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The art/science of experimental evolution

CHRISTOPHER MARX

ORGANISMIC AND EVOLUTIONARY BIOLOGY FAS CENTER FOR SYSTEMS BIOLOGY HARVARD UNIVERSITY CMARX@OEB.HARVARD.EDU WWW.OEB.HARVARD.EDU/FACULTY/MARX/

Experimental evolution: basics and examples

- 1. How cultures are started and why
- 2. Bacterial growth and fitness competitions
- 3. Identifying beneficial mutations via genome resequencing
- 4. Mutations are not just SNPs
- Selective coefficients of mutations are not constants, but functions of other competitors, environment, and other alleles (*i.e.*, epistasis)

Establishing populations: Lenski LTs as example

Dynamics of bacterial growth

High-throughput culturing...



Fitness determined via competitions

Fluorescent fitness assay

The alternative...

v Cytometry

Fluor. ancestor





(David Chou)

(Lee et al., 2009. Evolution)

Calculating fitness (W) and dynamics of W_{ave}

Genetic basis via re-sequencing

-GATCATGTCGCGGTGGACGGAGCCGAGCTCTCCCCC	CTTCACGAGCACGACCGAATGTCCTGGCACGTGGAAG
TCATGTCGCGGTGGACGGAGCCGAGCTCTCTCCC	TT Reference sequence
CATGTCGCGGTGGACGGAGCCGAGCTCTCCCCC	TTT
TT GCGGGGTGGACGGAGCCGAGCT CT CCCCC	TTTCA
GTCGCGGTGGACGGAGCCGCGCTCCCCCC	CTTCCTIndividualieads
TCGCGGGGGACGGAGCCGAGCTCTCCCCC	TTTCACG
CGCGGTGGACGGAGCCGAGCTCTCTCTC	TTTCCCGA
GCGGGGGACGGAGCCGAGCTCTCCCCC	TTTCACGAG
GGGGGGACGGAGCCGAGCTCTCCCCC	TTTCACGAGC
CGGTGGACGGAGCCGAGCTCTCCCCC	TTTCACGAGC
GTGGACGGAGCCGAGCTCTCCCCC	TTTCACGAGCAC
TGGACGGAGCCGAGCTCTCCCCC	TTTCACTAGCACG
TGGACGGAGCCGAGCTCTCCCCC	TTTCACGAGCAAG
GGACGGAGCCGAGCTCTCCCCC	TTTCACGAGCACGA
GACGGAGCCGAGCCCTCCCCC	TTTCACGAGCACGAC
ACGGAGGCGAGCTCTCCCCC	TTTCACGCGCACGACC
GGAGCCGCGCTCTCCCCC	TTTCACGAGCACGACCGA
GATCCGACCTCGCCCCC	TTTCACGAGCACGACCGAA
GCCGAGCTCTCCCCC	TTTCACGAGCACGACCGAATG
CCGAGCTCTCCCCC	TTTCACGAGCACGACCGACTGT
CCGAGCTCTCCCCC	TTTCACGAGCACGACCGAATGT
CGAGACCCCCCC	TTTCACGAGCACGACCGAATGTC
GAGCTCTCCCCC	TTTCACGAGCACGACCGAATGTCC
GAGATCTCACCC	TTTAACGAGCACGACCGAATGTCC
CTCTCCCCC	TTTCACGAGCACGACCGAATGTCCTGG
CGCTCCCCC	TTTCACGAGCACGACCGAATGTCCTGC
TCTCCCCC	TTTCACGAGCACGACCGAATGTCCTGGC
TCTCCCCC	TTTCACGAGCACGACCGAATGTCCTGGC
CTCCCAC	TTTCACGAGCACGACCGCATGTCCTGGTC
CTCCACC	TTTCACGAGCACGACCGAATGTCCTGGCA
TCCCCC	TTTCACGAGCACGACCGAATGTCCTGGCAC
CCCC	TTTAACGAGCACGACCGAATGTCCTGGCACGT
	TTTCACGAGCACGACCGAATGTCCTGGCACGTGG
CC	TTTAAAGAGCACGACCGAATGTCCTGGCACGTGG
	TTTCACGAGCACGACCGAATGTCCTGGCACGTGGAA-

(Nigel Delaney)

Sequence data from 20K gen. E. coli isolate



(Barrick et al., 2009. Nature)

Sequence data from 20K gen. E. coli isolate



Table 1 | Frequency of parallel mutations in 11 other independently evolved lines

Gene or region	Function	Parallel mutations (%)	Source
nadR	Transcriptional regulator	100	Ref. 42
pykF	Pyruvate kinase	100	Ref. 42
rbs operon	Ribose catabolism	100	Ref. 43
malT	Transcriptional regulator	64	Ref. 44
spoT	Stringent response regulator	64	Ref. 31
mrdA	Cell-wall biosynthesis	45	Ref. 42
infB	Translation initiation factor 2	45*	This study
fis	Nucleoid-associated protein	27	E. Crozat, D.S., unpublished
topA	DNA topoisomerase I	27	E. Crozat, D.S., unpublished
pcnB	Poly(A) polymerase	27	This study
ompF	Outer-membrane porin	18*	This study
rpsD	30S ribosomal protein	18*	This study
rpsM	30S ribosomal protein	0	This study
glmU promoter	Cell-wall biosynthesis	0	M. Stanek, R.E.L., unpublished

* In addition to populations with substitutions, one or more others were polymorphic.

Table 2 | Tests of fitness effect in competition between isogenic constructs

Gene or region	Fitness effect (%)	Significance	Source
topA	13.3	***	Ref. 32
pykF*	11.1	***	D.S., R.E.L., unpublished
spoT	9.4	***	Ref. 31
nadR†	8.1	***	D.S., R.E.L., unpublished
glmU promoter	4.9	***	M. Stanek, T. Cooper, R.E.L., unpublished
fis	2.9	***	Ref. 32
rbs operon†	2.1	***	Ref. 43
malT	0.4	**	Ref. 44
ompF‡	-9.7	**	D.S., R.E.L., unpublished

(Barrick et al., 2009. Nature)

Selective effect (s) can be determined by constructing a strain with particular evolved allele

s is not a constant, but can depend upon several factors:

- 1. Identity and frequency of other competitors (*i.e.*, non-transitive)
- 2. The selective environment (*i.e.*, GxE interaction)
- 3. Other alleles (*i.e.*, epistasis or 'GxG')

Fitness as a function of frequency

An example of tradeoffs: *Methylobacterium*

- Evolved 8 populations on methanol (C₁) or succinate (multi-C) for 1500 generations
- Examined substrate use
- Half of S-evolved populations lost C₁ use!
 - • C_1 use quite labile
 - •Nonmethylobacterium erlenmeyeri?



(Lee et al., 2009. Evolution)

Other research interests I'd love to discuss...

- Predicting fitness consequences, optimality and epistasis in metabolism
- Selective basis of codon bias
- Determining qualities of the DFE and rate of beneficial mutations
- HGT and evolution in particular of metabolism and transposable elements
- Cooperation and coevolution in spatially-structured, synthetic microbial consortia

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MARX LAB

Tami Lieberman Lewis Ward

Alex Bradley

Dipti Roxana Nayak Tarnita Ming-Chun (Miki) Lee

Tony Blair

Deepa Nigel Agashe Will Delaney Harcombe

Hsin-Hung (David) Chou

Sean Carrol

<u>Not shown:</u> Lon Chubiz Maryska Kaczmarek Sarah Douglas

> David Robinson