

STOCHASTIC PROCESSES IN POPULATION GENETICS

<http://physics.ucsd.edu/students/courses/spring2015/physics274/>

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Time and Location: Tue and Thu

09:30 am – 10:50 am

Mayer Hall 2623

Homework: Around 6 problem sets, with a week to do each.

There will be a final presentation as exam

Grade will be a combination of homework, final project/exam and participation

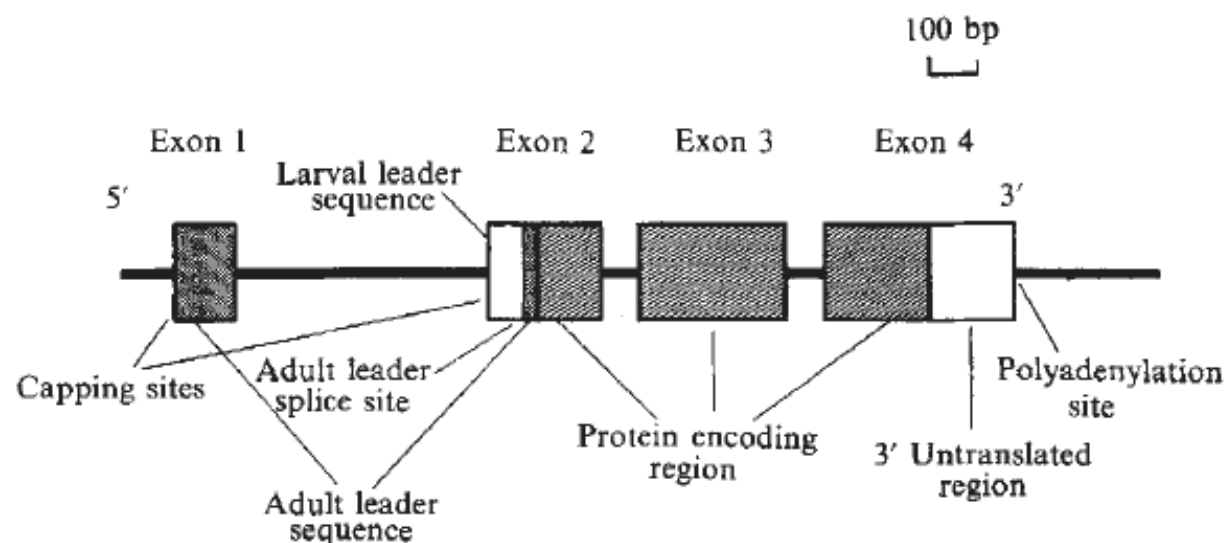
- A walk through the main mechanisms of evolution in population genetics
- Genetic variation and Hardy-Weinberg law
- Genetic drift and coalescent
- Natural selection
- Multi-loci dynamics
- Non-random mating and migration
- Quantitative genetics
- Evolutionary advantage of sex
- Mathematically more advanced discussion of selected topics

Nucleotide polymorphism at the alcohol dehydrogenase locus of *Drosophila melanogaster*

Martin Kreitman

Museum of Comparative Zoology, Harvard University, Cambridge, Massachusetts 02138, USA

The sequencing of eleven cloned Drosophila melanogaster alcohol dehydrogenase (Adh) genes from five natural populations has revealed a large number of previously hidden polymorphisms. Only one of the 43 polymorphisms results in an amino acid change, the one responsible for the two electrophoretic variants (fast, Adh-f, and slow, Adh-s) found in nearly all natural populations. The implication is that most amino acid changes in Adh would be selectively deleterious.



