

### III. INFORMATION ON STRAINS (保存株関連情報)

#### 1. Phylogenetic position of the cyanobacterial strains (シアノバクテリア保存株の系統的位位置)

Neighbor-joining (NJ) tree based on 16S rDNA sequences: The tree contains 78 strains of NIES cyanobacteria. Some cyanobacterial genera such as *Synechococcus* and *Phormidium* are polyphyletic in this tree. Strains showing identical or more than 99% identical sequences are listed in the same branch. Bootstrap values >50 are shown near branches (maximum parsimony (MP) / NJ). Sequences were aligned by using ClustalX (Thompson *et al.* 1997) and edited manually with BioEdit 7.01 (Hall 1999). Phylogenetic analysis was conducted with PHYLIP ver.

3.66 (Felsenstein 1993). NJ analysis using “dnadist” and MP analysis using “dnapars” were performed. Bootstrap values (100 replicates) were obtained by using “seqboot” in PHYLIP.

#### REFERENCES

- Hall, T. A. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. *Nucleic Acids Symposium Series* 41: 95–98.
- Thompson, J. D., Gibson, T. J., Plewniak, F., Jeanmougin, F. & Higgins, D. G. 1997. The ClustalX windows interface: flexible strategies for multiple sequence alignment aided by quality analysis tools. *Nucleic Acids Research* 24: 4876–4882.
- Felsenstein, J. 1993. PHYLIP (phylogeny Inference Package) University of Washington, Seattle.

