Evolutionary Genetics

Darwin and Genetics

- Darwin studied snapdragons
  - Came up with an incoherent theory of genetics
  - Blending inheritance
  - Lamarckian
  - Pangenesis
- Mendel studied peas

Gregor Mendel

- Austrian monk
- Did experiments from 1856 – 1863
- Published his findings in obscure journal
- Mendel's laws rediscovered in 1900
  - Mendel given credit
- Rise of biometricians
  - Focus on variation
  - Downplayed Mendel
- Reconciliation during the Modern Synthesis
  - Polygenic inheritance

Genetics Review

- Gene
- Locus
- Allele
- Genotype
- Phenotype
- Homozygous
- Heterozygous
- Dominant
- Recessive
Mendel’s Laws

- Law of Segregation
  - For each trait there is a gene with two copies (alleles)
  - Alleles separate during gamete production
- Law of Independent Assortment
  - Loci are independent
  - Doesn’t work if genes are linked

Mendel’s importance to evolution

- Particulate inheritance
  - Collapse of blending
  - Blending would make natural selection untenable

DNA

- Polymer of nucleotides
- Deoxyribose, base, phosphate group
- Pyrimidines (cytosine [C], and thymine [T])
- Purines (adenine [A], guanine [G])
- Antiparallel strands held together by H bonds
- A – T (two H bonds), C – G (three H bonds)

DNA vs. RNA

- DNA
  - double helix
  - Relatively stable
- RNA
  - Single strand
  - Unstable
- Few RNA-based lifeforms
DNA to Proteins

- Portion of DNA unzips
  - An RNA transcript is produced
  - Complementary base pairing except uracil (U) for T
  - Messenger RNA (mRNA)
  - Ribosomal RNA (rRNA)
  - Transfer RNA (tRNA)
  - microRNA

mRNA to Protein

- Codons
- 3rd position wobble

Genetic variability

- Crossing over
  - Creates new combinations of alleles at different loci
Mutations

- Ultimate source of variability
- Base substitution
  - Transitions
    - One purine to another
    - One pyrimidine to another
  - Transversions
    - Purine to a pyrimidine
    - Pyrimidine to purine
  - Silent or synonymous mutations
  - Missense mutations
  - Nonsense
Fig. 4. Best estimate phylogeny based on combined analysis of cytochrome b and c- myc. Topology is the majority rule consensus tree from the combined ML bootstrap analyses (i.e., nodes with support below 50% are collapsed). Numbers above branches are ML bootstrap values.

Aneuploidy

- The result of nondisjunction
Polyploidy


Mutations are random

• Mutations are random!
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Mutations and fitness

• Generally classified as
  – Beneficial
  – Neutral
  – Deleterious
• However fitness is a continuous trait
• The frequency of each type of mutation depends on the context
Mutation and Fitness

- The frequency of each type of mutation depends on the context
- In general, most are deleterious or neutral
- In stable environment, beneficial mutations are rarer
- In changing environment, greater probability of having beneficial mutations
  – Could be the same mutation that would be deleterious in a stable environment!!!