Population Genetics, Systematics and Conservation of Endangered Species

Discuss Population Genetics and Systematics

Describe how DNA is used in species management

- Wild vs. Captive populations

Data Generation:

- PCR / Fragment Analysis
- DNA Sequencing

Data Analysis

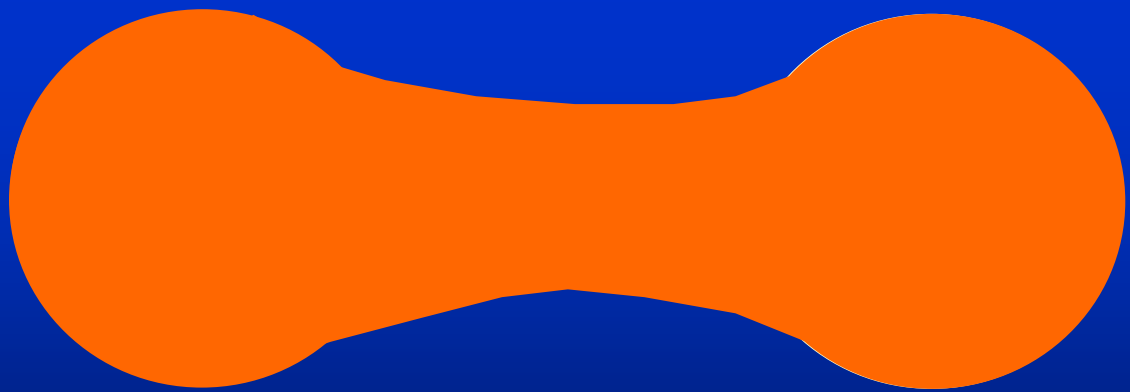
Case Studies

Population Genetics

- Analysis of the amount and partitioning of genetic variation between populations
- Data analysis is typically based upon the similarity of allele frequencies between samples
- Similarity of allele frequencies is an accepted proxy for gene flow between populations

Population Genetics

- Analysis of the amount and partitioning of genetic variation between populations



Population Genetics

- Similarity of allele frequencies between samples is an accepted proxy for gene flow between populations
- In the absence of gene flow, drift and/or selection will cause allele frequencies in the two populations to diverge
- Caveat: Differences accrue slowly; data reflect average historic conditions not necessarily the current status

Systematics

- In systematics, genetic distance is estimated by comparing similarity of DNA sequences

Systematics

- Analysis of genetic distance between groups of animals, generally above the species level

- Caveat: Sequence divergence is assumed to be uniform – selection of correct sequence is critical

Genetic Data is Used to Manage both Wild and Captive Populations

Wild Population

Assessment of population structure

Detection of vulnerable populations

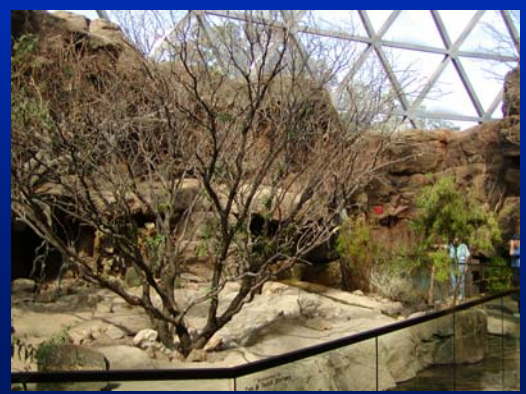
Tailoring of conservation efforts

Captive Population

Assessment of genetic diversity

Management of breeding programs

Maximize retention of genetic diversity



Data Generation – Population Genetics

- Begins with Polymerase Chain Reaction (PCR)

Denaturation (96ºC)

Data Generation – Population Genetics

Annealing (~55ºC)

