1
00:00:04,470 --> 00:00:02,310
during this presentation i will be

2
00:00:06,630 --> 00:00:04,480
talking about the possibility for

3
00:00:08,390 --> 00:00:06,640
spontaneous peptide bond formation at

4
00:00:10,470 --> 00:00:08,400
the water surface

5
00:00:13,270 --> 00:00:10,480
specifically i'm interested in this type

6
00:00:15,589 --> 00:00:13,280
of chemistry for its potential relevance

7
00:00:16,710 --> 00:00:15,599
to prebiotic chemistry and the origins

8
00:00:18,550 --> 00:00:16,720
of life

9
00:00:21,029 --> 00:00:18,560
i've put my email here on this first

10
00:00:23,349 --> 00:00:21,039
slide please feel free to email me with

11
00:00:26,710 --> 00:00:23,359
any questions or just to follow up and

12
00:00:28,390 --> 00:00:26,720
see where this research has gone

13
00:00:30,390 --> 00:00:28,400

to begin i want to share the three

14
00:00:31,429 --> 00:00:30,400
assumptions that we make about prebiotic

15
00:00:33,270 --> 00:00:31,439
earth

16
00:00:34,630 --> 00:00:33,280
first we assume that liquid water would

17
00:00:36,790 --> 00:00:34,640
have been present

18
00:00:39,030 --> 00:00:36,800
second we assume that the small monomers

19
00:00:40,869 --> 00:00:39,040
necessary for the formation of life

20
00:00:42,150 --> 00:00:40,879
including amino acids would have been

21
00:00:44,950 --> 00:00:42,160
present

22
00:00:46,229 --> 00:00:44,960
and third we assume that at least to

23
00:00:48,630 --> 00:00:46,239
some degree

24
00:00:51,110 --> 00:00:48,640
these small monomers would have been in

25
00:00:52,869 --> 00:00:51,120
the liquid water

26
00:00:55,270 --> 00:00:52,879
one of the questions that we have

27
00:00:56,709 --> 00:00:55,280
however about the origins of life is how

28
00:00:58,950 --> 00:00:56,719
we would have gone

29
00:01:01,670 --> 00:00:58,960
from these simple monomers to the more

30
00:01:02,950 --> 00:01:01,680
complex oligomers and biopolymers that

31
00:01:05,350 --> 00:01:02,960
would have been necessary for the

32
00:01:07,030 --> 00:01:05,360
origins of life

33
00:01:09,190 --> 00:01:07,040
as i mentioned earlier the small

34
00:01:11,270 --> 00:01:09,200
monomers present on early earth likely

35
00:01:14,550 --> 00:01:11,280
would have been in the liquid water of

36
00:01:16,789 --> 00:01:14,560
the earth this is really problematic for

37
00:01:18,630 --> 00:01:16,799
condensation chemistries like i've drawn

38
00:01:19,910 --> 00:01:18,640

here where you have a monomer a and

39
00:01:22,070 --> 00:01:19,920
monomer b

40
00:01:24,789 --> 00:01:22,080
combining to form some sort of larger

41
00:01:26,550 --> 00:01:24,799
more complex molecule a b

42
00:01:28,870 --> 00:01:26,560
and the reason that this is

43
00:01:30,390 --> 00:01:28,880
prohibitive to this type of chemistry is

44
00:01:32,870 --> 00:01:30,400
that when

45
00:01:35,749 --> 00:01:32,880
these two monomers combine

46
00:01:37,190 --> 00:01:35,759
very often they also eliminate a water

47
00:01:39,910 --> 00:01:37,200
molecule now

48
00:01:42,950 --> 00:01:39,920
eliminating a water molecule into bulk

49
00:01:44,469 --> 00:01:42,960
water is thermodynamically prohibitive

50
00:01:47,030 --> 00:01:44,479
meaning that a lot of these types of

51
00:01:49,270 --> 00:01:47,040
chemistries would have had difficulties

52
00:01:51,429 --> 00:01:49,280
occurring without some sort of

53
00:01:52,789 --> 00:01:51,439
