

What factors contribute to phenotypic variation?

The world's tallest man, Sultan Kösen (8 feet 1 inch) towers over the world's smallest, He Ping (2 feet 5 inches).




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## WHERE DOES THE VARIATION COME FROM IN THE FIRST PLACE?

- The environment plays a significant role in the patterns of variation among individuals.

However,

- The ultimate source of variation that is the fuel for evolutionary change is **MUTATION**.

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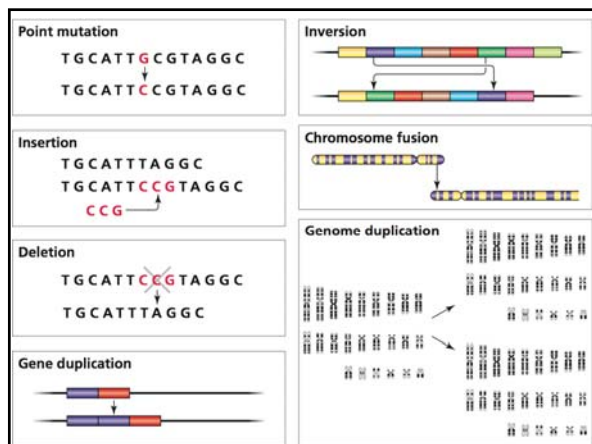
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## MAJOR SOURCES OF GENETIC CHANGE: MUTATION "THE FUEL FOR EVOLUTION"

Name	Description	Cause	Significance
1) Point mutation	Base-pair substitutions in DNA sequences	Chance errors during DNA synthesis or during repair of damaged DNA	Creates new alleles
2) Chromosome inversion	Flipping of a chromosome segment, so that the order of genes along the chromosome is altered	Breaks in DNA caused by radiation	Alleles inside the inversion are "locked together" into a unit
3) Gene duplication	Duplication of a short stretch of DNA, creating an additional copy of a gene	Unequal crossing over during meiosis (see Fig. 4.3)	The "extra" gene is free to mutate and perhaps gain new function
4) Polyploidy	Addition of a complete set of chromosomes	Errors in meiosis or (in plants) mitosis	Can create new species

## The Phenotypic Effect of Mutations Depends on the Location of the Mutation

TABLE 5.3 Sources of Heritable Genetic Variation

Location of Mutation	Type of Mutation	Consequence for Gene Action
Coding region	Substitution, insertion, deletion, duplication.	Alters the <b>product</b> of the gene, and thus its function or activity.
cis-Regulatory Regions	Substitution, insertion, deletion, duplication that alters the binding affinity of promoters, activators, repressors, etc.	Alters the timing, location, or level of expression of the gene.
trans-Regulatory Regions	Mutation to <b>coding regions</b> of trans-acting factor	Alters the binding affinity and thus the activity of a promoter, activator, repressor, etc.
	Mutation to <b>cis- or trans-regulatory regions</b> of trans-acting factors	Alters where, when, or to what extent inhibitory, activating, or other trans-acting regulatory factors are expressed.
Physiological Pathways (e.g., hormones)	Mutation (Mutations alter where, when, or how much an endocrine signal is produced)	Alters the timing, location, or level of expression of the gene. Alters the developmental or environmental context in which the gene is expressed.

### POINT MUTATIONS:

ACA ATG GTA CGA CAA



ACA ATT GTA CGA CAA

- Changes in the nucleotide sequence can alter the amino acid sequence and change protein structure **OR** introduce stop codons.
- Point mutations in regulatory regions can alter the timing and levels of gene expression.



Fig. 5.14 in Z&E

## Transposable Elements: “Jumping Genes”

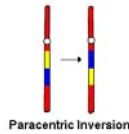


Barbara McClintock – Nobel Laureate 1983

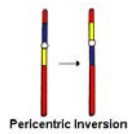
	Length	Jumping?	Number in genome	Fraction of genome
LINEs	6–8 kb	Yes	850 000	21%
SINEs	100–300 bp	No	1.5 million	12%
Retrovirus-like elements (LTR)		Yes	450 000	8%
	6–11 kb			
		No		
	1.5–3 kb			
		Yes	300 000	3%
	2–3 kb			
		No		
	80–3000 bp			

Orange blocks represent gene-like sequences; purple blocks represent flanking repeat sequences

## Chromosomal Inversions

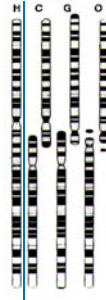


Paracentric Inversion



Pericentric Inversion

## Chromosomal Fusions



## GENE DUPLICATION:

Table 4.3 Some gene families

In this table, the “Number of duplicate genes” column refers to the number of loci in various gene families. These loci are presumed to be the result of duplication events. They have high sequence homology, code for products with closely related functions, and are often clustered close to one another on the same chromosome.

