,820
that it's growing on but at the very

200
00:10:23,520 --> 00:10:21,190
least now we've developed a system where

201
00:10:26,340 --> 00:10:23,530
previously the people studying

202
00:10:30,390 --> 00:10:26,350
tripeptide fibril assembly didn't really

203
00:10:32,760 --> 00:10:30,400
consider studying really specifically

204
00:10:35,760 --> 00:10:32,770
the dynamics of the assembly process

205
00:10:38,970 --> 00:10:35,770
itself but now we have a direct binding

206
00:10:42,330 --> 00:10:38,980
reporter and we can further probe this

207
00:10:45,600 --> 00:10:42,340
system and kind of study interesting

208
00:10:48,179 --> 00:10:45,610
things about it it's pretty nice to look

209
00:10:54,039 --> 00:10:51,160
yeah and so one of the things that I'm

210
00:10:55,900 --> 00:10:54,049
interested in working on next is using a

211
00:10:58,509 --> 00:10:55,910
system that's been developed called

212
00:11:02,109 --> 00:10:58,519
dynamic peptide libraries which actually

213
00:11:05,410 --> 00:11:02,119

you're able to start with a pool of very

214
00:11:07,840 --> 00:11:05,420
diverse small peptides and over time you

215
00:11:10,840 --> 00:11:07,850
can select out those peptides that form

216
00:11:13,329 --> 00:11:10,850
vibrator or other macro structures and

217
00:11:15,669 --> 00:11:13,339
so in that case where we want to try to

218
00:11:18,850 --> 00:11:15,679
find other peptides that have other

219
00:11:21,429 --> 00:11:18,860
interesting assembled structures with

220
00:11:24,939 --> 00:11:21,439
assembled functions for example RNA DNA

221
00:11:28,329 --> 00:11:24,949
binding or even structures that are more

222
00:11:30,519 --> 00:11:28,339
heat stable or that assemble in under

223
00:11:33,989 --> 00:11:30,529
specific you know metal iron conditions

224
00:11:37,900 --> 00:11:33,999
and also different mineral surfaces

225
00:11:40,900 --> 00:11:37,910
scaffolded by different different things

226
00:11:43,449 --> 00:11:40,910
and also finally to see if the

227
00:11:46,840 --> 00:11:43,459
localization of RNA onto these fibrils

228
00:11:49,989 --> 00:11:46,850
can somehow affect evolution of RNA or

229
00:11:52,119 --> 00:11:49,999
even template its polymerization so I'd

230
00:11:54,879 --> 00:11:52,129
like to thank my collaborators at

231
00:11:57,429 --> 00:11:54,889
Harvard at City College New York and

232
00:12:00,039 --> 00:11:57,439
University of Strathclyde and at growing

233
00:12:02,710 --> 00:12:00,049
again in the Netherlands and also this

234
00:12:05,650 --> 00:12:02,720
is my home Institute LC I have some

235
00:12:09,729 --> 00:12:05,660
funding support from LC origins network

236
00:12:11,799 --> 00:12:09,739
Eon and Tokyo Tech and so I have to plug

237
00:12:14,829 --> 00:12:11,809
this now if you want to know more about

238
00:12:17,859 --> 00:12:14,839

LC please come talk to me so every year

239
00:12:19,239 --> 00:12:17,869
we have a symposium in January the this

240
00:12:21,369 --> 00:12:19,249
following January there's going to be a

241
00:12:23,470 --> 00:12:21,379
winter school which is a two-week

242
00:12:25,919 --> 00:12:23,480
hands-on course that will be really cool

243
00:12:28,600 --> 00:12:25,929
and year round there's workshops and

244
00:12:31,090 --> 00:12:28,610
they're always hiring so if you're

245
00:12:33,579 --> 00:12:31,100
interested in doing a postdoc over at LC

246
00:12:35,710 --> 00:12:33,589
there's information out there or also

247
00:12:37,059 --> 00:12:35,720
come please please come talk to me so

248
00:12:39,210 --> 00:12:37,069
thank you very much for all your time

249
00:12:50,180 --> 00:12:39,220
happy to take questions

250
00:12:56,580 --> 00:12:53,670
questions about your movie uh mostly was

251
00:12:58,140 --> 00:12:56,590
it come focal microscopy secondly how

252
00:13:00,270 --> 00:12:58,150
thick is the structure that's going and

253
00:13:02,070 --> 00:13:00,280
is it an artifact of the imaging that

254
00:13:06,570 --> 00:13:02,080
everything looks like parallel to the

255
00:13:17,400 --> 00:13:06,580
glass surface so this is a confocal

256
00:13:21,990 --> 00:13:17,410
microscope image second question I'm not

257
00:13:24,270 --> 00:13:22,000
sure but in a 3d in a tube structure the

258
00:13:27,960 --> 00:13:24,280
entire structure forms a gel-like state

259
00:13:29,670 --> 00:13:27,970
so it can it should be very large three

260
00:13:39,240 --> 00:13:29,680
dimensionally it could be and third

261
00:13:44,620 --> 00:13:42,790
um I don't know the answer to that and

262
00:13:46,720 --> 00:13:44,630
we're actually right now probing also

263
00:13:49,710 --> 00:13:46,730

like whether different substrates have

264
00:13:56,310 --> 00:13:49,720
some effect on the assembly properties

265
00:14:00,580 --> 00:13:56,320
um I have a question about from the

266
00:14:02,830 --> 00:14:00,590
paper published by your collaborator the

267