help so in modern biology of course we

54
00:01:55,990 --> 00:01:52,799
have enzymes but that would not have

55
00:01:57,830 --> 00:01:56,000
been present on early earth

56
00:02:00,389 --> 00:01:57,840
peptide bond formation as i will be

57
00:02:01,990 --> 00:02:00,399
talking about today is a great example

58
00:02:04,469 --> 00:02:02,000
of one of these types of chemistries

59
00:02:07,270 --> 00:02:04,479
that is thermodynamically unfavorable in

60
00:02:09,669 --> 00:02:07,280
bulk water so as i've drawn here

61
00:02:12,790 --> 00:02:09,679
two amino acid monomers combining to

62
00:02:14,949 --> 00:02:12,800
make a peptide releases water

63
00:02:17,430 --> 00:02:14,959

this reaction has a small equilibrium

64
00:02:19,190 --> 00:02:17,440
constant in bulk solution as depicted by

65
00:02:22,070 --> 00:02:19,200
the arrows in the middle

66
00:02:23,830 --> 00:02:22,080
so as shown by the big arrow on top it

67
00:02:25,510 --> 00:02:23,840
is much more likely that these amino

68
00:02:27,510 --> 00:02:25,520
acids would stay as their individual

69
00:02:29,510 --> 00:02:27,520
monomer form

70
00:02:31,509 --> 00:02:29,520
however there's a very interesting

71
00:02:33,430 --> 00:02:31,519
emerging body of research that shows

72
00:02:34,390 --> 00:02:33,440
chemistries that are prohibited in bulk

73
00:02:38,309 --> 00:02:34,400
water

74
00:02:40,150 --> 00:02:38,319
interface

75
00:02:42,309 --> 00:02:40,160
first i want to mention that many

76
00:02:44,630 --> 00:02:42,319
organic molecules are found at the water

77
00:02:46,869 --> 00:02:44,640
surface and this does include even the

78
00:02:49,670 --> 00:02:46,879
small amino acids that are necessary for

79
00:02:51,830 --> 00:02:49,680
peptide bond formation

80
00:02:54,390 --> 00:02:51,840
at the air water interface

81
00:02:56,070 --> 00:02:54,400
molecules are in contact with bulk water

82
00:02:58,309 --> 00:02:56,080
but they are also in contact with the

83
00:03:01,430 --> 00:02:58,319
vapor phase where the concentration of

84
00:03:03,270 --> 00:03:01,440
water would be much lower

85
00:03:05,270 --> 00:03:03,280
this makes it much more likely that

86
00:03:07,430 --> 00:03:05,280
condensation reactions

87
00:03:09,509 --> 00:03:07,440
can easily eliminate water molecules

88
00:03:11,509 --> 00:03:09,519

into the vapor phase and makes the air

89
00:03:14,550 --> 00:03:11,519
water interface a very interesting

90
00:03:16,790 --> 00:03:14,560
environment for peptide bond formation

91
00:03:19,270 --> 00:03:16,800
in fact our group released a study in

92
00:03:21,589 --> 00:03:19,280
2012 that did show that peptide bond

93
00:03:23,110 --> 00:03:21,599
formation can occur spontaneously at the

94
00:03:25,750 --> 00:03:23,120
water interface

95
00:03:27,670 --> 00:03:25,760
when using activated amino acid esters

96
00:03:30,390 --> 00:03:27,680
and a transition metal

97
00:03:32,229 --> 00:03:30,400
so first the amino acid esters formal

98
00:03:33,830 --> 00:03:32,239
complex with the transition metal at the

99
00:03:37,190 --> 00:03:33,840
water interface

100
00:03:39,350 --> 00:03:37,200
this aligns the amino acids in a way

101
00:03:41,509 --> 00:03:39,360
that is favorable for

102
00:03:43,430 --> 00:03:41,519
peptide bond formation

103
00:03:46,070 --> 00:03:43,440
an ethanol molecule is subsequently

104
00:03:48,869 --> 00:03:46,080
