Genetics Underlying de novo Origins of Multicellularity

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1
00:00:00,820 --> 00:00:08,980
[Music]

2
00:00:18,260 --> 00:00:12,799
Thank You Candace so Pedro makes the

3
00:00:21,050 --> 00:00:18,270
transition to organizers so how why the

4
00:00:25,330 --> 00:00:21,060
more complex life has evolved over time

5
00:00:28,130 --> 00:00:25,340
back in 1995 - made and thought Mary

6
00:00:30,859 --> 00:00:28,140
proposes this can be can be achieved

7
00:00:33,770 --> 00:00:30,869
through a serious major evolutionary

8
00:00:37,040 --> 00:00:33,780
transitions including the origins of

9
00:00:37,869 --> 00:00:37,050
cells genomes genetic code eukaryotes

10
00:00:40,639 --> 00:00:37,879
sex

11
00:00:42,110 --> 00:00:40,649
multicellularity social groups such as

12
00:00:45,920 --> 00:00:42,120
social insects

13
00:00:49,639 --> 00:00:45,930

among those transitions the origin of

14
00:00:53,930 --> 00:00:49,649
motifs errantly and allows opportunities

15
00:00:57,200 --> 00:00:53,940
for further complexity to evolve and led

16
00:01:02,330 --> 00:00:57,210
to more complex life we see today like

17
00:01:05,410 --> 00:01:02,340
animals and plants across the Tree of

18
00:01:08,750 --> 00:01:05,420
Life our earth multicellularity has

19
00:01:12,859 --> 00:01:08,760
originated independently a number of

20
00:01:16,460 --> 00:01:12,869
times the thing we want to know is that

21
00:01:20,929 --> 00:01:16,470
what our minimum necessary steps that

22
00:01:23,690 --> 00:01:20,939
are required at first usually people do

23
00:01:27,280 --> 00:01:23,700
this by comparing those Modi's thermal

24
00:01:29,840 --> 00:01:27,290
images with their unicellular relatives

25
00:01:31,969 --> 00:01:29,850
but the problem is that those things

26
00:01:35,719 --> 00:01:31,979
happened long time ago and many changes

27
00:01:39,560 --> 00:01:35,729
have occurred in the extant species and

28
00:01:45,289 --> 00:01:39,570
which makes a typical to infer infirmity

29
00:01:48,230 --> 00:01:45,299
happens in the beginning so one of those

30
00:01:50,210 --> 00:01:48,240
multicellular lineages it's green algae

31
00:01:54,020 --> 00:01:50,220
which includes bobasa

32
00:01:57,289 --> 00:01:54,030
LG this group of algae contains species

33
00:02:00,050 --> 00:01:57,299
with different levels of complexity from

34
00:02:01,310 --> 00:02:00,060
unicellular Chlamydomonas to fully

35
00:02:05,120 --> 00:02:01,320
differentiated

36
00:02:09,619 --> 00:02:05,130
Volvox so with this unicellular algae

37
00:02:11,500 --> 00:02:09,629
and how we can replay lights - like tape

38
00:02:12,890 --> 00:02:11,510

to see how mori celerity

39
00:02:18,830 --> 00:02:12,900
originates

40
00:02:21,890 --> 00:02:18,840
in the first place the model species of

41
00:02:26,210 --> 00:02:21,900
the unicellular algae is law

42
00:02:29,530 --> 00:02:26,220
chemita Moniz Ryan hardy I it's a model

43
00:02:33,589 --> 00:02:29,540
system for photosynthesis and motility

44
00:02:36,199 --> 00:02:33,599
their vegetative cells or asexual cells

45
00:02:40,699 --> 00:02:36,209
are haploid and their genome has been

46
00:02:42,979 --> 00:02:40,709
sequenced and annotated which make them

47
00:02:45,619 --> 00:02:42,989
a great system to do evolution

48
00:02:47,390 --> 00:02:45,629
experiment experiment ways so that we

49
00:02:52,699 --> 00:02:47,400
can see how they are phenotypes and

50
00:02:56,119 --> 00:02:52,709
genotypes change in real time among the

51
00:02:59,449 --> 00:02:56,129
possible selective pressures and might

52
00:03:02,119 --> 00:02:59,459
generate multicellularity predation has

53
