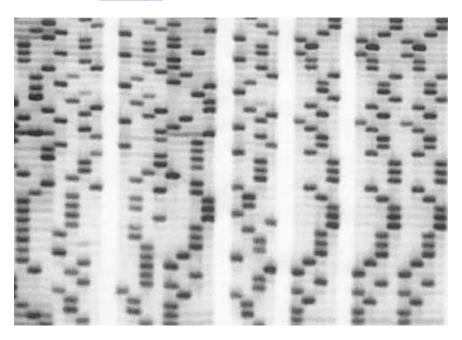
# **DNA** sequencing with chain-terminating inhibitors

F. Sanger, S. Nicklen, and A. R. Coulson



Presented by Kim Butt, Yumiko Komatsu, and Amelia Parrott

### Nobel Prize in Chemistry (1980)

"for his fundamental studies of the biochemistry of nucleic acids, with particular regard to recombinant-DNA"

"for their contributions concerning the determination of base sequences in nucleic acids"

Paul Berg

Walter Gilbert Fred Sanger

# **DNA Sequencing Timeline**

1953 – Structure of DNA double helix deduced by Watson and Crick

1972 - Development of recombinate DNA technology by Berg

1975 – Plus and minus method of DNA sequencing developed by Sanger

<u>1977</u> – DNA sequencing dideoxy method developed by Sanger

1986 – PCR developed by Mullis

1986 - First semi-automated DNA sequencing machine announced

2000 - Drosophila genome is completed

2003 – Human genome sequence is released

# The Dideoxy Method

#### PRINCIPLE BEHIND THE METHOD

**Sanger method** - DNA sequencing using <u>chain-terminating inhibitors</u> to terminate DNA synthesis at a specific site

- also known as the dideoxy method

### How did Sanger come up with this method?

### **Method**

### 1. Preparation of ddNTPs

Complex chemistry

Now: A lot of materials are commercially available

## 2. Sequencing procedure:

#### **Chain termination method:**

- Primer annealed to tDNA in H buffer
- Template DNA from Phage Phi X174

Make 5 separate mixtures and incubate as follows:

**dATP** chase—put additional dATP into each of the tube & incubate.

A critical step to avoid random termination at A residues

Figure 1: Small primer, no further splitting required

Figure 2: Longer primer, further splitting was necessary to separate the primer from synthesized DNA.

• Used restriction enzyme, Hae III.

Electrophoresis on 12% acrylamide gel to separate fragments of different sizes

Autoradiograph was used to visualize bands

# **Results**

- Figure 1 Small primers do not need to be removed before sequencing.
- Figure 2 Long primers must be removed before sequencing.
- Figure 3 Fragments with multiple restriction sites close together are problematic.
  - Problems can be avoided with single site ribosubstitution.

# **Discussion**

The dideoxy method is the **simplest**, **fastest**, and **most effecient** method of sequencing DNA to date.

#### **However**

This paper was written in 1977.

DNA sequencing has significantly advanced since this paper was written.

Modern techniques are based on the **same principles** as the dideoxy method.

See cycle sequencing.

The Phi X174 genome has been synthesized as of 2003.

Biology 4241 Homepage