Family	Number of duplicate genes
<i>Locs found in many organisms</i>	
Actins	5–30
Tubulins (α and β)	5–15
Myosin, heavy chain	5–10
Histones	100–1000
Keratins	~ 20
Heat-shock proteins	3
<i>Insects</i>	
Eggshell proteins (silk moth and fruit fly)	> 50
<i>Vertebrates</i>	
Globins (many species)	
α-like	1–5
β-like	≥ 50
Ovalbumin (chicken)	3
Vitellogenin (frog, chicken)	5
Immunoglobulins, variable regions (many species)	> 500
Transplantation antigens (mouse and human)	50–100

### THE FATE OF DUPLICATE GENES:

- Retain their original function and provide an additional copy of the parent locus.
- Accumulate point mutations and become functionless pseudogenes.
- Gain a new function through mutation and selection (neofunctionalization).
- While Humans and chimpanzees are ~1-2% different at the nucleotide level they are more than 3% different in gene copy number variants (CNV). Within Human populations many disease phenotypes are linked to CNVs.

- Different classes of mutation occur at different rates in humans, and affect different proportions of the genome.

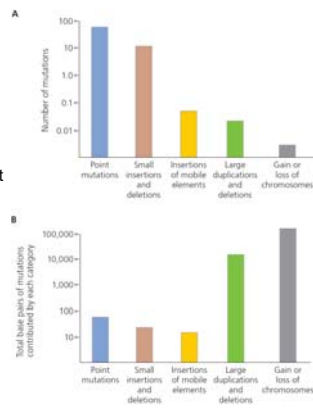


Fig. 5.15 Z&E

- The genomic mutation rate appears to be roughly constant in haploid microbes and simple eukaryotes:

ORGANISM	GENOME SIZE	PER BASE <sup>1</sup>	PER GENOME <sup>1</sup>
Phage M13	$6.4 \times 10^3$	$7.2 \times 10^{-7}$	0.0046
Phage lambda	$4.8 \times 10^4$	$7.7 \times 10^{-8}$	0.0038
Phage T2, T4	$1.6 \times 10^5$	$2.4 \times 10^{-8}$	0.0038
E. coli	$4.7 \times 10^6$	$5.4 \times 10^{-10}$	0.0025
Yeast	$1.4 \times 10^7$	$2.2 \times 10^{-10}$	0.0031
Neurospora	$4.2 \times 10^7$	$7.2 \times 10^{-11}$	0.0030

<sup>1</sup>per generation

- These results suggest that as genome size has increased the DNA replication – repair machinery has increased in efficiency.

From: J. W. Drake, 1991, Proc. Natl. Acad. Sci. USA 88:7160-7164.

## Constancy of Mutation Rates?

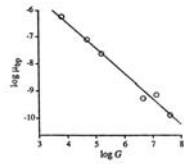


FIG. 1. Average mutation rate  $\mu_{bp}$  per base pair as a function of genome size  $G$  in bp.

- The genomic deleterious mutation rate:
  - $\approx 0.004/\text{cell division}$  in *E. coli*
  - $\approx 1.5/\text{generation}$  in *D. melanogaster*
- High rates in flies and humans suggest **Drake's constancy hypothesis** cannot be extended to higher organisms.

## THE MUTATION RATE IN HUMANS

- The mutation rate in males is on the order of 10x that in females, probably because of a higher number of cell divisions from zygote to gamete.

Female Cell divisions	$\approx 24$ (independent of age)
Male Cell Divisions	$\approx 36 + ((\text{Age}-13) \times 23)$
	$\approx 200$ @ Age 20
	$\approx 770$ @ Age 45
- The male rate of **point** mutations is approx.  $1.2 \times 10^{-8}$  per base per generation, or approx  $1 \times 10^{-10}$  per cell division.
- The genomic mutation rate is approx.  $(1.2 \times 10^{-8}) \times (3 \times 10^9 \text{ bases/genome}) \approx 36$ .
- More than 6% of newly fertilized eggs carry a gross chromosomal abnormality.
  - Approx. 5.5% of these terminate as spontaneous abortions.