00:03:05,390 --> 00:03:02,129
long been her has hypothesized as a

54
00:03:08,449 --> 00:03:05,400
major cause for motor celerity because

55
00:03:11,420 --> 00:03:08,459
it favors bigger sites such as groups of

56
00:03:12,289 --> 00:03:11,430
cells over single cells so here's a

57
00:03:16,069 --> 00:03:12,299
picture of

58
00:03:16,789 --> 00:03:16,079
Silius and algae those feed her feelings

59
00:03:19,580 --> 00:03:16,799
ciliates

60
00:03:22,670 --> 00:03:19,590
they are also unitl they can feed on

61
00:03:26,270 --> 00:03:22,680
those single-celled algae however if we

62
00:03:29,030 --> 00:03:26,280
continuously exposing those algae to

63
00:03:32,479 --> 00:03:29,040

ciliates and that will generate the

64
00:03:38,170 --> 00:03:32,489
selective pressure to make them become

65
00:03:44,890 --> 00:03:42,289
so a few years ago my advisor matt and

66
00:03:48,199 --> 00:03:44,900
jacob a graduate student in our lab

67
00:03:50,930 --> 00:03:48,209
disease evolution experiments to say

68
00:03:55,520 --> 00:03:50,940
select four multicellularity using

69
00:03:58,849 --> 00:03:55,530
predators so the experiment was started

70
00:04:01,159 --> 00:03:58,859
with out cross population by making two

71
00:04:04,039 --> 00:04:01,169
different algae strands so we have

72
00:04:06,920 --> 00:04:04,049
genetic diversity in the beginning the

73
00:04:09,229 --> 00:04:06,930
starting population was split into five

74
00:04:11,990 --> 00:04:09,239
experimental probation that were

75
00:04:14,240 --> 00:04:12,000
cultured with predators and three

76
00:04:18,050 --> 00:04:14,250
control populations that were cultured

77
00:04:20,810 --> 00:04:18,060
without predators those cultures were

78
00:04:22,159 --> 00:04:20,820
transferred into fresh media every week

79
00:04:26,570 --> 00:04:22,169
over a year

80
00:04:29,899 --> 00:04:26,580
at the end of the experiment we two of

81
00:04:33,230 --> 00:04:29,909
the experimental populations P 2 and P

82
00:04:36,529 --> 00:04:33,240
five population they involve those multi

83
00:04:41,899 --> 00:04:36,539
cellular structures not observed in any

84
00:04:46,760 --> 00:04:41,909
of the control populations so here's a

85
00:04:50,149 --> 00:04:46,770
time-lapse video over 72 hours of a

86
00:04:52,640 --> 00:04:50,159
unicellular algae strip strength so you

87
00:04:54,709 --> 00:04:52,650
can see that when cells go through cell

88
00:04:58,249 --> 00:04:54,719

division there are some little clumsy

89
00:05:06,439 --> 00:04:58,259
but soon after that the total cells will

90
00:05:09,070 --> 00:05:06,449
separate and console division here's one

91
00:05:12,019 --> 00:05:09,080
of our evolved more tea seller strengths

92
00:05:15,469 --> 00:05:12,029
and you can see that the cells stayed

93
00:05:18,980 --> 00:05:15,479
together for a while and then they start

94
00:05:25,820 --> 00:05:18,990
to pop out those smaller multicellular

95
00:05:28,640 --> 00:05:25,830
puppeteers here's another multicellular

96
00:05:32,709 --> 00:05:28,650
strands from the other extreme to

97
00:05:35,420 --> 00:05:32,719
population p5 they also stay together

98
00:05:38,689 --> 00:05:35,430
for a while and then they start to pop

99
00:05:41,149 --> 00:05:38,699
out single motile cells and then they

100
00:05:44,800 --> 00:05:41,159
start to form those multi solar coasters

101
00:05:47,179 --> 00:05:44,810
again so there are these two the

102
00:05:50,360 --> 00:05:47,189
medicinal strands from those two

103
00:05:53,149 --> 00:05:50,370
populations differ in their life cycles

104
00:05:55,490 --> 00:05:53,159
but they both from those structures by

105
00:05:59,570 --> 00:05:55,500
the failure of daughter cells to

