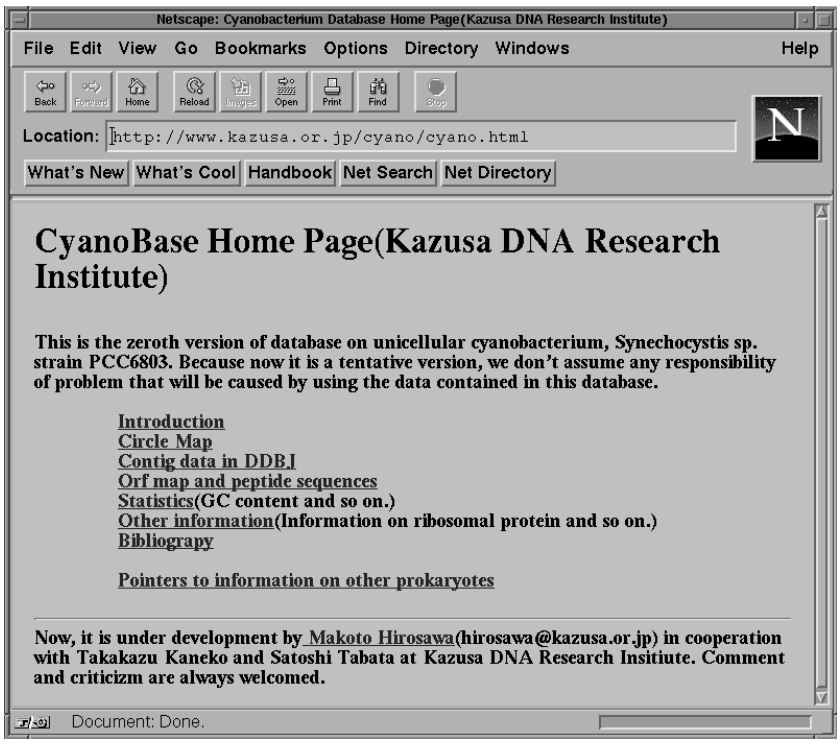

Figure 1: Home page of CyanoBase

of a single organism. The sequence data we gained have been registered in public databases and published in journals. However, the information available through the databases are very limited. There exist several frameworks of presenting sequence information(e.g. AceDB, Genomatica), but we selected the presentation through WWW because of easy access and manipulation (http://www.kazusa.or.jp/cyano/cyano.html).

CyanoBase provides information registered in public databases and related publications, additional information gained through the project, and information on related organisms which can access by pointing to proper sources in WWW. Thanks to WWW technology, users can see desired information in CyanoBase just by clicking a proper place in the windows and retrieve any information by utilizing facilities in WWW. The information stored in CyanoBase at present are in the above figure.

References

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CyanoBase: Visual presentation of information on the genome of Cyanobacterium Synechocystis sp. strain PCC6803 through WWW

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Abstract

Kazusa DNA Research Institute launched a project of sequencing the entire genome of an unicellular cyanobacterium Synechocystis sp. strain PCC6803 in 1994. The data that we gained through the project have been registered in public databases. But, it is not easy to properly grasp information on the cyanobacterium genome with only the information in the databases.

Now, we constructed CyanoBase, a data presentation system through WWW, that enables users to visualize the genomic information of this species. CyanoBase includes the additional information that are not described in public databases.

Overview of CyanoBase

The advance of technology of Internet enables biologists to collect necessary information through computer terminals. The trend demands the providers of data more sophisticated presentation of sequence data. Our institute, Kazusa DNA Research Institute, launched a project of sequencing the entire genome(3.6 Mb) of a unicellular cyanobacterium Synechocystis sp. strain PCC6803[1]. We determined a continuous 1.0 Mb sequence of this strain and assigned 818 ORFs tentatively[2]. We will finish determination of the whole genome until the first half of the next year.

The cyanobacterium has been used as a model organism for the study of oxygenic photosynthesis because it carries a complete set of genes for oxygenic photosynthesis. The deduction of its entire genome sequence will not only be a great contribution to the study of the mechanism of oxygenic photosynthesis but also the comprehensive understanding of genome organization

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