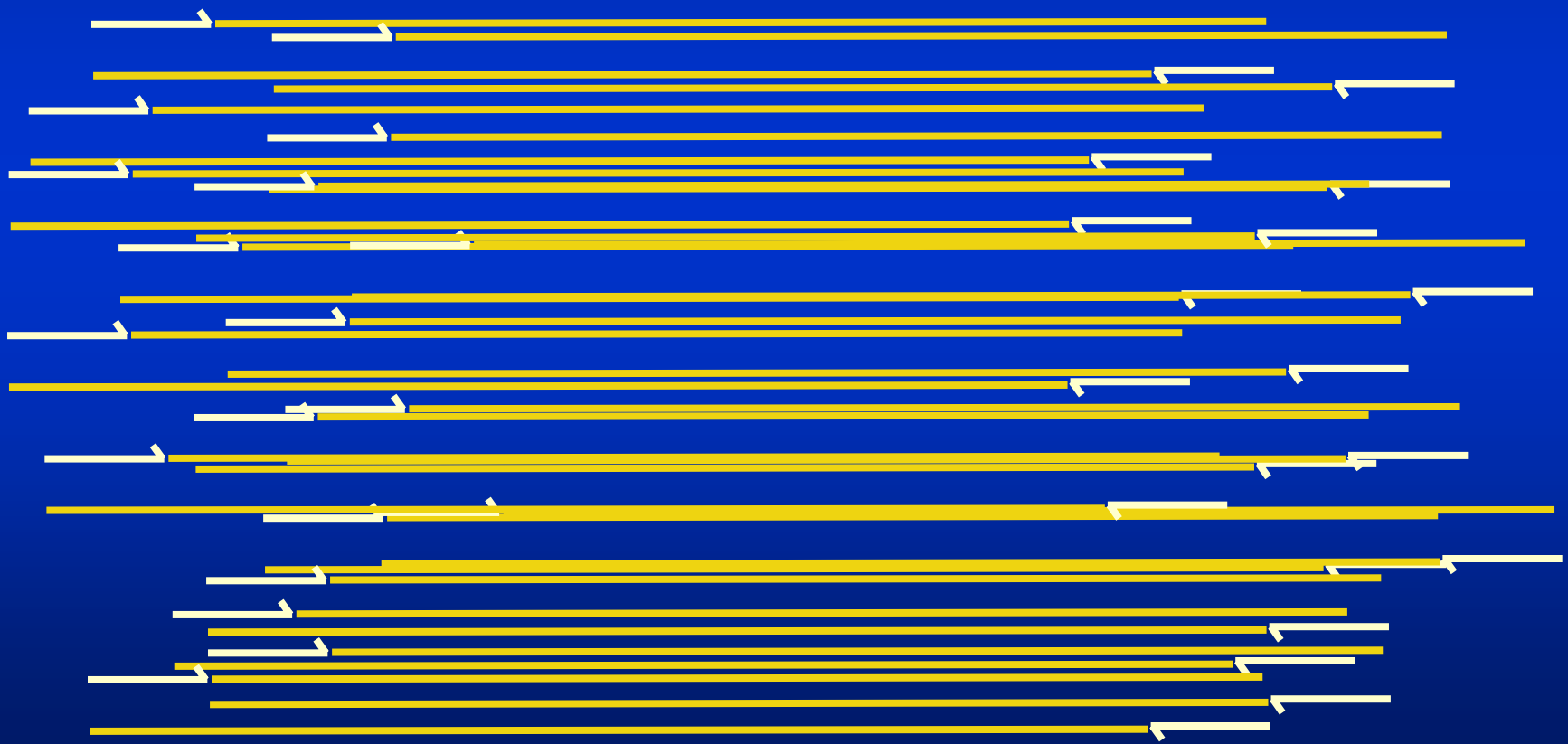
Data Generation – Population Genetics

Extension (72ºC)

Data Generation – Population Genetics

These three steps are repeated 35-40 times

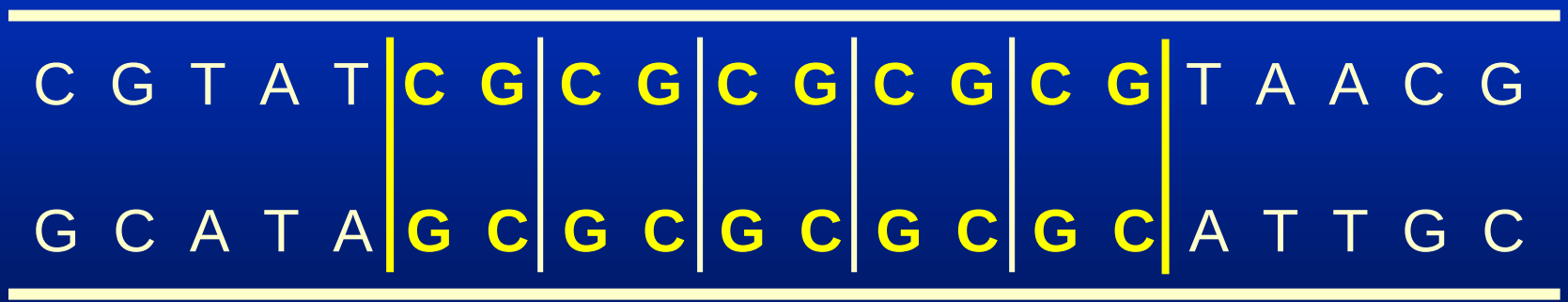
The region between the primers is exponentially amplified



Data Generation – Population Genetics

Microsatellites

- Commonly used in population genetic studies
- Repeated DNA elements
- Repeated units are typically 2 to 4 nucleotides long