106
00:06:01,760 --> 00:05:59,580
separate among cell division and most

107
00:06:03,980 --> 00:06:01,770
importantly they from those structures

108
00:06:05,329 --> 00:06:03,990
in even when their predators are not

109
00:06:07,689 --> 00:06:05,339
around anymore

110
00:06:12,909 --> 00:06:07,699
meaning that there's a genetic basis

111
00:06:19,189 --> 00:06:15,829
so to find out what kind of mutations

112
00:06:22,360 --> 00:06:19,199
happened in those evolved LG LG strands

113
00:06:26,119 --> 00:06:22,370

with it Illumina whole genome sequencing

114
00:06:28,790 --> 00:06:26,129
so for the 2x raindrop operation one

115
00:06:31,699 --> 00:06:28,800
control population we pick up multiple

116
00:06:34,580 --> 00:06:31,709
colonies to do whole genome sequencing

117
00:06:37,280 --> 00:06:34,590
we also sequence the

118
00:06:40,480 --> 00:06:37,290
- ancestral strength to know what

119
00:06:43,430 --> 00:06:40,490
genetic gration existed in the beginning

120
00:06:50,660 --> 00:06:43,440
so that we can know what actually

121
00:06:54,020 --> 00:06:50,670
happened in those evolved algae so what

122
00:06:56,870 --> 00:06:54,030
we found out is that appear that is two

123
00:07:00,200 --> 00:06:56,880
different genetic basis underlying two

124
00:07:03,740 --> 00:07:00,210
origins of multicellularity in your

125
00:07:07,490 --> 00:07:03,750
experiment so here are the mutations

126
00:07:11,180 --> 00:07:07,500
occurring each strand each Royces is an

127
00:07:14,020 --> 00:07:11,190
evolved isolate the first four are from

128
00:07:16,940 --> 00:07:14,030
the beetle permission that about

129
00:07:19,400 --> 00:07:16,950
medicinal properties the next four are

130
00:07:22,940 --> 00:07:19,410
from the be pipe operation that part

131
00:07:25,730 --> 00:07:22,950
about single cell properties and the

132
00:07:28,790 --> 00:07:25,740
last four are come from control

133
00:07:32,120 --> 00:07:28,800
population that are Romanian insulin and

134
00:07:35,540 --> 00:07:32,130
each prize mutation happened in their

135
00:07:39,610 --> 00:07:35,550
genomes and you can see that for the

136
00:07:42,910 --> 00:07:39,620
multicellular isolate in the b2 and b5

137
00:07:46,820 --> 00:07:42,920
populations they shared certain set of

138
00:07:49,910 --> 00:07:46,830

mutation all together suggesting that

139
00:07:56,750 --> 00:07:49,920
those are or any thousand are important

140
00:08:00,710 --> 00:07:56,760
for those medicinal phenotypes so how do

141
00:08:03,530 --> 00:08:00,720
we know that which which mutations are

142
00:08:06,820 --> 00:08:03,540
actually responsible for those most

143
00:08:11,330 --> 00:08:06,830
logical changes with it so these

144
00:08:15,470 --> 00:08:11,340
analyzers code park second analyzes the

145
00:08:19,610 --> 00:08:15,480
idea is that say let free meat mutations

146
00:08:24,290 --> 00:08:19,620
in all evolve isolate and we want to

147
00:08:27,140 --> 00:08:24,300
know whether it's a PC or a BP CAC or

148
00:08:29,930 --> 00:08:27,150
ABC together that are you responsible

149
00:08:33,230 --> 00:08:29,940
for the phenotype you can make it with

150
00:08:35,540 --> 00:08:33,240
the wild-type strength to generate a

151
00:08:38,600 --> 00:08:35,550
group of cells with different

152
00:08:41,900 --> 00:08:38,610
combinations of those mutations and then

153
00:08:44,780 --> 00:08:41,910
we can select full of phenotype we are

154
00:08:48,500 --> 00:08:44,790
interested in put summary cell phenotype

155
00:08:51,610 --> 00:08:48,510
and then those

156
00:08:57,200 --> 00:08:51,620
you know hats associate associated with

157
00:09:00,680 --> 00:08:57,210