released and then the dipeptide shown on

105
00:03:52,390 --> 00:03:48,879
the right is formed and with the new

106
00:03:54,550 --> 00:03:52,400
peptide bond as i've circled

107
00:03:56,630 --> 00:03:54,560
this study used the surface-specific

108
00:03:59,429 --> 00:03:56,640
technique infrared reflection absorption

109
00:04:01,670 --> 00:03:59,439
spectroscopy also known as iris

110
00:04:03,429 --> 00:04:01,680
iris works by reflecting light off of

111
00:04:05,830 --> 00:04:03,439
the water surface and obtaining a

112
00:04:07,429 --> 00:04:05,840
reflection absorption spectrum

113
00:04:09,030 --> 00:04:07,439

these spectra are very similar to

114
00:04:11,190 --> 00:04:09,040
vibrational spectra that you might have

115
00:04:12,789 --> 00:04:11,200
seen in the gas phase

116
00:04:14,470 --> 00:04:12,799
however they give us structural

117
00:04:18,629 --> 00:04:14,480
information for molecules that

118
00:04:20,469 --> 00:04:18,639
specifically sit at the water surface

119
00:04:21,430 --> 00:04:20,479
here i'm showing the results from this

120
00:04:23,990 --> 00:04:21,440
study

121
00:04:26,710 --> 00:04:24,000
in box a is the iris spectrum for the

122
00:04:28,790 --> 00:04:26,720
transition metal complex and in box b is

123
00:04:30,629 --> 00:04:28,800
the spectrum of the water surface after

124
00:04:32,550 --> 00:04:30,639
the solution has been allowed to sit on

125
00:04:34,310 --> 00:04:32,560
the trough overnight

126
00:04:37,110 --> 00:04:34,320
specifically i'd like to point out this

127
00:04:39,749 --> 00:04:37,120
red dash line which corresponds to a new

128
00:04:42,629 --> 00:04:39,759
peak that grew in overnight

129
00:04:45,189 --> 00:04:42,639
this peak corresponds to the amide one

130
00:04:46,710 --> 00:04:45,199
band of a peptide bond so on the right

131
00:04:49,189 --> 00:04:46,720
i'm showing you the molecule that we

132
00:04:51,110 --> 00:04:49,199
believe was produced and i've circled

133
00:04:52,790 --> 00:04:51,120
the specific bond that we're detecting

134
00:04:54,550 --> 00:04:52,800
with this new p

135
00:04:56,230 --> 00:04:54,560
while this study is exciting as it

136
00:04:58,310 --> 00:04:56,240
showed spontaneous peptide bond

137
00:05:01,110 --> 00:04:58,320
formation at the water surface

138
00:05:02,870 --> 00:05:01,120

it did use activated amino acids

139
00:05:05,029 --> 00:05:02,880
so now the question is can the water

140
00:05:09,590 --> 00:05:05,039
surface promote peptide bond formation

141
00:05:13,350 --> 00:05:11,510
as many of you will be aware there have

142
00:05:15,670 --> 00:05:13,360
been many interesting studies coming out

143
00:05:17,670 --> 00:05:15,680
of the georgia pec group recently

144
00:05:19,909 --> 00:05:17,680
specifically i'd like to discuss this

145
00:05:21,670 --> 00:05:19,919
one by forsyth at all that came out in

146
00:05:24,790 --> 00:05:21,680
2015

147
00:05:27,430 --> 00:05:24,800
so they used mixtures of

148
00:05:30,310 --> 00:05:27,440
lactic acid and various amino acids and

149
00:05:31,430 --> 00:05:30,320
they found that by wet dry cycling these

150
00:05:35,590 --> 00:05:31,440
mixtures

151
00:05:40,790 --> 00:05:37,430
as you can see in this graph

152
00:05:43,350 --> 00:05:40,800
after just one cycle they already saw

153
00:05:45,590 --> 00:05:43,360
some mi bond yield and with subsequent

154
00:05:48,950 --> 00:05:45,600