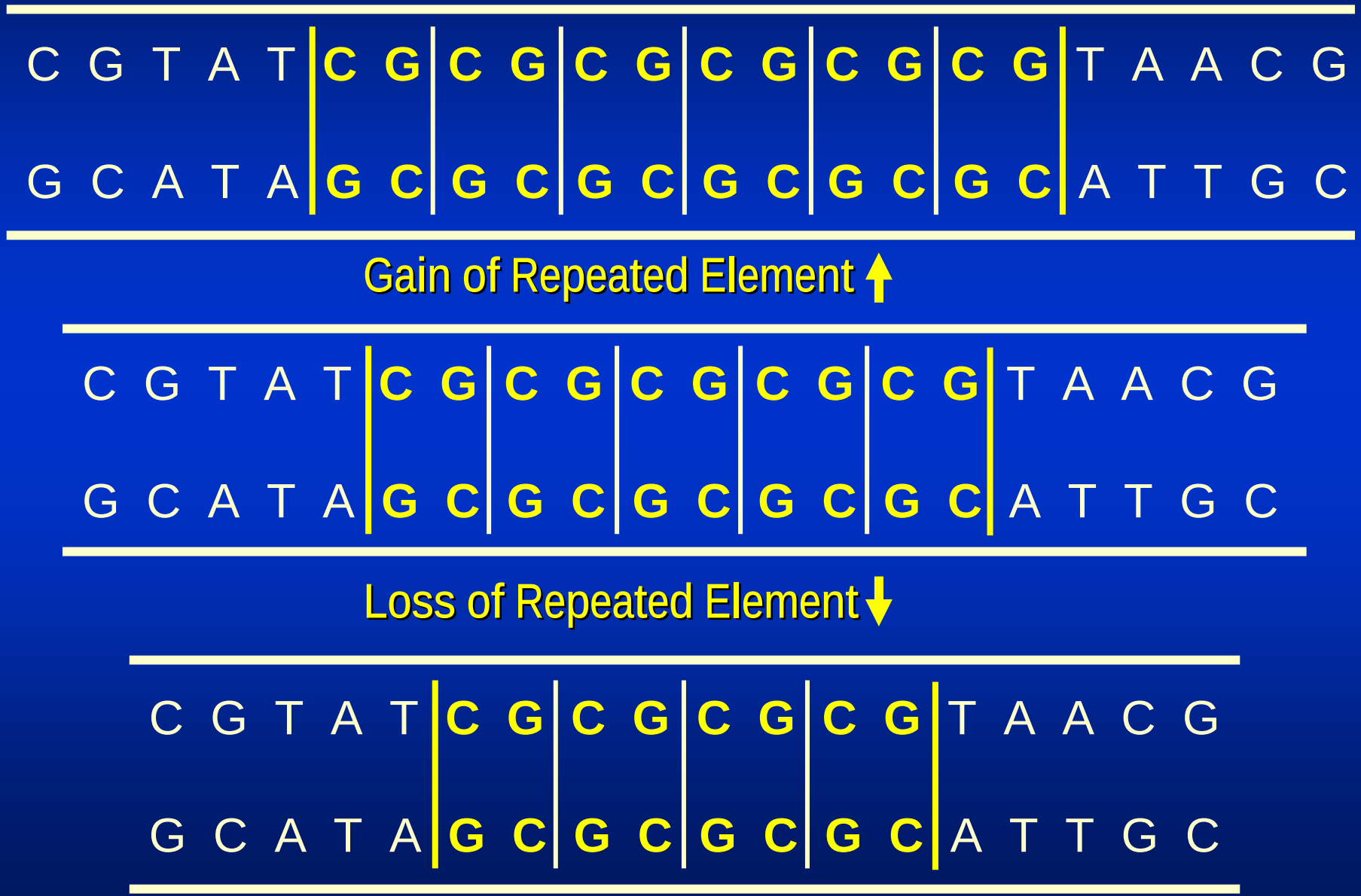


Data Generation – Population Genetics

Advantages of Microsatellites

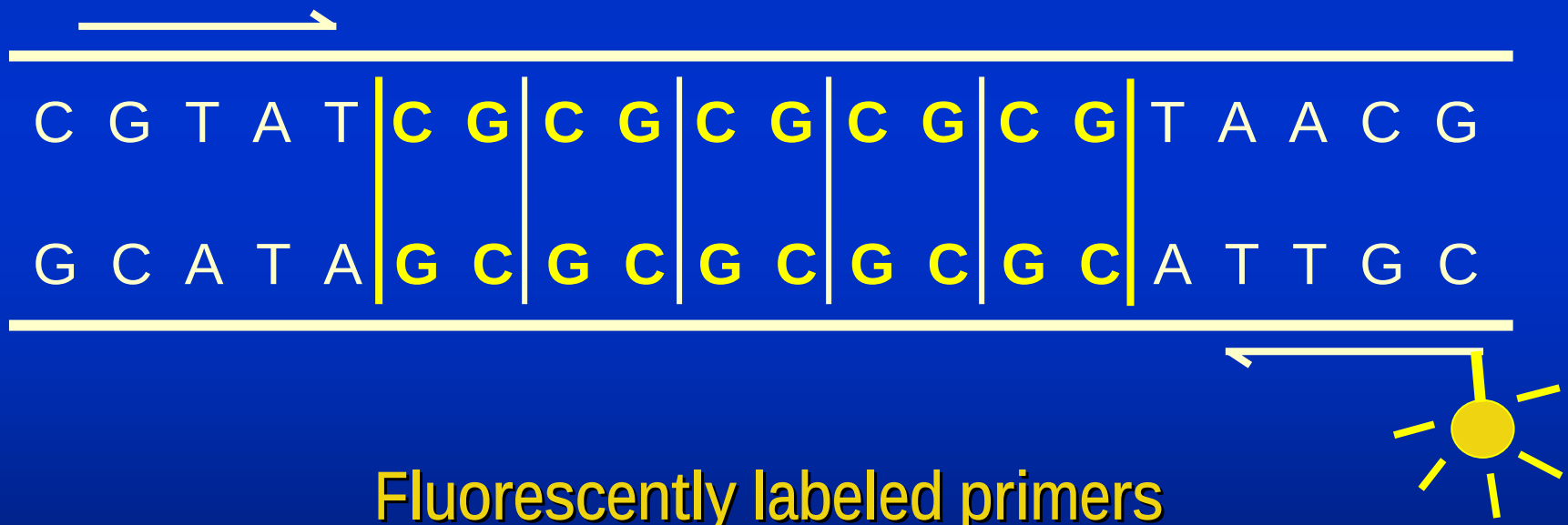
- Occur at high frequency throughout mammalian genomes
- Randomly located across all chromosomes
- Highly polymorphic (variable) due to replication errors

