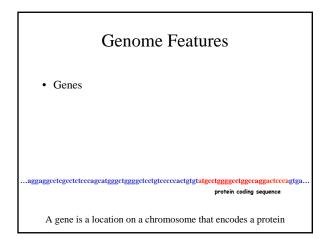
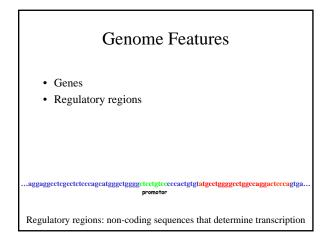


| Genome Complexity | | | |
|------------------------|--------|-------------|--|
| Organism: | Mbases | # of genes: | |
| E. Coli | 4.6 | ~4,000 | |
| Baker's yeast | 12.1 | ~6,000 | |
| Fruit fly | 180.0 | ~13,000 | |
| Worm | 97.0 | ~18,000 | |
| Human | 3200.0 | ~30,000 | |
| Human mitochondrion | 17kb | 37 | |





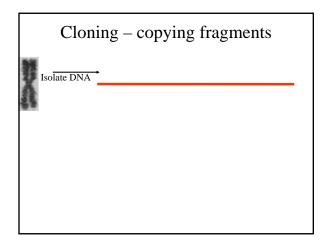


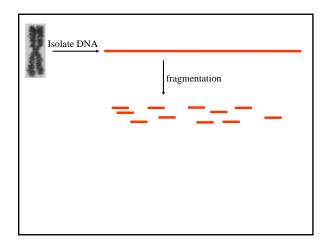
DNA Sequencing

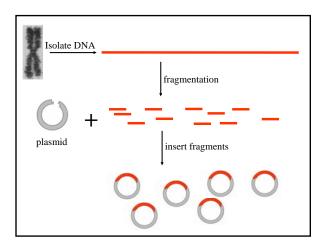
- Tools for manipulating DNA Enzymes that cut, paste and modify
- Methods for copying DNA fragments
- Methods for determining the sequence of fragments
- Assembling fragments into finished sequence

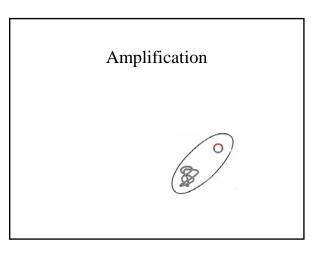
DNA Sequencing

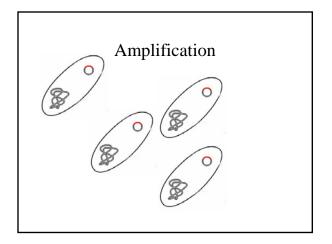
- Tools for manipulating DNA Enzymes that cut, paste and modify
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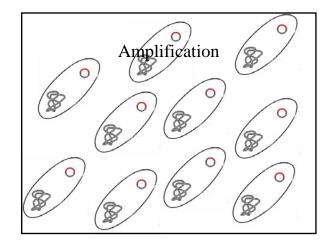












Cloning vectors

Properties

- Size of insertHost
- Stability of insert

Examples

| – Plasmids | 5-10 Kb |
|-------------------------------------|------------|
| Lambda Phage | 20 Kb |
| - BAC (Bacterial Artificial Chrom.) | 100-200 Kb |

– YAC (Yeast Artificial Chrom.)

Fragment Sequencing

- Tools for manipulating DNA Enzymes that cut, paste and modify
- Methods for copying DNA fragments
- Methods for determining the sequence of fragments