cycling they see more and more percent

155
00:05:53,830 --> 00:05:50,629
they proposed that this happens by a

156
00:05:57,029 --> 00:05:53,840
two-step mechanism first the lactic acid

157
00:05:58,870 --> 00:05:57,039
monomers oligomerized to form an ester

158
00:06:01,029 --> 00:05:58,880
and then the trailing lactic acid

159
00:06:02,469 --> 00:06:01,039
monomer is replaced by an amino acid

160
00:06:05,350 --> 00:06:02,479
monomer

161
00:06:08,230 --> 00:06:05,360
this forms what's called a pepsi peptide

162
00:06:10,390 --> 00:06:08,240
and interestingly as cycling continues

163
00:06:12,469 --> 00:06:10,400

the amino acids will continue to add to

164
00:06:14,870 --> 00:06:12,479
the end of the chain forming longer and

165
00:06:16,710 --> 00:06:14,880
longer peptides

166
00:06:18,629 --> 00:06:16,720
this is particularly interesting in

167
00:06:21,110 --> 00:06:18,639
light of a study that we released

168
00:06:24,550 --> 00:06:21,120
earlier this year this study was looking

169
00:06:27,350 --> 00:06:24,560
at solutions of pyruvic acid however we

170
00:06:29,749 --> 00:06:27,360
noticed that pyruvic acid seemed to be

171
00:06:31,189 --> 00:06:29,759
spontaneously forming lactic acid at the

172
00:06:33,350 --> 00:06:31,199
water surface

173
00:06:36,070 --> 00:06:33,360
and then those lactic acid monomers

174
00:06:37,830 --> 00:06:36,080
appear to be forming lactic acid

175
00:06:42,150 --> 00:06:37,840
oligomers

176
00:06:46,550 --> 00:06:44,070
this study was performed in a languare

177
00:06:49,029 --> 00:06:46,560
trough which maximizes the surface area

178
00:06:51,110 --> 00:06:49,039
to volume ratio of the solution

179
00:06:53,189 --> 00:06:51,120
and a blodget attachment which allows us

180
00:06:54,790 --> 00:06:53,199
to collect molecules specifically from

181
00:06:56,790 --> 00:06:54,800
the surface

182
00:06:58,950 --> 00:06:56,800
whenever surface molecules are collected

183
00:07:00,550 --> 00:06:58,960
we simultaneously collect molecules from

184
00:07:04,309 --> 00:07:00,560
the bulk solution

185
00:07:07,189 --> 00:07:04,319
and then both surface and bulk samples

186
00:07:09,430 --> 00:07:07,199
are run through esi mass spectrometry to

187
00:07:12,790 --> 00:07:09,440
identify the species present

188
00:07:18,309 --> 00:07:14,550

here i'm showing some of the results

189
00:07:21,589 --> 00:07:18,319
from this study in red are the bulk

190
00:07:23,990 --> 00:07:21,599
results and in blue are the

191
00:07:25,749 --> 00:07:24,000
surface results and the darker color is

192
00:07:27,270 --> 00:07:25,759
after three hours of the solution

193
00:07:29,909 --> 00:07:27,280
sitting on the trough and the lighter

194
00:07:33,270 --> 00:07:29,919
color is immediately after the solution

195
00:07:38,950 --> 00:07:36,070
this peak in particular is interesting

196
00:07:41,029 --> 00:07:38,960
as the mass to charge ratio corresponds

197
00:07:43,189 --> 00:07:41,039
to a molecule that could be formed by

198
00:07:45,029 --> 00:07:43,199
two lactic acids combining

199
00:07:47,189 --> 00:07:45,039
and releasing a water molecule so

200
00:07:49,909 --> 00:07:47,199
potentially this peak corresponds to the

201
00:07:51,909 --> 00:07:49,919
esters that we may need to form depth

202
00:07:53,589 --> 00:07:51,919
peptides

203
00:07:54,629 --> 00:07:53,599
to summarize everything that i've just

204
00:07:56,309 --> 00:07:54,639
