Comparative Study of DNA Methylation in Three Unicellular Eucaryotes

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We have analyzed the nature/content of methylated bases in the nuclear DNA of three unicellular eucaryotes. The pattern of methylation was different for each of the three organisms studied: Saccharomyces cerevisiae contained only 5-methylcytosine; Tetrahymena pyriformis contained only N\textsuperscript{6}-methyladenine; and Chlamydomonas reinhardi contained both modified bases.

The occurrence of methylated bases in cellular DNA appears to be universal (5, 17). In procaryotes both N\textsuperscript{6}-methyladenine (MeAde) and 5-methylcytosine (MeCyt) have been observed; in contrast, in plants and higher animals only MeCyt has been detected with certainty. However, in a study of green algae, Pakhomova et al. (13) reported the presence of very low levels of MeAde also (approximately 1 MeAde per 500 Ade residues). The methods used in that study relied on measurement of differences in spectral absorption ratios. Using radioisotope labeling, we demonstrated that the ciliated protozoan, Tetrahymena pyriformis, contains MeAde in its macronuclear DNA (1 MeAde per 120 Ade residues), whereas micronuclear DNA has little or no MeAde (6). MeAde has also been found in the DNA of Paramecium aurelia, but unlike other eucaryotes Paramecium DNA is devoid of MeCyt (4). The DNA of the dinoflagellate, Peridinium triquetrum, has also been observed to contain MeAde (14). The present communication describes a comparative analysis of the nature and level of methylated bases in the DNA of several unicellular eucaryotes (a preliminary account of part of these studies has been reported [C. Kenny and S. Hattman, Abstr. Annu. Meet. Am. Soc. Microbiol. 1977, Abstr. no. K245, p. 227]).

The results of these studies are summarized in Table 1. We repeated the observation that Tetrahymena macronuclear DNA contains MeAde. In contrast, Tetrahymena DNA appears to lack MeCyt; i.e., there is less than 1 MeCyt per 5,000 Cyt residues (Table 1). This conclusion was confirmed by examining DNA from cells labeled in the presence of [methyl-\textsuperscript{3}H]methionine. We observed 49,000 cpn in [\textsuperscript{3}H]MeAde and no detectable radioactivity in MeCyt (data not shown). This pattern of DNA methylation is similar to that of another ciliated protozoan, P. aurelia (4); we have also confirmed that MeAde (1.5 mol%) is present in P. aurelia macronuclear DNA (data not shown).

It has been reported that yeast DNA lacks modified bases (8, 17). On the contrary, we were able to show that MeCyt is present in the main-band DNA of the haploid strain, D273-10b, of Saccharomyces cerevisiae (Table 1); however, there appears to be no MeAde (less than 1 MeAde per 2,000 Ade residues). These conclusions were confirmed by analyzing DNA from yeast labeled in the presence of [methyl-\textsuperscript{3}H]methionine. The precise level of MeCyt in yeast main-band DNA was not clearly established; in two independent investigations the average MeCyt composition was 0.3 and 1.0 mol%, respectively. Although the cause for this discrepancy remains undetermined, it is clear that MeCyt is present in yeast main-band DNA. We have not yet investigated methylation in mitochondrial DNA.

As shown in Table 1, both MeCyt and MeAde are present in the nuclear DNA of the green alga, Chlamydomonas reinhardi. The level of each modified base was similar for the mt\textsuperscript{+} and the mt\textsuperscript{−} mating type (data not shown). In contrast, chloroplast DNA appears to be devoid of MeAde (<1 MeAde per 2,000 Ade residues); we were unable to obtain a sufficient quantity of radioactively labeled chloroplast DNA to determine the MeCyt content.

Other green algae have been studied with respect to DNA methylation; e.g., the nuclear DNA of Euglena gracilis has been shown to contain only MeCyt (1, 2, 15), whereas chloroplast DNA lacks MeCyt. It is interesting to note that chloroplast DNA from higher plants has never been observed to contain MeCyt, even though the nuclear DNA may contain high levels of this base.

The results presented in this paper show that...
Table 1. Content of methylated bases in the DNAs of uncellular eucaryotes

<table>
<thead>
<tr>
<th>Organism</th>
<th>DNA</th>
<th>mol% MeAdenine</th>
<th>mol% Methylcytosine</th>
</tr>
</thead>
<tbody>
<tr>
<td>T. pyriformis</td>
<td>Macronuclear</td>
<td>0.80</td>
<td>&lt;0.02</td>
</tr>
<tr>
<td>C. reinhardtii</td>
<td>Nuclear</td>
<td>0.50</td>
<td>0.70</td>
</tr>
<tr>
<td>C. reinhardtii</td>
<td>Chloroplast</td>
<td>&lt;0.06</td>
<td>Not analyzed</td>
</tr>
<tr>
<td>S. cerevisiae</td>
<td>Main band</td>
<td>&lt;0.05</td>
<td>0.3-1.0</td>
</tr>
</tbody>
</table>

* T. pyriformis (B-1868-VII) was grown axenically at 28°C in enriched protease peptone supplemented with [6-3H]uridine or [2-3H]adenine. The DNA was isolated from purified macronuclei (7) essentially according to the method of Kavnenoff and Zimm (11). C. reinhardtii (mt* and mt* mating types of strain 137c) was grown at 25°C in minimal medium (12) under continuous illumination with cool-white fluorescent light; radiisotope labeling was with [2-3H]adenine or [6-3H]uracil during growth through late log phase. The DNA was isolated from detergent-lysed cells by phenol extraction and ethanol precipitation. After extensive pancreatic and T1 ribonuclease digestion, the DNA was centrifuged to equilibrium in a CsCl gradient. The nuclear and chloroplast DNA peaks (p = 1.723 and p = 1.691 g/cm³, respectively) were purified by a second centrifugation. S. cerevisiae (haploid strain D273-10B) was grown at 30°C in Difco yeast nitrogen base (without amino acids) containing 0.6% (wt/vol) glucose and 40 μg of streptomycin sulfate per ml. Radiisotope labeling was with [2-3H]adenine or [6-3H]uracil. The DNA was isolated by phenol extraction of lyzed spheroplasts prepared essentially as described by Cryer et al. (3). After pancreatic and T1 ribonuclease digestion, nuclear DNA was separated from mitochondrial DNA by centrifugation in a CsCl gradient. We estimate that there was less than 10% mitochondrial DNA contamination of the nuclear DNA preparation. Since the nuclear DNA is separated from the cytoplasmic 2-μm DNA circles (16), which comprise about 5% of the total DNA, this fraction is referred to as main-band DNA.

The various labeled DNAs were made 0.5 N in NaOH, and any traces of remaining RNA were hydrolyzed at 37°C for 18 h. The acid-precipitable DNA was collected and hydrolyzed in 1 N HCl (for MeAdenine determination) or 70% perchloric acid; the bases were separated by descending paper chromatography as described earlier (9, 10).

1 mol% MeAdenine and mol% Methylcytosine are calculated on the basis of total Ade and Cyt residues, respectively. The values shown are the averages of analysis of several independent preparations; except for the MeCyt content of yeast, the range was not greater than ±10% of the mean.

Each of the three organisms studied has a different pattern of modified bases in DNA. Thus, among other uncellular eucaryotes there is likely to be diversity in DNA methylation similar to that found here. In procaryotes some of the DNA methylation is known to be involved in host-specific restriction/modification; however, in eucaryotes a biological function has not yet been definitively established.

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LITERATURE CITED