Microsatellite



Microsatellite

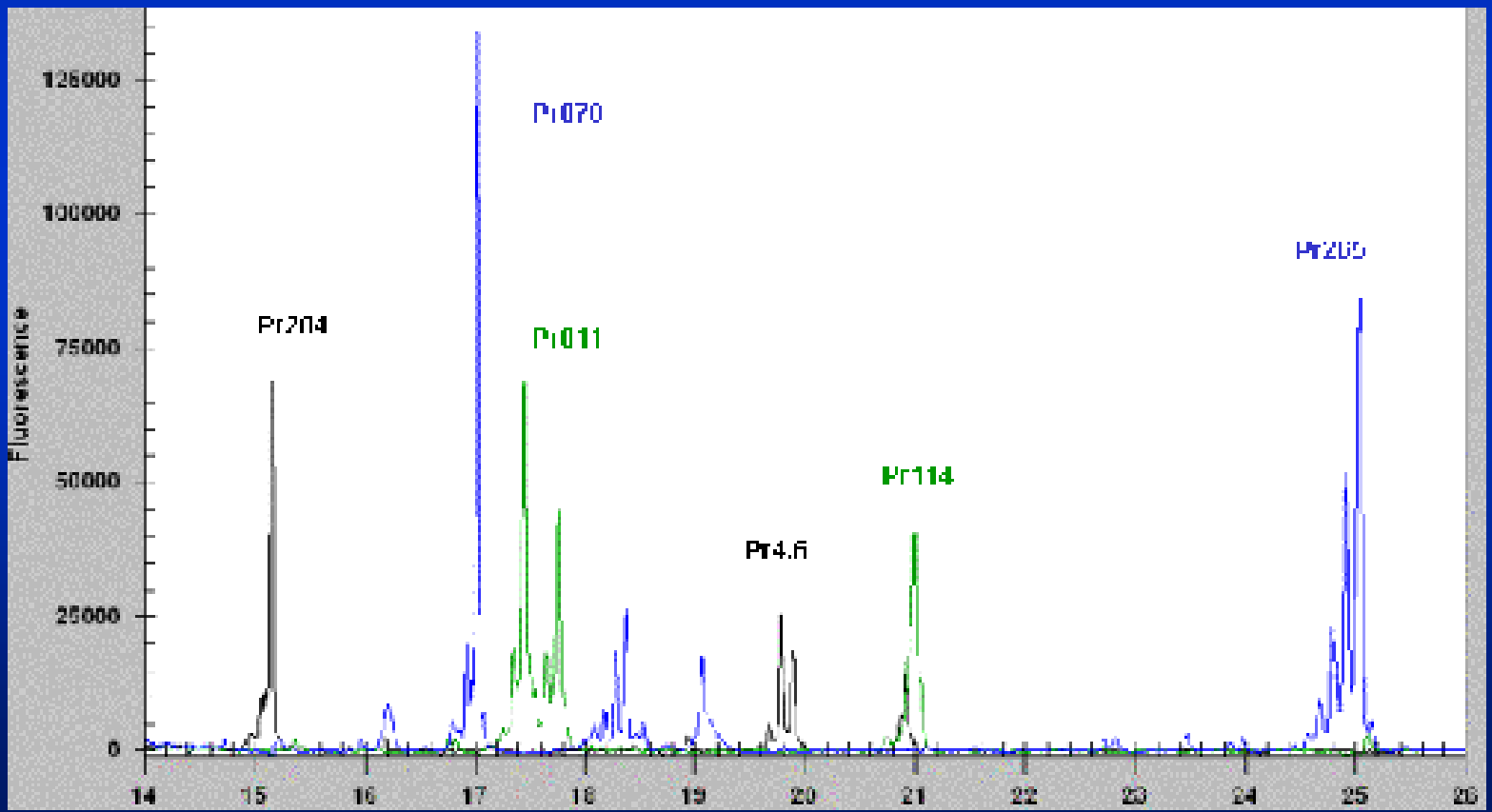
The number of repeats can be assessed by designing PCR primers that flank the repeated region



