

## Notes to Instructors

### Chapter 21 Genomes and Their Evolution

#### What is the focus of this activity?

While the Sanger method for sequencing DNA and the modifications that follow are conceptually fairly simple, most students don't understand them. As noted previously, in order for most students to understand unfamiliar processes, they need to build models for themselves to discover what it is they understand and, more important, what they don't.

#### What is this particular activity designed to do?

##### Activity 21.1 How can we discover the sequence of an organism's DNA?

This activity allows students to interpret the results of a classic Sanger method for sequencing a DNA molecule only 20 bp long. It then asks them to translate these results into the results they would expect using more modern fluorescently tagged ddNTP methods.

#### What misconceptions or difficulties can this activity reveal?

Because much of the methodology and information in this area is relatively new, students tend to lack conceptions in this area rather than have misconceptions. Walking them through how sequencing is done and how it is interpreted should overcome this.

## Answers



##### Activity 21.1 How can we discover the sequence of an organism's DNA?

Bacterial genomes have between 1 million and 6 million base pairs (Mb). Most plants and animals have about 100 Mb; humans have approximately 2,900 Mb. Individual chromosomes may therefore contain millions of base pairs. It is difficult to work with DNA sequences this large, so for study purposes the DNA is broken into smaller pieces (approximately 500 to 1,000 bp each). These pieces are sequenced and then the sequenced pieces are examined and aligned based on overlapping sequence homology at their ends.

# Genomes And Their Evolution Answer Key

**Xiaolong Qi**



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