talked about

205
00:07:58,230 --> 00:07:56,319
we know that the water surface can

206
00:08:00,469 --> 00:07:58,240
promote peptide bond formation under

207
00:08:02,950 --> 00:08:00,479
certain circumstances

208
00:08:05,749 --> 00:08:02,960
we know that wet dry cycling of lactic

209
00:08:07,110 --> 00:08:05,759
acid amino acid mixtures forms depth c

210
00:08:09,589 --> 00:08:07,120
peptides

211
00:08:12,629 --> 00:08:09,599
and we know that lactic acid appears to

212
00:08:14,150 --> 00:08:12,639
form esters at the air water interface

213
00:08:16,390 --> 00:08:14,160

combining all of this

214
00:08:18,469 --> 00:08:16,400
it's reasonable to ask well can the

215
00:08:19,589 --> 00:08:18,479
water surface promote deficient

216
00:08:22,790 --> 00:08:19,599
formation

217
00:08:27,189 --> 00:08:22,800
from lactic acid and amino acid mixtures

218
00:08:29,430 --> 00:08:27,199
without the need for wet dry cycling

219
00:08:31,830 --> 00:08:29,440
going forward we plan to study mixtures

220
00:08:34,310 --> 00:08:31,840
of alpha hydroxy acids and amino acids

221
00:08:37,670 --> 00:08:34,320
at the water surface using both our iris

222
00:08:39,670 --> 00:08:37,680
and logic collection techniques

223
00:08:42,230 --> 00:08:39,680
we have also obtained and planned to use

224
00:08:43,909 --> 00:08:42,240
a series of alpha hydroxy acids with

225
00:08:49,269 --> 00:08:43,919
changing tail length

226
00:08:51,750 --> 00:08:49,279
longer molecules more surface active

227
00:08:54,630 --> 00:08:51,760
thereby allowing us to select for

228
00:08:57,110 --> 00:08:54,640
surface specific chemistry

229
00:08:59,670 --> 00:08:57,120
we have been able to obtain ira spectra

230
00:09:02,070 --> 00:08:59,680
of the series of hydroxy acids

231
00:09:03,829 --> 00:09:02,080
both lactic acid and hydroxyactinoic

232
00:09:05,910 --> 00:09:03,839
acid are soluble so they're placed on

233
00:09:08,550 --> 00:09:05,920
the trough in solution

234
00:09:10,550 --> 00:09:08,560
while hydroxy stearic acid is insoluble

235
00:09:12,550 --> 00:09:10,560
so it's placed on top of a clean water

236
00:09:14,710 --> 00:09:12,560
surface by way of chloroform which is

237
00:09:18,949 --> 00:09:14,720
subsequently evaporated leaving a

238
00:09:20,949 --> 00:09:18,959

disordered monolayer of these molecules

239
00:09:22,710 --> 00:09:20,959
here i'm showing the carbonyl section of

240
00:09:24,310 --> 00:09:22,720
the iris spectrum for the series of

241
00:09:27,030 --> 00:09:24,320
hydroxy acids

242
00:09:29,670 --> 00:09:27,040
on top we have lactic acid in black and

243
00:09:31,990 --> 00:09:29,680
then hydroxyoptinoic in blue that

244
00:09:33,829 --> 00:09:32,000
clearly show the carbonyl stretch

245
00:09:35,829 --> 00:09:33,839
on the bottom in green i have hydroxy

246
00:09:37,430 --> 00:09:35,839
stearic acid which does not show the

247
00:09:40,070 --> 00:09:37,440
carbonyl stretch

248
00:09:41,910 --> 00:09:40,080
however given that the

249
00:09:43,030 --> 00:09:41,920
hydrochloric acid is a disordered

250
00:09:44,550 --> 00:09:43,040
monolayer

251
00:09:46,310 --> 00:09:44,560
it is reasonable to assume that there

252
00:09:48,949 --> 00:09:46,320
are fewer molecules

253
00:09:51,430 --> 00:09:48,959
in the sample pathway

254
00:09:54,550 --> 00:09:51,440
so that we may not see the carbonyl

255
00:09:56,790 --> 00:09:54,560
