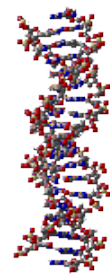


Genomics



An Introduction to Genomics

- Genomics in Medicine, part I;
ASCB iBioseminar by Dr. Brian Druker from
Oregon Health & Science University Cancer Institute
- Human Genome Project
- Genomics in Medicine, part II
- Genome Organization
- Bioinformatics
- Gene Expression in a Model Organism

Mapping Human Disease Genes

- Approximately 12 disease genes mapped by 1989
- Thousands of human disease genes have been identified and mapped as a result of the Human Genome Project (completed in 2003)

**What have we learned about
ourselves from sequencing model
organism genomes?**

Just how unique are humans?

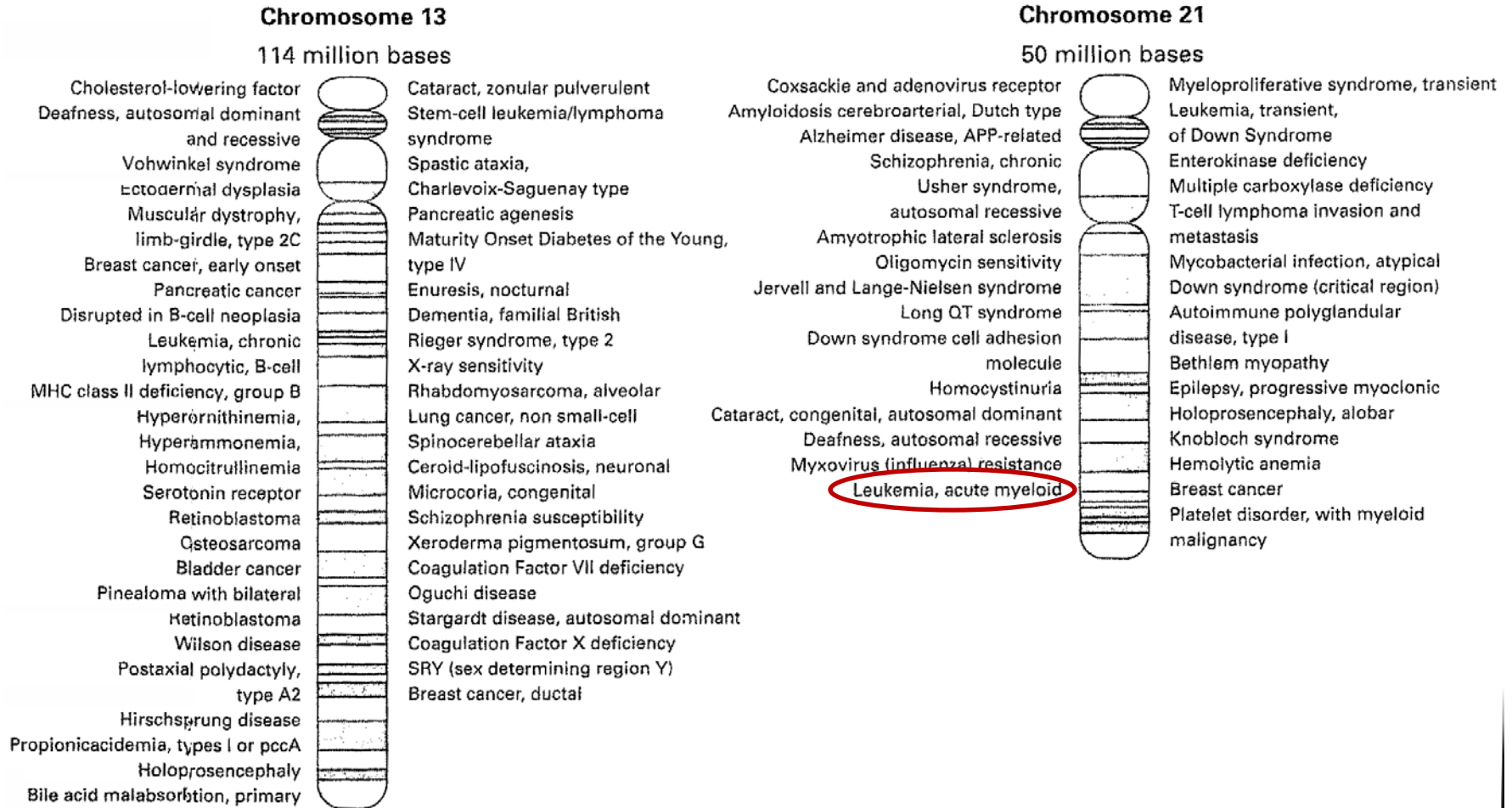
- Large numbers of genes are in common with other organisms
 - ~50% of our genes are also found in fruit flies
 - ~40% of our genes are also found in roundworms
 - ~30% of our genes are also found in yeast
 - ~80% of our genes are shared with the mouse and ~96% of our genes are shared with chimpanzees
 - ~100 of our genes are even shared with bacteria

What else can we learn using model organisms?

Many genes determining body plan, organ development, and aging are nearly identical to genes in the fruit fly

~61% of genes mutated in nearly 300 human disease conditions are found in the fruit fly. Genes include those involved in prostate cancer, pancreatic cancer, cardiac disease, cystic fibrosis, leukemia, and many other human genetic disorders.

Disease genes on chromosomes 13 and 21



Mapping the Cancer Genome

DNA sequencing of a cytogenetically normal acute myeloid leukaemia genome

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Acute myeloid leukaemia is a highly malignant haematopoietic tumour that affects about 13,000 adults in the United States each year. The treatment of this disease has changed little in the past two decades, because most of the genetic events that initiate the disease remain undiscovered. Whole-genome sequencing is now possible at a reasonable cost and timeframe to use this approach for the unbiased discovery of tumour-specific somatic mutations that alter the protein-coding genes. Here we present the results obtained from sequencing a typical acute myeloid leukaemia genome, and its matched normal counterpart obtained from the same patient's skin. We discovered ten genes with acquired mutations; two were previously described mutations that are thought to contribute to tumour progression, and eight were new mutations present in virtually all tumour cells at presentation and relapse, the function of which is not yet known. Our study establishes whole-genome sequencing as an unbiased method for discovering cancer-initiating mutations in previously unidentified genes that may respond to targeted therapies.

Major findings of AML study

- Comparison of genome from normal skin compared to tumor cell from same patient
- 10 protein-coding gene differences: 2 already identified genetic alterations and 8 previously unknown mutations
- Alterations also noted in non-coding DNA
- Differences noted in genes from other AML patients suggests complex and diverse pathways to cancer onset and progression
- Prospect for *personalized treatment strategies* over time

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iBioSeminar by [Dr. Brian Druker](#)

***"Imatinib (Gleevec) as a
Paradigm of Targeted
Cancer Therapies"***