Fluorescently labeled primers enable automated analysis

Data Generation – Population Genetics

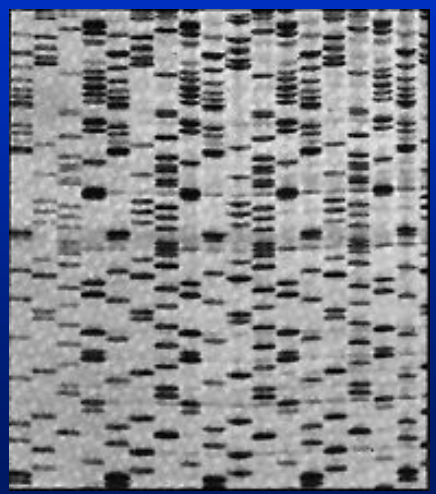
- PCR amplification is followed by automated fragment analysis

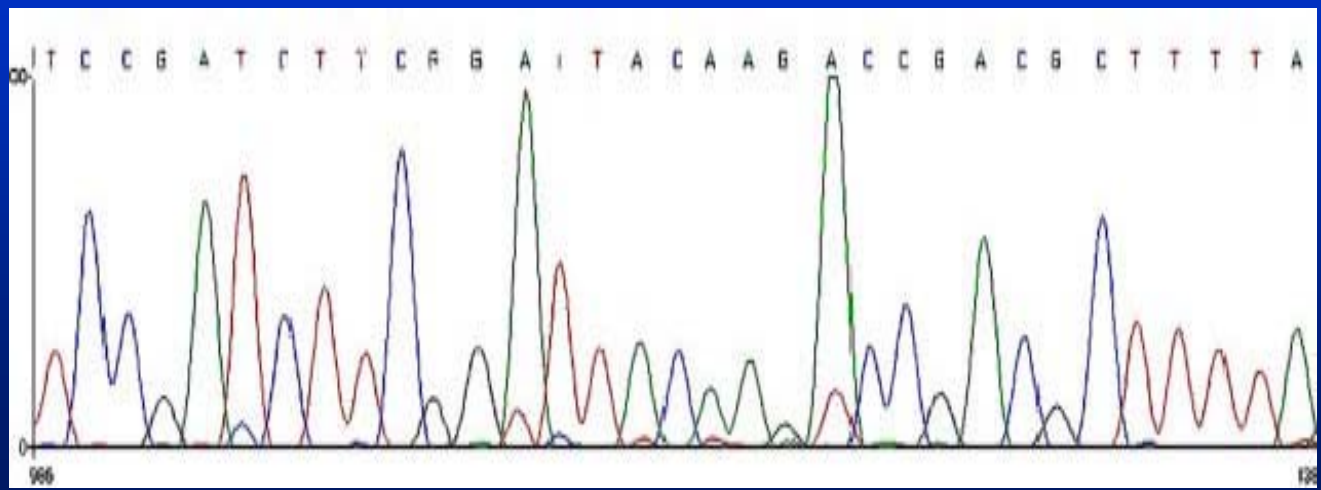


Data Generation – Systematics

DNA sequence analysis

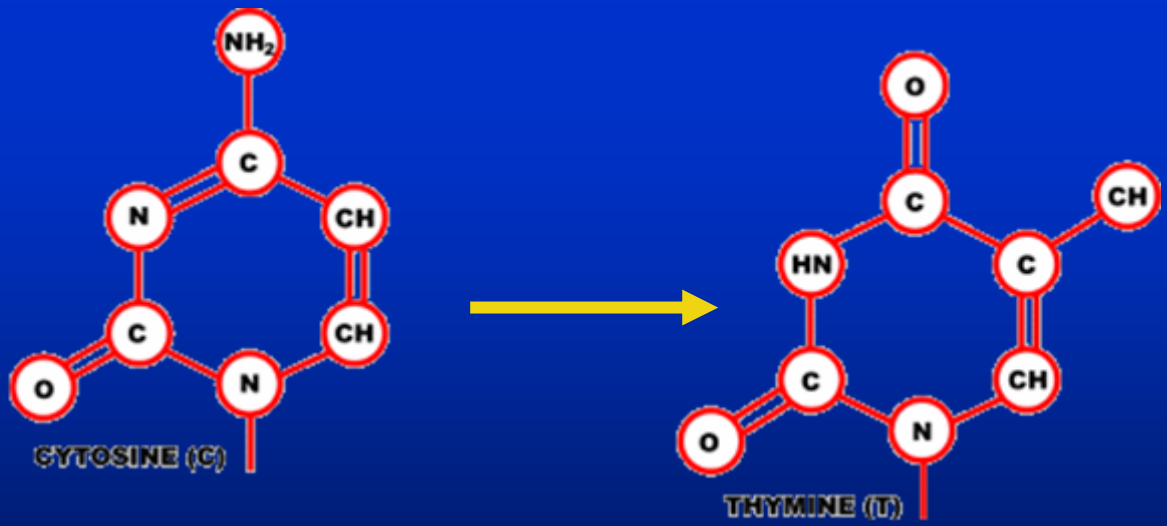
- Begins with PCR, same as in fragment analysis
- Followed by di-deoxy nucleotide (Sanger) sequencing
- Uses fluorescently labeled nucleotides (4 colors; 1 per base)