stretch for hydroxy stearic acid

256
00:09:59,190 --> 00:09:56,800
now i'm showing the ch stretch region of

257
00:10:01,269 --> 00:09:59,200
the spectrum for all three molecules the

258
00:10:03,509 --> 00:10:01,279
lactic acid does not show signals in

259
00:10:04,470 --> 00:10:03,519
this region about the hydroxyactinoic

260
00:10:06,470 --> 00:10:04,480
acid

261
00:10:09,750 --> 00:10:06,480
starts to show signal and the hydroxyl

262
00:10:11,509 --> 00:10:09,760
steric acid has quite strong signals

263
00:10:14,630 --> 00:10:11,519

and this makes sense just due to the

264
00:10:16,949 --> 00:10:14,640
shear number of ch stretches that the

265
00:10:20,389 --> 00:10:16,959
hydroxy stearic acid has in comparison

266
00:10:22,870 --> 00:10:20,399
with say lactic acid

267
00:10:24,870 --> 00:10:22,880
additionally we've modified our iris

268
00:10:28,230 --> 00:10:24,880
setup and we've added

269
00:10:30,550 --> 00:10:28,240
a polarizer this polarizer allows us to

270
00:10:33,269 --> 00:10:30,560
get orientation in addition to

271
00:10:36,790 --> 00:10:33,279
structural information

272
00:10:37,829 --> 00:10:36,800
so briefly the s polarized light will

273
00:10:39,990 --> 00:10:37,839
tell us

274
00:10:41,990 --> 00:10:40,000
which bonds are sitting parallel to the

275
00:10:43,990 --> 00:10:42,000
surface and the p-polarized light will

276
00:10:46,870 --> 00:10:44,000
tell us which bonds are sitting

277
00:10:48,949 --> 00:10:46,880
not parallel to the surface

278
00:10:51,190 --> 00:10:48,959
here's a quick depiction of what the

279
00:10:52,870 --> 00:10:51,200
hydroxy stearic acid molecules might

280
00:10:54,870 --> 00:10:52,880
look at the surface we are in a

281
00:10:57,430 --> 00:10:54,880
disordered regime so we would expect

282
00:10:59,350 --> 00:10:57,440
these tails to be quote unquote floppy

283
00:11:02,790 --> 00:10:59,360
and not necessarily

284
00:11:04,550 --> 00:11:02,800
perpendicular to the surface

285
00:11:07,030 --> 00:11:04,560
and this is exactly what we see in the

286
00:11:10,069 --> 00:11:07,040
polarized spectrum for

287
00:11:13,110 --> 00:11:10,079
hydroxy steric acid on top i'm showing

288
00:11:14,710 --> 00:11:13,120

the p polarized light in dark green so

289
00:11:17,190 --> 00:11:14,720
these are the

290
00:11:18,949 --> 00:11:17,200
bonds that are sitting not parallel to

291
00:11:21,590 --> 00:11:18,959
the surface and on the bottom i'm

292
00:11:23,350 --> 00:11:21,600
showing the s-polarized results

293
00:11:24,949 --> 00:11:23,360
which show the bonds that are sitting

294
00:11:25,829 --> 00:11:24,959
parallel to the surface and we have a

295
00:11:28,710 --> 00:11:25,839
mix

296
00:11:31,590 --> 00:11:28,720
which is exactly what we expect for a

297
00:11:34,550 --> 00:11:31,600
disordered monolayer

298
00:11:36,870 --> 00:11:34,560
now that we have been able to obtain the

299
00:11:38,550 --> 00:11:36,880
iris spectra for the hydroxy acids we

300
00:11:41,110 --> 00:11:38,560
will be moving on to

301
00:11:43,269 --> 00:11:41,120
mixtures of hydroxiasis with the amino

302
00:11:44,470 --> 00:11:43,279
acids and looking for pepsi peptide

303
00:11:48,230 --> 00:11:44,480
formation

304
00:11:51,829 --> 00:11:50,230
finally i'd like to acknowledge our

305
00:11:54,949 --> 00:11:51,839
funding sources and the mass

306
00:11:56,790 --> 00:11:54,959
spectrometry facility at cu boulder