

## Shimadzu Developments in Biotechnology

# DNA Analysis Activities Contributes to 21st Century Genetic Research

Protein Structural Analysis on Consignment Service Commenced Spring 2001

The success of the Human Genome Project in reading all the base sequences of the human genome is still a recent memory. However, even this brilliant achievement is no more than the first step into the exciting world of biotechnology that humans are destined to explore. Basic research into determining which of the 3 billion base pairs carry out which genetic functions is not even halfway complete. In addition, decoding the genetic make-up of most of the world's plants and organisms also remains a task for the future.

### Decoding Base Sequences Demands Significant Time and Money

DNA analysis (reading the base sequence) is the foundation of genetic research, but this work requires great time and effort. Even the smallest amount of DNA extracted from cells is made up of tens of millions of bases that cannot be read directly. First, the DNA must be broken into fragments of several hundred base pairs. Second, a large number of copies of these fragments must be made and subjected to a special pretreatment in order to create a sample for the automatic sequencer. Finally, the information from the analysis is processed by a computer and recombined to correspond to the length of the original DNA. Only then is the decoding process of the base sequence of the DNA complete. This total process requires a wide range of equipment, including an automatic base sequence analyzer.

Many Shimadzu products, including RISA-384, the world's fastest automatic DNA sequencer, have contributed significantly to genetic research throughout the world.

Based on these important products and a rich store of knowledge, Shimadzu launched the Genomic Research Department in April 2000, to further contribute to genetic research in the 21st century.

### Excellence in Algal Genome Analysis and Other In-House Research

The role of the Genomic Research Department fall into two main categories. One is to conduct analysis on consignment for universities and public research institutions. The facilities, which include four RISA-384 units, are capable of analyzing two to three million base pairs per day. The Genomic Research Department offers three types of service on consignment, including analysis with pretreatment. (Fig. 1)

The other role of the Genomic



Fig. 1 Analysis on Consignment Services Offered by the Genomic Research Department

Fig. 2 Blue-green Algae *Synechococcus* (courtesy of Graduate School of Human Informatics, Nagoya University)

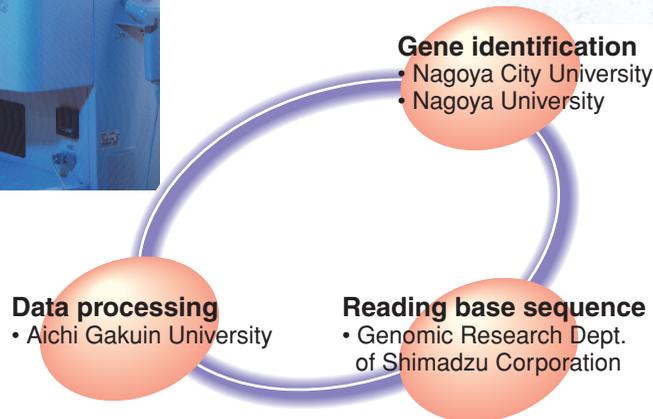


Fig. 3 Blue-green Algae *Synechococcus* (No. 6301) Genome Analysis Project

Research Department is to conduct in-house research with the cooperation of other DNA research organizations. Work on decoding the DNA of the blue-green algae *Synechococcus* is already complete. (Fig. 2) Blue-green algal bacteria are widely distributed throughout the hydrosphere, and some 1600 types are known at present. Blue-green algae are said to be the first organisms on Earth that formed oxygen and carbohydrates through photosynthesis, and thus knowledge about their genetic functions may give rise to developments in immobilization technologies for atmospheric CO<sub>2</sub>. Such research is also extremely important in clarifying the process of evolution from bacteria to plants. The Genomic Research Department initiated a joint-research project with Nagoya University to decode the DNA base sequence (Fig. 3), which was completed early in 2001. Nagoya University is currently continuing

research into the genetic functions. However, the results of the base sequence analysis indicate that *Synechococcus* followed a very different evolutionary path than other blue-green algae.

### Technology under Development for SNPs Analysis

The genome of *Synechococcus* contains approximately 27 million base pairs, but in practice the DNA shotgun sequencing used in the project required ten times this number of base analyses.

The fact that fish genomes contain anywhere from several hundred million to ten billion base pairs, and that some plant genomes have 100 billion base pairs, illustrates the importance of efficient base sequence analysis. Such work, however, cannot be efficiently conducted by a single research organization due to the high costs and personnel demands, which means that the Shimadzu

Genomic Research Department can play a major role in this research. Indeed, the number of analyses requested has grown rapidly since Shimadzu launched this service, and the Genomic Research Department is now running at full capacity. After genome analysis, the next most significant research topic for the Genomic Research Department is the analysis of protein structures. Through the introduction of cutting-edge mass spectrometers and cooperation with overseas partners, the Genomic Research Department also began a protein structure analysis on consignment service in April 2001. Shimadzu is also developing SNPs (Single Nucleotide Polymorphisms) analysis technology that is expected to find widespread medical applications, and will offer an SNPs analysis on consignment service in the future.

(Editorial supervision: Mr. Jun Takano, General Manager, Genomic Research Dept. of Shimadzu Corporation)