SHORT COMMUNICATION

Genetic Relationships among Cyanobacterial Strains Originally Designated as 'Anacystis nidulans' and Some Other Synechococcus Strains

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(Received 14 June 1984)

Determinations of the genetic relationships between six Synechococcus strains demonstrated that three strains, originally designated as 'Anacystis nidulans', belong to one and the same species. The other three strains belong to other species and/or genera. This conclusion is discussed with regard to a recently proposed revised classification of the genus Synechococcus.

INTRODUCTION

Rippka et al. (1979) provisionally recognized only two genera of unicellular cyanobacteria (blue-green algae) that possess thylakoids and divide by equal binary fission in one plane: Gloeothecae and Synechococcus. On the basis of the DNA base compositions of the strains belonging to the latter genus, three compositional subgroups, with spans of 39–43, 47–56 and 66–71 mol% GC, were recognized (Herdman et al., 1979; Rippka et al., 1979), which already indicated that generic separations could be justified.

In a revised classification, based mainly on the differences in GC content, Rippka & Cohen-Bazire (1983) proposed that the genus Synechococcus should be split into four genera: Cyanobacterium, with a relatively low GC content (39–41 mol%) and a relatively low cell width (about 2 μm); Cyanothecae, with a mol% GC of 42 and relatively wider cells (4–6 μm); Synechococcus, with 47–56 mol% GC; and Cyanobium with 66–71 mol% GC. The recognition of these four genera is more or less supported by mutual differences in a number of phenetic properties. However, Rippka & Cohen-Bazire (1983) did not exclude the possibility of further generic subdivisions of the newly defined genus Synechococcus.

The differences in GC contents used for the revised classification indicate considerable genetic differences both between the proposed genera Cyanobacterium, Cyanobium and Synechococcus and within the latter genus. This paper describes results obtained from DNA–DNA reassociation experiments with DNA from six strains, one representative of Cyanobium, one of Cyanobacterium and four of Synechococcus, including those strains originally, but erroneously, designated 'Anacystis nidulans', viz. strains Tx20 (UTEX 625), R2 and 602.

METHODS

Strains. All strains (Table 1) were obtained from the Pasteur Culture Collection (PCC), Paris, France. Table 1 also includes the original designation of the strains and their generic identity as proposed by Rippka & Cohen-Bazire (1983). Growth conditions were described by Stulp & Stam (1984), except that strains were mass-cultured in BG-11 medium (Rippka et al., 1979).

Extraction of DNA and determination of base composition. DNA was extracted as described by Stulp & Stam (1984), except that the cells were disrupted in a French press only. The DNA base composition of strain 7942 was determined from the UV absorbance–temperature profile (Mandel & Marmur, 1968; de Bont et al., 1981).

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Table 1. Synechococcus strains used

For more detailed information on strain histories and properties see Rippka et al. (1979) and Rippka & Cohen-Bazire (1983). PCC, Pasteur Culture Collection, Paris, France; UTEX, University of Texas Culture Collection, Austin, Tex., USA.

<table>
<thead>
<tr>
<th>PCC strain no.</th>
<th>Original designation</th>
<th>Proposed generic identity*</th>
</tr>
</thead>
<tbody>
<tr>
<td>7502</td>
<td>Synechococcus sp.</td>
<td>'Cyanobacterium'</td>
</tr>
<tr>
<td>6301</td>
<td>Anacystis nidulans Tx20; UTEX 625 and 1550</td>
<td>'Synechococcus'</td>
</tr>
<tr>
<td>6312</td>
<td>Synechococcus sp.</td>
<td>'Synechococcus'</td>
</tr>
<tr>
<td>7942</td>
<td>Anacystis nidulans R2</td>
<td>'Synechococcus'</td>
</tr>
<tr>
<td>7943</td>
<td>Anacystis nidulans 602</td>
<td>'Synechococcus'</td>
</tr>
<tr>
<td>6307</td>
<td>Coccochloris penicystis 120; UTEX 1548</td>
<td>'Cyanobium'</td>
</tr>
</tbody>
</table>


Labelling of DNA and DNA-DNA hybridizations. Nick-labelled [\(^3\)H]DNA samples (Stulp & Stam, 1984) were purified by passage through a Sephadex G100 (Pharmacia) column eluted with 0-03 M-sodium phosphate buffer (NaPB) containing 0-15 M-NaCl. After heat denaturation (100 °C, 10 min) the [\(^3\)H]DNA was loaded onto a hydroxypatite micro-column. After prewashing with 0-03 M-NaPB + 0-135 M-NaCl at 50 °C and 0-03 M-NaPB at 60 °C, the single-stranded (ss) [\(^3\)H]DNA was eluted with 0-15 M-NaPB at 60 °C.