FROM: J. F. Crow, 1993, Environ. Mol. Mutagenesis 21:122-129 & F. Vogel and R. Rathenberg, 1975, Adv. Human Genetics 5:223-318.

NATURE | NEWS

## Fathers bequeath more mutations as they age

Genome study may explain links between paternal age and conditions such as autism.

In the 1930s, the pioneering geneticist **J. B. S. Haldane** noticed a peculiar inheritance pattern in families with long histories of haemophilia. The faulty mutation responsible for the blood-clotting disorder tended to arise on the X chromosomes that fathers passed to their daughters, rather than on those that mothers passed down. Haldane subsequently proposed that **children inherit more mutations from their fathers than their mothers**, although he acknowledged that "it is difficult to see how this could be proved or disproved for many years to come".

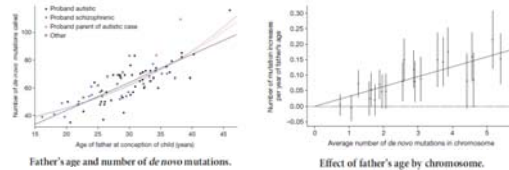


Haldane, J. B. S. Ann. Eugen. 13, 262-271 (1947).

## Rate of *de novo* mutations and the importance of father's age to disease risk

Augustine King<sup>1</sup>, Michael L. Frigge<sup>2</sup>, Gadi Maass<sup>3</sup>, Soren Brennerhauer<sup>2,3</sup>, Patrick Sulem<sup>1</sup>, Guðr Magnússon<sup>1</sup>, Sigrún A. Gudjonsson<sup>1</sup>, Asgeir Sigurðsson<sup>1</sup>, Aslaug Jonasdóttir<sup>1</sup>, Adalbjörg Jonasdóttir<sup>1</sup>, Wendy S. W. Wong<sup>4</sup>, Gunnar Sigurdsson<sup>5</sup>, G. Bragi Walters<sup>1</sup>, Stacy Steinberg<sup>1</sup>, Harnes Helgason<sup>1</sup>, Gudmar Thorleifsson<sup>1</sup>, Daniel F. Gudbjartsson<sup>1</sup>, Agnar Helgason<sup>1</sup>, Olafur Th. Magnússon<sup>1</sup>, Unnur Thorsteinsdóttir<sup>2,3</sup> & Karl Stefansson<sup>1,3</sup>

Mutations generate sequence diversity and provide a substrate for selection. The rate of *de novo* mutations is therefore of major importance to evolution. Here we conduct a study of genome-wide mutation rates by sequencing the entire genomes of 78 Icelandic parent-offspring trios at high coverage. We show that in our samples, with an average father's age of 29.7, the average *de novo* mutation rate is  $1.20 \times 10^{-8}$  per nucleotide per generation. Most notably, the diversity in mutation rate of single nucleotide polymorphisms is dominated by the age of the father at conception of the child. The effect is an increase of about two mutations per year. An exponential model estimates paternal mutations doubling every 16.5 years. After accounting for random Poisson variation, father's age is estimated to explain nearly all of the remaining variation in the *de novo* mutation counts. These observations shed light on the importance of the father's age on the risk of diseases such as schizophrenia and autism.



## DIRECTED MUTATION

- Do mutations arise spontaneously **OR** in response to selective challenges???



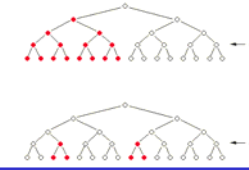
The Luria-Delbruck Fluctuation test (1943):