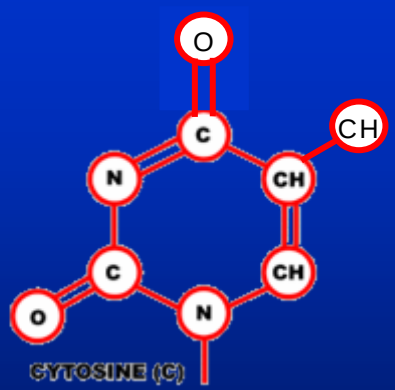
DNA Mutation

- The most common mutation in mammals and most higher vertebrates is cytosine to thymine



DNA Mutation

- This transition substitution is caused by deamination of methylated cytosine



Data Generation – Systematics

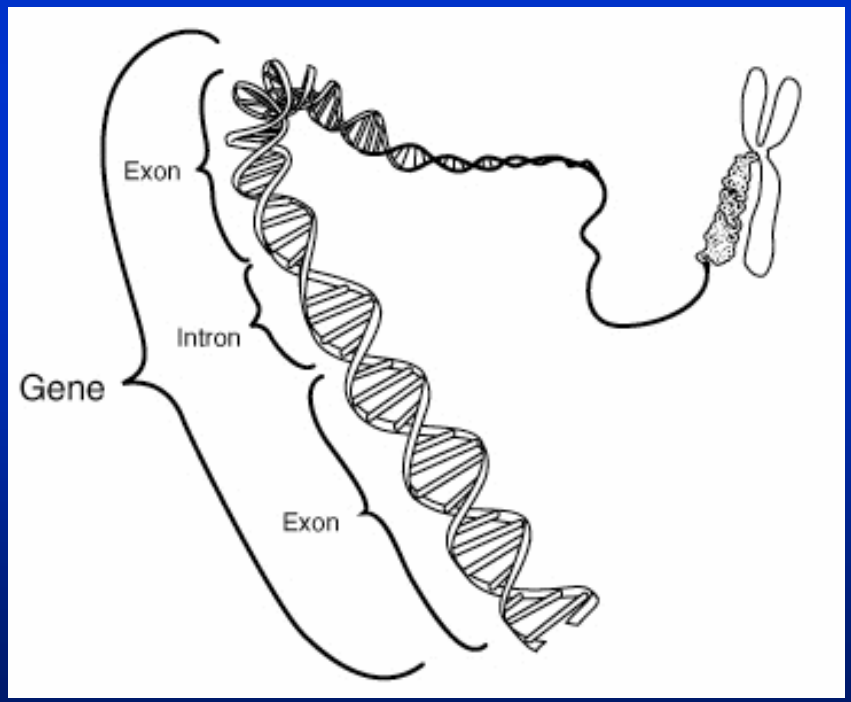
- Not all genes accrue mutations (evolve) at the same rate
- Some genes are prone to rapid rates of evolution
- Faster evolving genes are more useful for recent events
- Mitochondrial genes are more sensitive to change

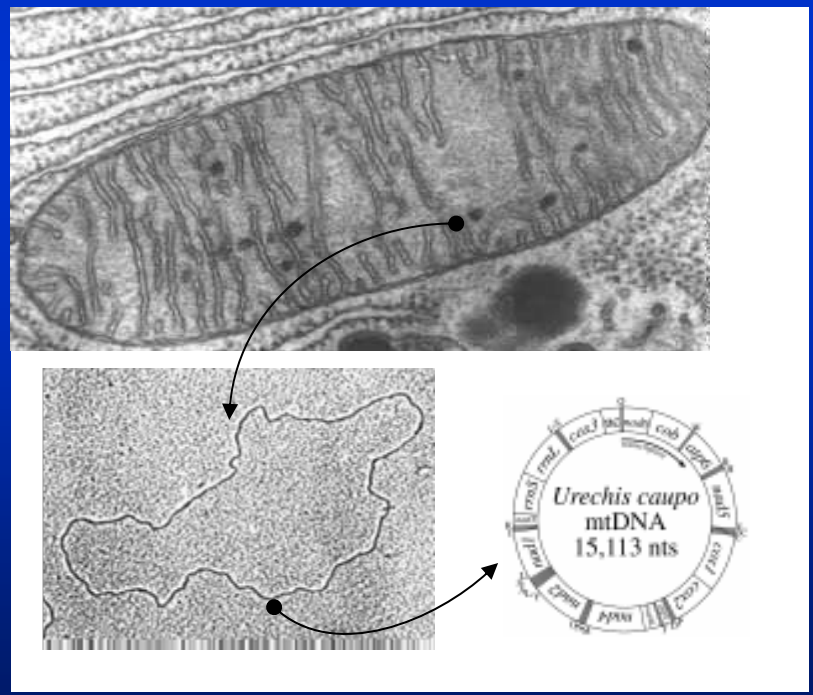
Data Generation – Systematics

- Selection of DNA segment (gene) is critical
- For species with ancient species radiation events, such as crocodiles, a slowly evolving gene is selected
- A faster evolving gene is used for species with recent radiations, such as African gerbils and other mammals