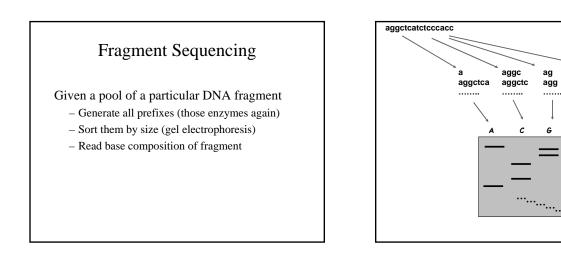
aggct

т

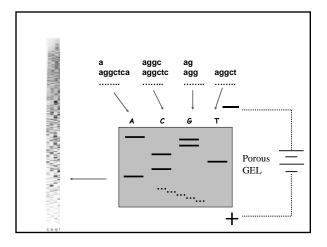
+

Porous GEL

• Assembling fragments into finished sequence

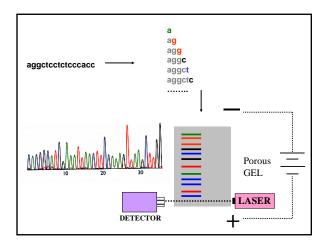


1000 Kb



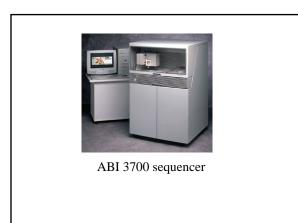
Improvements in Sequencing Technology

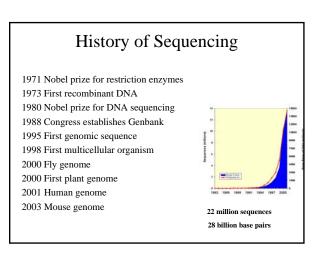
• Fluorescent bases



Improvements in Sequencing Technology

- Fluorescence bases
- Automation
- Polymerase Chain Reaction (PCR)
- Capillary-based sequencing machines

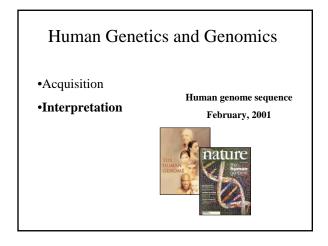




DNA Sequencing

- Tools for manipulating DNA Enzymes that cut, paste and modify
- Methods for copying DNA fragments
- Methods for determining the sequence of fragments
- Assembling fragments into finished sequence

Sequence Assembly Limits of gel electrophoresis: ~ 500bp in one "read" To sequence more than 500 bp: Sequence 500bp fragments separately Combine *computationally* using sequence comparison



Variation within the Human Genome

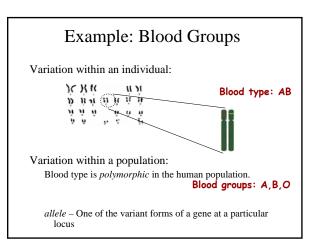
Polymorphism -

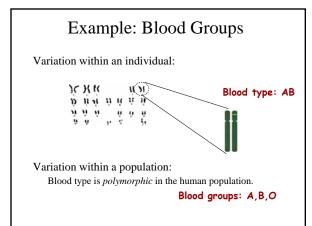
- Occurrence of more than one type of genetic feature within a population.
- A common variation in the sequence of DNA among individuals.

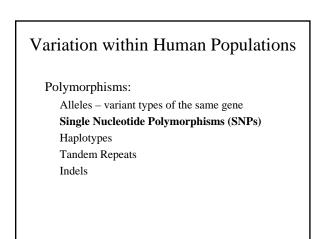
Variation within Human Populations

Polymorphisms:

Alleles – variant types of the same gene Single Nucleotide Polymorphisms (SNPs) Haplotypes Tandem Repeats Indels







Single Nucleotide Polymorphisms

SNP:

Variation at a single nucleotide position. Roughly one every 1,000 bases in the human genome.

Variation within Human Populations

Polymorphisms: Alleles – variant types of the same gene Single Nucleotide Polymorphisms (SNPs)

Haplotypes Tandem Repeats

Indels

Haplotypes

GCTTTAATTATCACGATATAATATAATAACGATT GCTTTAATTTTCACTATATAATAATAACGATT GCTTTAATTTTCACGATATACTATAACGATT GCTTTAATTATCACGATATAATAAACGATT GCTTTAATTTTCACCATATAATAAACGATT

A genomic region that is inherited as a unit

Variation within Human Populations

Polymorphisms:

Alleles – variant types of the same gene Single Nucleotide Polymorphisms (SNPs) Haplotypes **Tandem Repeats (copy number)** Indels

Variation within Human Populations

Polymorphisms:

Alleles – variant types of the same gene Single Nucleotide Polymorphisms (SNPs) Haplotypes Tandem Repeats **Insertions and deletions**

gccaggctgagagcctgctcctgtccaga

...aggcgcctggacttgtgcctggccaggctgagagcctgctcctgtccagagtgag...

Interpretation of genomic variation

- · Genetic basis for disease
- History
 - Patterns of migration, epidemics, population subdivision
- Anthropology

 Linguistics, religion
- Evolution

Interpretation of genomic variation

Use polymorphism to address questions like:

- Are all jews biologically related?
- Where did the Basques come from?
- Did humans originate only in Africa?
- When did humans come to the new world?
- Why is sickle cell disease more prevalent among African Americans?
- Did humans interbreed with Neanderthals?

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- Annette McCleod
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