721 GCCCTCTTCCAATTGAAACAGATCGAAAGAGAGCTGCTAAAGCAAAAAAGAAGTCACCATGTCGTTTACTTTGACCAACAA
 MetSerPheThrLeuThrAsnLy

801 GAACGTGATTTTCGTTGCCGGTCTGGGAGGCATTGGTCTGGACACCAGCAAGGAGCTGCTCAAGCGCGATCTGAAGGTAA
 sAsnValIlePheValAlaGlyLeuGlyGlyIleGlyLeuAspThrSerLysGluLeuLeuLysArgAspLeuLys

881 CTATGCGATGCCACAGGCTCCATGCAGCGATGGAGGTTAATCTCGTGTATTCAATCCTAGAACCTGGTGATCCTCGACC
 AsnLeuValIleLeuAspA

961 GCATTGAGAACCCGGCTGCCATTGCCGAGCTGAAGGCAATCAATCCAAAGGTGACCGTCACCTTCTACCCCTATGATGTG
 rgIleGluAsnProAlaAlaIleAlaGluLeuLysAlaIleAsnProLysValThrValThrPheTyrProTyrAspVal

1041 ACCGTGCCCATTTGCCGAGACCACCAAGCTGCTGAAGACCATCTTCGCCAGCTGAAGACCGTCGATGTCCTGATCAACGG
 ThrValProIleAlaGluThrThrLysLeuLeuLysThrIlePheAlaGlnLeuLysThrValAspValLeuIleAsnGly

1121 AGCTGGTATCCTGGACGATCACCAGATCGAGCGCACCATTGCCGTCAACTACACTGGCCTGGTCAACACCACGACGGCCA
 yAlaGlyIleLeuAspAspHisGlnIleGluArgThrIleAlaValAsnTyrThrGlyLeuValAsnThrThrThrAlaI

1201 TTCTGGACTTCTGGGACAAGCGCAAGGGCGGTCCCGGTGGTATCATCTGCAACATTGGATCCGTCACTGGATTCAATGCC
 leLeuAspPheTrpAspLysArgLysGlyGlyProGlyGlyIleIleCysAsnIleGlySerValThrGlyPheAsnAla

1281 ATCTACCAGGTGCCCGTCTACTCCGGCACCAAGGCCGCCGTGGTCAACTTCACCAGCTCCCTGGCCGTAAGTTGATCAA
 IleTyrGlnValProValTyrSerGlyThrLysAlaAlaValValAsnPheThrSerSerLeuAla

1361 GGAACGCAAAGTTTTCAAGAAAAACAAAATAATTTGATTTATAACACCTTTAGAAACTGGCCCCCATTACCGGCGTG
 LysLeuAlaProIleThrGlyVal

1441 ACCGCTTACACCGTGAACCCCGGCATCACCCGCACCACCTGGTGCACAAGTTCAACTCCTGGTTGGATGTTGAGCCCCA
 ThrAlaTyrThrValAsnProGlyIleThrArgThrThrLeuValHisLysPheAsnSerTrpLeuAspValGluProGly

1521 GGTGCTGAGAAGCTCCTGGCTCATCCACCCAGCCATCGTTGGCCTGCGCCGAGAAGTTCGTCAAGGCTATCGAGCTGA
 nValAlaGluLysLeuLeuAlaHisProThrGlnProSerLeuAlaCysAlaGluAsnPheValLysAlaIleGluLeuA

1601 ACCAGAACGGAGCCATCTGGAAGTGGACTTGGGCACCCTGGAGGCCATCCAGTGGACCAAGCACTGGGACTCCGGCATC
 snGlnAsnGlyAlaIleTrpLysLeuAspLeuGlyThrLeuGluAlaIleGlnTrpThrLysHisTrpAspSerGlyIle

What are the evolutionary forces that lead to this pattern of divergence and selection?

Why preponderance of silent over replacements?

Can we tell anything meaningful out of 11 alleles?

Do intra-species patterns have anything to do with inter-species?

Mel vs erecta	Polymorphic	Fixed
Silent	13	26
Replacement	1	10

Loci and alleles

Differences by origin, state and descent

- Origin: Same locus, different chromosomes
 - State difference (sequence, phenotype, etc)
 - Descent: Do not share a common ancestor (within a relevant past timespan)
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- Hetero vs homozygous