00:14:07,000 --> 00:14:02,840
Nature Chemistry paper in which they has

268
00:14:11,980 --> 00:14:07,010
the yeah this exact one so it seems like

269
00:14:14,370 --> 00:14:11,990
um tryptophan rich tripeptides have the

270
00:14:16,120 --> 00:14:14,380
highest propensity for forming the

271
00:14:18,460 --> 00:14:16,130
self-assemble structure because it's

272
00:14:24,250 --> 00:14:18,470
like the w w is like all the way down

273
00:14:28,960 --> 00:14:24,260
the in the left lower left-hand side and

274
00:14:32,470 --> 00:14:28,970
i was wondering why the try peptide that

275
00:14:36,640 --> 00:14:32,480
you studied don't have any trip to vent

276
00:14:41,380 --> 00:14:36,650
um yeah so these were a smattering of

277
00:14:43,240 --> 00:14:41,390
different candidates we would like I

278
00:14:46,030 --> 00:14:43,250
would like to test all of them but that

279
00:14:47,830 --> 00:14:46,040
wasn't possible and also from previous

280
00:14:49,900 --> 00:14:47,840
studies that they've done there are a

281
00:14:52,210 --> 00:14:49,910
lot of solubility issues with many of

282
00:14:54,010 --> 00:14:52,220
these really hydrophobic peptides so we

283
00:14:55,930 --> 00:14:54,020
also wanted to make sure that the

284
00:14:57,400 --> 00:14:55,940
peptides we were working with could

285
00:15:03,970 --> 00:14:57,410
actually be analyzed in some

286
00:15:05,770 --> 00:15:03,980
constructive way hey nice talk I had a

287
00:15:07,450 --> 00:15:05,780
question about the composition of the

288
00:15:10,260 --> 00:15:07,460

fibers themselves and how well you guys

289
00:15:12,820 --> 00:15:10,270
understand what those actually are and

290
00:15:14,590 --> 00:15:12,830
how thick they are for instance if are

291
00:15:16,420 --> 00:15:14,600
they single fibers or they double fibers

292
00:15:19,300 --> 00:15:16,430
or do an idea

293
00:15:22,870 --> 00:15:19,310
um I don't specifically know a lot about

294
00:15:25,120 --> 00:15:22,880
this but I'm sure that the people in the

295
00:15:26,650 --> 00:15:25,130
lab in the U n lab at New York there are

296
00:15:30,220 --> 00:15:26,660
some people that are certainly studying

297
00:15:32,590 --> 00:15:30,230
this and they probably have a much

298
00:15:34,890 --> 00:15:32,600
better idea than I would have a guess

299
00:15:37,930 --> 00:15:34,900
it seems so it seems like the fibers are

300
00:15:40,020 --> 00:15:37,940
consistent between the different runs

301
00:15:43,450 --> 00:15:40,030
that you used to create them for

302
00:15:45,290 --> 00:15:43,460
specific conditions generally yes

303
00:15:47,420 --> 00:15:45,300
they're very highly conditioned

304
00:15:51,949 --> 00:15:47,430
dependent for example changing the

305
00:15:55,880 --> 00:15:51,959
buffer system could lead to no growth or

306
00:15:57,710 --> 00:15:55,890
like much denser growth okay thanks um

307
00:15:59,090 --> 00:15:57,720
and sort of following on that I have

308
00:16:00,949 --> 00:15:59,100
another question about the the fibril

309
00:16:02,540 --> 00:16:00,959
formation there have been some

310
00:16:05,120 --> 00:16:02,550
suggestions in the literature that just

311
00:16:07,160 --> 00:16:05,130
phenylalanine amino acids themselves can

312
00:16:08,180 --> 00:16:07,170
make fibrils so I was wondering what

313
00:16:09,650 --> 00:16:08,190

would the rationale for picking

314
00:16:11,750 --> 00:16:09,660
tripeptides was and whether you think

315
00:16:14,990 --> 00:16:11,760
some of this might happen with with just

316
00:16:16,819 --> 00:16:15,000
single or double amino yeah um yeah it

317
00:16:19,009 --> 00:16:16,829
would be really interesting if single or

318
00:16:22,100 --> 00:16:19,019
double if like we could study more about

319
00:16:25,130 --> 00:16:22,110
these like single amino acid diet I

320
00:16:26,900 --> 00:16:25,140
peptide assemblies

321
00:16:28,910 --> 00:16:26,910
I guess specifically for this study we

322
00:16:30,530 --> 00:16:28,920
we just wanted to make sure to include a

323
00:16:32,240 --> 00:16:30,540
cationic group because we were looking

324
00:16:34,699 --> 00:16:32,250
for RNA binding but if you're looking

325
00:16:36,560 --> 00:16:34,709
for something else like formation of a

326
00:16:38,030 --> 00:16:36,570
gel state for whatever reason to prevent

327
00:16:41,870 --> 00:16:38,040
diffusion or something you might be able

328
00:16:44,180 --> 00:16:41,880
to select out a single peptide single

329
00:16:46,940 --> 00:16:44,190
amino acid or die peptide and so this

330
00:16:49,730 --> 00:16:46,950
dynamic peptide library technique that's

331
00:16:50,720 --> 00:16:49,740
been developed they've they're able to

332
00:16:52,850 --> 00:16:50,730
you're able to start with a lot of

333
00:16:58,850 --> 00:16:52,860
different components and select out

334
00:17:00,480 --> 00:16:58,860
something that you want so cool alright

335
00:17:03,830 --> 00:17:00,490
thank you very much thank you