Luria & Delbruck

### Pattern A: Mutation is Directed

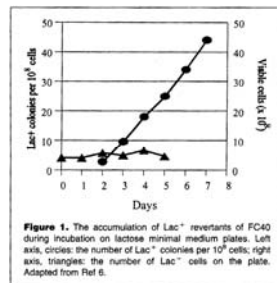


### Pattern B: Mutation is Random



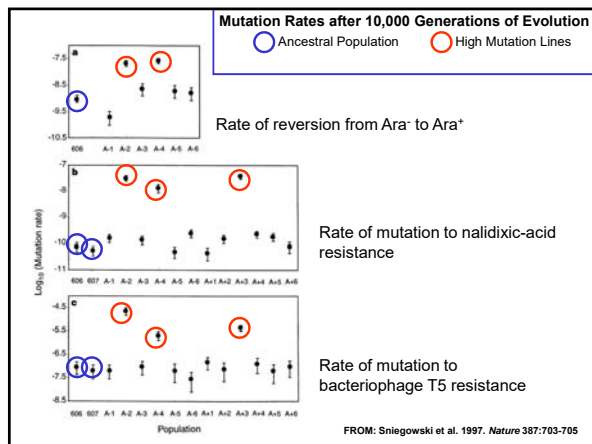
## Are Mutations Random?

- Cairns et al. (1988) exposed a Lac<sup>-</sup> strain of *E. coli* to Lactose media and measured the rate of mutation to Lac<sup>+</sup>.



- Is this evidence of "Adaptive Mutation"???

FROM: Cairns, J., & P. L. Foster. 1991. Adaptive reversion of a frameshift mutation in *Escherichia coli*. *Genetics* 128:695-701




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### What Is Going On?

- Recent studies by Rosenberg and Foster suggest that alteration of the recombination-repair pathway is essential for this result.
- Starvation is mutagenic – either as an unavoidable consequence of physiological deterioration OR increasing the mutation rate may be adaptive in the sense that not mutating is certain death.
- These mutator strains may have a **short term** advantage coping with environmental stress but over the **long term** they will be at a selective disadvantage.

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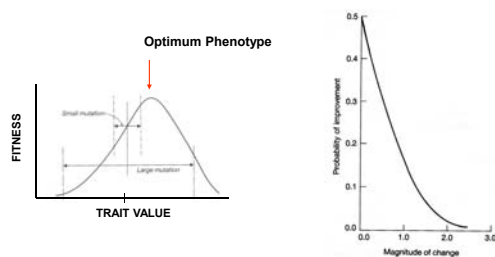
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**Mutational Effects:** Fisher argued that mutations of small effect are more likely the fuel for evolution by natural selection.



**Figure 87.5** Smaller mutations have a higher chance of being selectively advantageous. Macromutations are almost never advantageous. Most evolutionary change, therefore, is achieved by substituting mutations of small effect.

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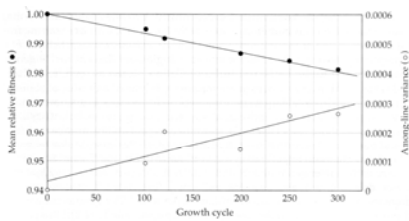
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### Mutation Accumulation Experiments



**Figure 12.7** Similar plots to Figure 12.6 for 50 lines of the bacterium *E. coli* taken through daily single-cell bottlenecks for 300 days (with approximately 22 cell divisions per day). Here fitness is measured as the exponential rate of clonal expansion in liquid medium. (From Kibota and Lynch 1996.)

FROM: Lynch & Walsh 1998

### Conclusions from mutation accumulation studies:

- The majority of spontaneous mutations have a **slightly** deleterious effect on fitness.
- The average effect of spontaneous deleterious mutations is a 1-2% decrease in fitness (Houle *et al.* 1997).

### SUMMARY OF KNOWLEDGE ON MUTATION RATES

- The spectrum of mutations is enormous, ranging from chromosomal rearrangements (translocations and inversions) and duplications to insertion and excisions of transposable elements to single base substitutions, insertions, and deletions.
- The mutation rate is subject to evolutionary modification.
- The vast majority of mutations appear to be deleterious.
- Mildly deleterious mutations are much more common than lethals.
- The mutation rate per generation increases with the number of cell divisions --- in mammals, the point mutation rate is much higher in males than females.



#### SUMMARY OF KNOWLEDGE ON MUTATION RATES

- For polygenetic characters, the mutational rate of introduction of new variation is on the order of 0.1% to 1.0% of the standing variation.
- The adaptive value of mutations changes with the ecological circumstances.
- Mutations arise randomly with respect to their utility.
- The mutation rate can be modified greatly by the environment.

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