

## A COMPARISON OF THE AMINO-TERMINAL SEQUENCE OF THE L7/L12-TYPE PROTEINS OF *ARTEMIA SALINA* AND *SACCHAROMYCES CEREVISIAE*

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### 1. Introduction

The ribosomal protein L7/L12 functions in the GTP-dependent reactions of protein synthesis [1,2]. A comparison of its primary structure, both in prokaryotic and eucaryotic organisms, would be of great interest, not only for localizing active sites involved in protein biosynthesis, but also for tracing evolutionary changes of the protein moiety of the ribosome.

Up to now, only the complete primary structure of *Escherichia coli* L7/L12 protein has been published [3]. Visentin et al. [4] performed sequence studies of the amino-terminal region of the *Bacillus stearothermophilus* protein, and they found that the first 15 residues are highly homologous with residues 2-16 of the *E. coli* protein. Oda et al. [5] published partial sequences of an acidic protein, L20, of *Halobacterium cutirubrum* which appears to be homologous to L7/L12. The amino-terminal region of this protein shows a substantial degree of homology with the region, starting at residue 35 of the *E. coli* protein. The presence of acidic proteins in 60 S ribosomes of the brine shrimp *Artemia salina* was previously reported by Möller et al. [6]. These proteins were shown to function in the GTP-dependent reactions in ribosomes [6,7]. We therefore assume that these

proteins are equivalent to bacterial L7/L12 and we hereafter call them L7/L12-type proteins.

The present communication is concerned with the comparison of the aminoterminal region of the L7/L12-type proteins from *Artemia salina* and the yeast *Saccharomyces cerevisiae*. The results indicate a remarkable conservation of this region and a clear relationship to the aminoterminal part of the protein from the halophile.

### 2. Materials and methods

The 80 S ribosomes from *A. salina* cysts were prepared as described earlier [6]. The L7/L12-type proteins were extracted from 80 S ribosomes by the procedure of Hamel et al. [8] and purified by carboxymethylcellulose and diethylaminoethyl-cellulose chromatography, as will be described elsewhere.

The yeast L7/L12-type proteins were extracted from 80 S or 60 S ribosomes and purified by diethylaminoethyl-cellulose chromatography, as will be described in detail elsewhere.

#### 2.1. Sequence determination of *Artemia* protein

##### 2.1.1. Automated solid-phase Edman degradation

Various methods were applied to couple the intact protein to suitable matrices. The best results were



Comparison of the two eucaryotic sequences shows a remarkable degree of homology in this part of the protein molecule: 9–10 out of 16 residues are homologous and several of the other ones may be related through single-base point mutations. There exists also a homology with *H. cutirubrum* L20: 5–7 out of 16 residues of the yeast protein, and 8 out of 25 residues of the *A. salina* protein are homologous in this part of the polypeptide chains. The clustering of two tyrosine residues near the amino-terminal end is noteworthy as is the occurrence of hydrophobic residues in equivalent positions of the polypeptide chains. A homology between *H. cutirubrum* L20 and *E. coli* L7/L12 was reported earlier [5], if the two chains were aligned such that residue-35 of *E. coli* L7/L12 matched the aminoterminal methionine residue of *H. cutirubrum* L20: 9 out of 25 residues were homologous in this case. On the basis of its aminoterminal sequence there is no doubt that *H. cutirubrum* resembles a eucaryotic rather than a procaryotic organism. In this connection we like to mention the occurrence of a bacteriorhodopsin in the membrane of the halophile, and the fact that the biosynthesis of the proteins in this organism is initiated by Met-tRNA rather than fMet-tRNA (S. T. Bayley, personal communication).

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