phenotype huapi imaged this way so to

158
00:09:03,770 --> 00:09:00,690
actually do this with LG we made it our

159
00:09:07,100 --> 00:09:03,780
evolved multi server phenotypes with the

160
00:09:10,730 --> 00:09:07,110
unicellular strand to generate an actual

161
00:09:14,750 --> 00:09:10,740
population with different combination of

162
00:09:19,060 --> 00:09:14,760
the mutations so some details are multi

163
00:09:22,010 --> 00:09:19,070

seller and something on unit cell and

164
00:09:25,610 --> 00:09:22,020
then we select the multi cellular

165
00:09:27,500 --> 00:09:25,620
phenotype by centrifugation briefly so

166
00:09:31,280 --> 00:09:27,510
that's the bigger one should sink to the

167
00:09:33,650 --> 00:09:31,290
bottom more quickly and then so that the

168
00:09:36,920 --> 00:09:33,660
bottom ones go to the multi seller pool

169
00:09:40,130 --> 00:09:36,930
and the cells aren't have go to the

170
00:09:44,060 --> 00:09:40,140
single cell pool by repeating this for

171
00:09:47,930 --> 00:09:44,070
multiple times we can enrich the multi

172
00:09:51,230 --> 00:09:47,940
seller genotypes and unison what is the

173
00:09:54,770 --> 00:09:51,240
genotypes and then we sequence is two of

174
00:09:56,840 --> 00:09:54,780
pools of cells to see the allele

175
00:10:02,930 --> 00:09:56,850
frequency differences across their whole

176
00:10:05,840 --> 00:10:02,940
genomes and it turns out there are

177
00:10:08,690 --> 00:10:05,850
multiple regions in those LG's genome

178
00:10:11,960 --> 00:10:08,700
responsible for the motor severity

179
00:10:15,830 --> 00:10:11,970
evolved in your lab so it's a result

180
00:10:20,260 --> 00:10:15,840
from the multicellular isolates from the

181
00:10:23,840 --> 00:10:20,270
p2 population the y-axis means that

182
00:10:28,270 --> 00:10:23,850
given the overall allele frequency in

183
00:10:32,210 --> 00:10:28,280
both unicellular and multicellular pool

184
00:10:34,910 --> 00:10:32,220
these allele the transit alia appear in

185
00:10:38,900 --> 00:10:34,920
the MOTC report and the higher the dots

186
00:10:41,240 --> 00:10:38,910
are the laurel urchins are and the more

187
00:10:45,650 --> 00:10:41,250
likely they are associated with the

188
00:10:48,410 --> 00:10:45,660

multi cellular phenotypes so you can see

189
00:10:50,570 --> 00:10:48,420
several peaks here and three of them

190
00:10:52,280 --> 00:10:50,580
also match to the mutations we

191
00:10:57,150 --> 00:10:52,290
identified through whole genome

192
00:11:00,450 --> 00:10:57,160
sequencing approach and then there also

193
00:11:03,090 --> 00:11:00,460
other pics they're suggesting certain

194
00:11:08,190 --> 00:11:03,100
genetic background is important for

195
00:11:12,600 --> 00:11:08,200
those mute new mutations to arise here's

196
00:11:14,820 --> 00:11:12,610
the results from the b5 isolate and the

197
00:11:17,490 --> 00:11:14,830
other population that you bought

198
00:11:20,580 --> 00:11:17,500
multicellularity and we also see a

199
00:11:23,820 --> 00:11:20,590
similar trend so while the pigs match to

200
00:11:27,110 --> 00:11:23,830
one of the mutations we identified well

201
00:11:29,670 --> 00:11:27,120
there are several other pics that

202
00:11:32,480 --> 00:11:29,680
suggesting its ancestral genetic

203
00:11:37,830 --> 00:11:32,490
background plot the mute mutations

204
00:11:40,260 --> 00:11:37,840
responsible for those phenotypes both

205
00:11:44,340 --> 00:11:40,270
these mutations and the why I showed in

206
00:11:47,070 --> 00:11:44,350
the last slide now then they are either

207
00:11:50,730 --> 00:11:47,080
in introns or intergenic regions or none

208
00:11:53,580 --> 00:11:50,740