Data Generation – Systematics

- Nuclear or mitochondrial DNA may be sequenced



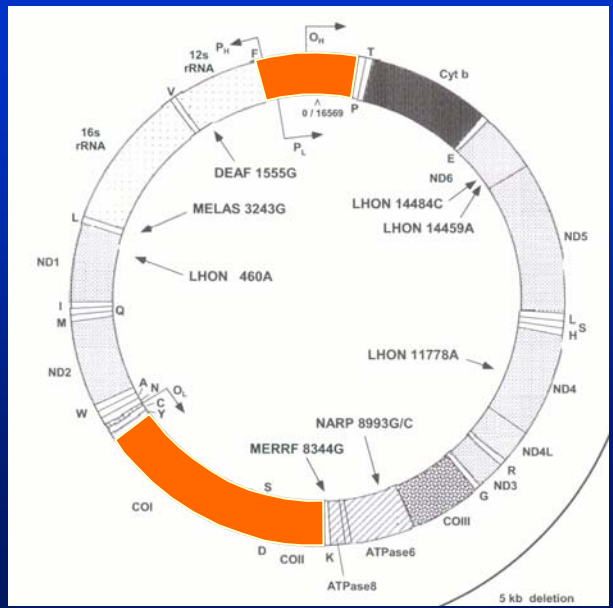


Mitochondrial DNA

- Mitochondrial DNA is ~4X more sensitive to change
- Mitochondrial DNA is haploid
- Maternally transmitted
- Can only reveal phylogeny of the maternal lineage
- Depending upon the gene studied, mitochondrial DNA can be used in population genetics or systematics

Data Generation – Systematics

- The displacement loop (D-loop) region evolves very quickly and has been used in many population genetic studies to resolve population substructure within species
- Cyotchrome oxidase subunits I and II evolve very slowly and have been used to resolve relationships between insect taxa, which have deep speciation nodes



Data Analysis

- Methods are based upon allele frequency or diversity

Population Genetics

- Haplotype Network
  Graphically represents population structure
- F_{ST} (Fixation index)
  Compares variation within a subpopulation to the total population

Systematics

- Phylogenetic Analysis
  Reconstructs ancestral history (speciation events)
- Maximum Parsimony
  Minimizes changes required to generate a given phylogentic tree