Hybridizations were performed, in duplicate, at 64 °C. Unreassociated DNA (ss fraction) was collected by hydroxypatite chromatography at 60 °C with 0-15 M-NaPB. The reassociated (double-stranded) DNA (ds fraction) was subjected to thermal elution with 0-15 M-NaPB (Stulp & Stam, 1984) including a final 0-3 M-NaPB elution at 95 °C. Total radioactivity in the ds fraction relative to the total radioactivity (ss fraction + ds fraction) gave the renaturation rate for each hybridization. The renaturation rate in a heteroduplex relative to that in the homoduplex gave the relative binding (RB, %) of a heteroduplex. The difference in thermal stability (\(\Delta T_{\text{m(\text{el})}}\)) between hetero- and homoduplexes was derived from computer-plotted thermal elution curves as the difference in temperature at 50% elution (Stulp & Stam, 1984).

**RESULTS AND DISCUSSION**

Table 2 presents the RB and \(\Delta T_{\text{m(\text{el})}}\) values of strains 7502 (Cyanobacterium); 6312, 7942 and 7943 (Synechococcus); and 6307 (Cyanobium) determined from reassociations of DNA from these strains with DNA from the reference strain 6301 (Synechococcus = 'Anacystis nidulans' 625). Strains 7942 (‘Anacystis nidulans’ R2) and 7943 (‘Anacystis nidulans’ 602) show high RB values (94 and 97%, respectively) and low \(\Delta T_{\text{m(\text{el})}}\) values (1.3 and 2.2 °C, respectively), which means that these strains are genotypically almost identical with strain 6301. Strain 6312 shows some genotypic relationship with strain 6301 (RB = 31%, \(\Delta T_{\text{m(\text{el})}}\) = 5-6 °C), while strains 7502 and 6307 are genotypically only slightly related to strain 6301 (RB = 13% for both). For strains 7502 and 6307 \(\Delta T_{\text{m(\text{el})}}\) was not calculated since the amount of heteroduplexes in the reassociation mixture was too low to obtain accurate thermal elution patterns.

The known GC contents of the strains (Table 2) are in agreement with the results discussed above, including the intermediate RB and \(\Delta T_{\text{m(\text{el})}}\) values for strain 6312 and its 6 mol% GC content difference from reference strain 6301.

These data permit the following taxonomic conclusions. Strains 6301, 7942 and 7943 belong to one and the same species. Strain 6312 is a member of the same genus as strain 6301 and strains 7502 and 6307 probably belong to other and mutually different genera. These conclusions are in agreement with the revised classification proposed by Rippka & Cohen-Bazire (1983) and confirm their doubt about the taxonomic homogeneity of the newly defined genus Synechococcus, although in the case of strain 6312 only specific, rather than generic, subdivision seems appropriate.

Following Stanier et al. (1971), Rippka & Cohen-Bazire (1983) proposed that strain 6301 be recognized as the neotype of Synechococcus elongatus. If this proposal is validated under the rules of the International Code of Nomenclature of Bacteria, strains 7942 and 7943 should be named...
The genetic difference between strains 7502 and 6301 (RB = 13%) in agreement with 16S RNA cataloguing data, which revealed that these strains are only distantly related (Doolittle, 1982). The taxonomic position of strain 7502 with regard to the newly proposed type strain *Cyanobacterium stanierii* PCC 7202 (Rippka & Cohen-Bazire, 1983) is still unclear and should be revealed by further DNA–DNA reassociation experiments.

The authors are grateful to R. Rippka for placing at their disposal both the *Synechococcus* strains used and information concerning these strains. During preparation of this paper A.M.R.W. was 'Aspirant du Fonds National Belge de la Recherche Scientifique.'

**REFERENCES**


HERDMAN, M., JANVIER, M., WATERBURY, J. B.,

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**Table 2. DNA base compositions of the *Synechococcus* strains and relative binding (RB) and \( \Delta T_{\text{m}} \) values determined from DNA–DNA reassociations using DNA from strain 6301 as reference**

<table>
<thead>
<tr>
<th>PCC strain no.</th>
<th>GC content* (mol%)</th>
<th>RB (%)</th>
<th>( \Delta T_{\text{m}} ) (°C)</th>
</tr>
</thead>
<tbody>
<tr>
<td>7502</td>
<td>41</td>
<td>13 ± 2.3</td>
<td>—</td>
</tr>
<tr>
<td>6301</td>
<td>56</td>
<td>(100)</td>
<td>0</td>
</tr>
<tr>
<td>6312</td>
<td>50</td>
<td>31 ± 2.4</td>
<td>5.6 ± 0.5</td>
</tr>
<tr>
<td>7942</td>
<td>55</td>
<td>94 ± 0.1</td>
<td>1.3 ± 0.1</td>
</tr>
<tr>
<td>7943</td>
<td>—</td>
<td>97 ± 3.1</td>
<td>2.2 ± 0.5</td>
</tr>
<tr>
<td>6307</td>
<td>70</td>
<td>13 ± 0.2</td>
<td>—</td>
</tr>
</tbody>
</table>

* From Herdman et al. (1979), except the GC content for strain 7942, which was determined by the present authors.