of them change amino acid sequences so I

209
00:11:58,670 --> 00:11:53,590
still working on what they actually do

210
00:12:02,670 --> 00:11:58,680
to change those phenotypes to summarize

211
00:12:05,490 --> 00:12:02,680
we evolved multicellularity black with

212
00:12:09,240 --> 00:12:05,500
predators we have identified mutations

213
00:12:13,590 --> 00:12:09,250

that ever happened in those evolved

214
00:12:16,910 --> 00:12:13,600
algae appear that is two different

215
00:12:21,180 --> 00:12:16,920
genetic bases undesigned those two

216
00:12:24,120 --> 00:12:21,190
different origins of multicellularity we

217
00:12:28,560 --> 00:12:24,130
are working on the functional relevance

218
00:12:31,800 --> 00:12:28,570
of those mutations at the moment for

219
00:12:34,950 --> 00:12:31,810
future directions now that we have

220
00:12:38,100 --> 00:12:34,960
evolved those simple modular structures

221
00:12:41,940 --> 00:12:38,110
we want to know how cellular

222
00:12:44,520 --> 00:12:41,950
differentiation would evolve and another

223
00:12:46,860 --> 00:12:44,530
postdoc in your lab is working on this

224
00:12:49,170 --> 00:12:46,870
project right now she's pretending a

225
00:12:54,780 --> 00:12:49,180
poster today if you haven't talked to

226
00:12:56,550 --> 00:12:54,790
her you should so what I presented today

227
00:13:00,260 --> 00:12:56,560
is multiple people's work especially

228
00:13:03,450 --> 00:13:00,270
Matt who oversees this whole project and

229
00:13:04,140 --> 00:13:03,460
we also like to paint our funding

230
00:13:09,810 --> 00:13:04,150
sources

231
00:13:09,820 --> 00:13:13,290
[Applause]

232
00:13:13,300 --> 00:13:19,520
we have time for some questions

233
00:13:33,760 --> 00:13:31,220
[Laughter]

234
00:13:36,100 --> 00:13:33,770
[Music]

235
00:13:38,230 --> 00:13:36,110
great talk thank you much I know you're

236
00:13:40,990 --> 00:13:38,240
working on hallucinating the genetic

237
00:13:42,760 --> 00:13:41,000
basis for the drive towards

238
00:13:45,190 --> 00:13:42,770

multicellularity under these

239
00:13:48,430 --> 00:13:45,200
circumstances but do you have any sort

240
00:13:51,700 --> 00:13:48,440
of predictions or hypotheses about what

241
00:13:54,630 --> 00:13:51,710
the phenotypic you know results of these

242
00:13:56,170 --> 00:13:54,640
genetic mutations are what would drive

243
00:14:04,660 --> 00:13:56,180
the con

244
00:14:08,710 --> 00:14:04,670
you know the collective nature can be

245
00:14:12,880 --> 00:14:08,720
something evolving cell lung cell cycle

246
00:14:14,740 --> 00:14:12,890
that one day what usually when cell goes

247
00:14:17,350 --> 00:14:14,750
through division there will from those

248
00:14:21,400 --> 00:14:17,360
two four or eight cell

249
00:14:23,830 --> 00:14:21,410
cops but then something else mutations

250
00:14:28,000 --> 00:14:23,840
might affect this process so that they

251
00:14:28,180 --> 00:14:28,010
couldn't separate after that great thank

252
00:14:32,020 --> 00:14:28,190
you

253
00:14:37,890 --> 00:14:32,030
but they don't look like it's in the

254
00:14:53,470 --> 00:14:49,540
other questions I have a question Green

255
00:14:57,430 --> 00:14:53,480
now is a bicones and all know this other

256
00:15:00,160 --> 00:14:57,440
organism say unique wants so is there

257
00:15:04,180 --> 00:15:00,170
any way that you can try to do any

258
00:15:08,320 --> 00:15:04,190
Studies on some single seller unicorns

259
00:15:10,500 --> 00:15:08,330
and try to see if you can do sort of

260
00:15:15,500 --> 00:15:10,510
explore the origin of multicellularity

261
00:15:30,550 --> 00:15:18,710
it's a fool major clades of eukaryotic