Data Analysis

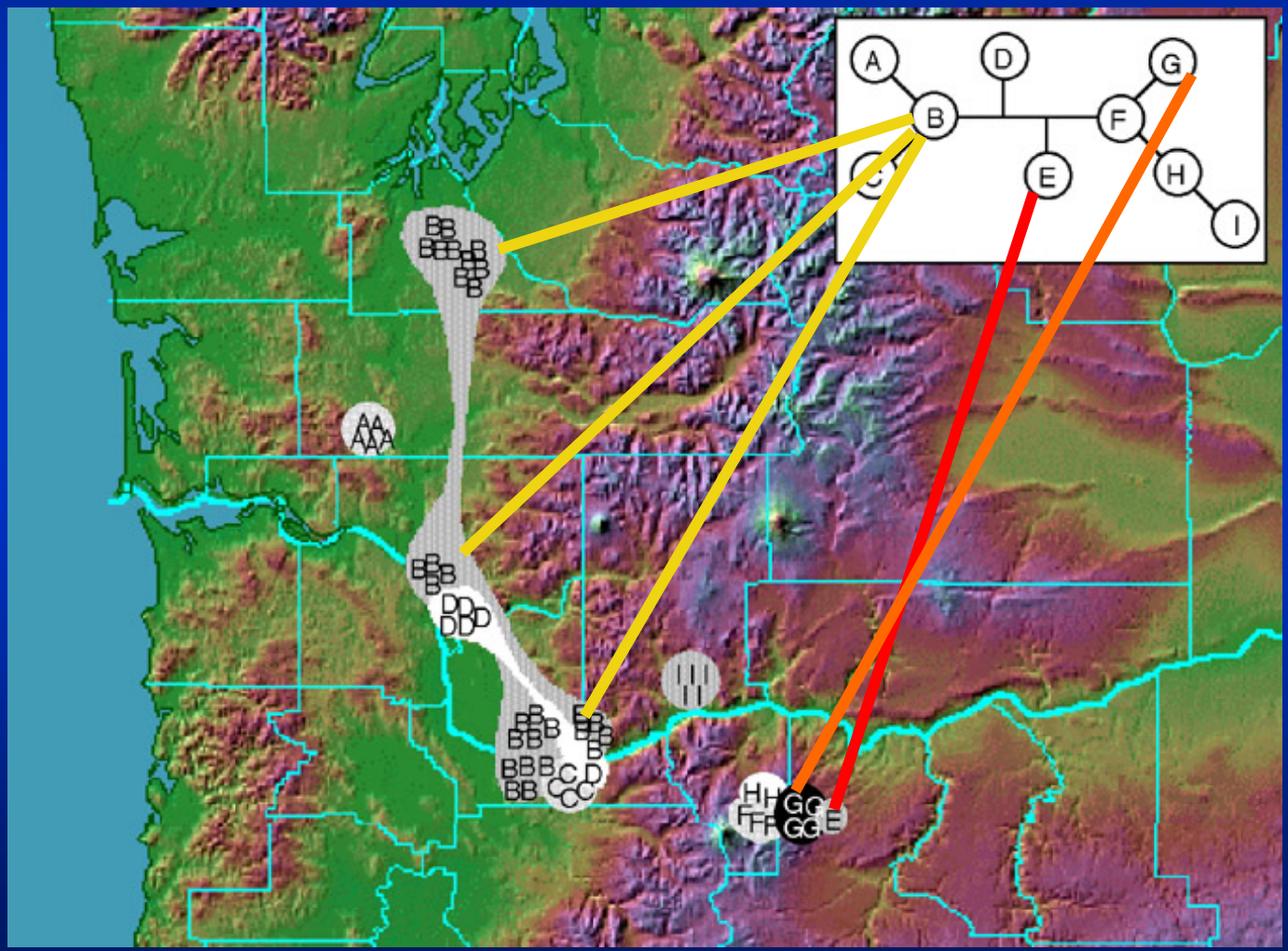
Population Genetics

- Generally used for management of captive populations
- Species Survival Plans require the creation of breeding recommendations

Systematics

- More useful for analysis and management of wild (in situ) populations
- Discover new species that may be unprotected and establish a new refuge

Example of a Haplotype Network for *Delphinium* from Washington State



Phylogentics of the *Hapalemur* (Bamboo Lemur)

Hapalemur griseus

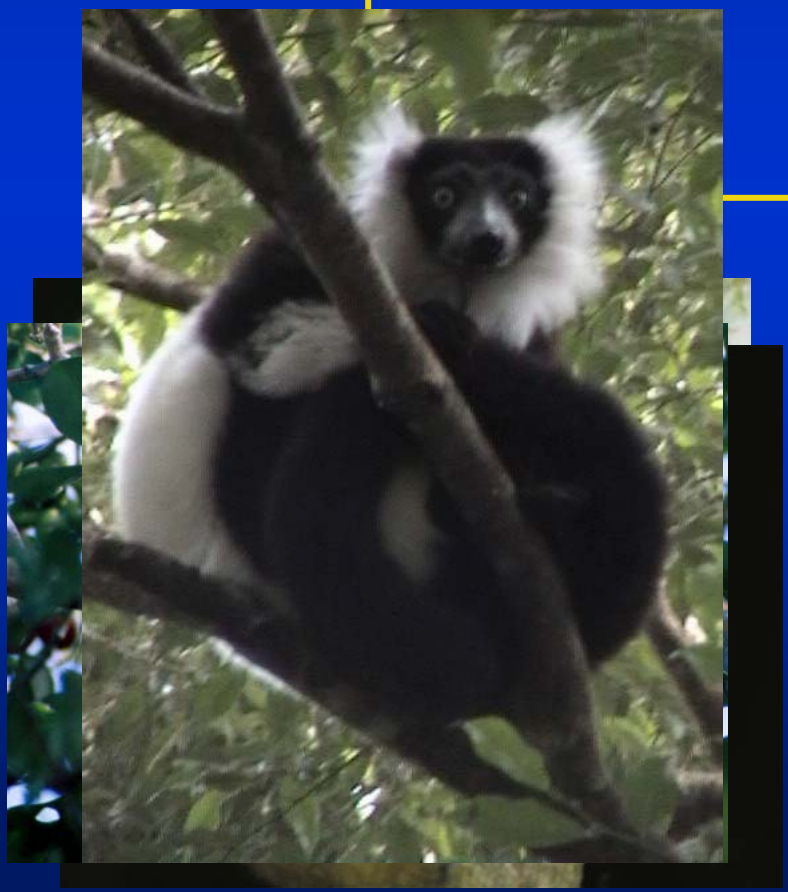
Hapalemur aureus

Hapalemur simus

Madagascar

Study Area

Phylogram for 3 Species of *Hapalemur*



5 changes

BET51VVV
BET52VVV
FAN9VVV
FAN15VVV
KIAN137VVV
KIAN45VVV

Rano83HG
Rano133HG
Rano134HG
Rano118HG
Sin6HG
Sin19HG
Rano311HG
Sin7HG
Sin8HG
Sin20HG
Sin24HG
Sin25HG
Rano117HG
Tra264HG
Tra265HG

Rano337HS
Rano338HS
Rano339HS
Rano340HS
Rano355HS
Rano356HS
KAR1HS
KAR2HS
KAR3HS
KIAN101HS
KIAN114HS
KIAN116HS
KIAN124HS
KIAN140HS
KIAN151HS
KIAN152HS
KIAN153HS

Rano334HA
Rano335HA
Rano349HA
Rano336HA
Rano350HA
Rano351HA
Rano352HA
Rano353HA
Rano354HA
Rano347HA
Tra267HA

Outgroup

H. griseus

H. simus

H. aureus