cDNA and predicted amino acid sequences of the human ribosomal protein genes rpS12 and rpL17

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Two new human ribosomal protein cDNAs have been isolated using heterologous differential screening. This method is based on the screening of a human cDNA library, at high stingency, with cDNA probes from avian cells. It should thus select for only highly evolutionary conserved sequences. The human cDNA library was constructed from Raji human lymphocytes (1), and was screened with a set of heterologous probes derived from quail neuroretina cells (QNR) induced to divide with a thermosensitive src mutant NYts68 of RSV-A (2). The differential hybridization technique was carried out with a couple of single stranded cDNA probes synthetized from poly(A+) RNA of RSV infected and actively dividing QNR cells (grown at 37°C) or from cells rendered quiescent by a 48 hours shift at 41.5°C.

Nucleotide sequence identified 4 differential clones as genes encoding components of the translation apparatus of the cell. Two were coding repectively for the human ribosomal protein S17 and the human elongation factor 1α whereas the last two cDNAs code for so far unknown human products. Molecular cloning of the complete cDNA sequences was subsequently achieved. Their nucleotide and deduced amino acid sequences shared high homology respectively with the rat small subunit ribosomal protein S12 (rpS12) and with the yeast large subunit ribosomal protein L17 (rpL17). The two r-proteins probes hybridize with an abundant transcript which shows that they belong to a family of highly expressed genes.

The human S12 protein contains 132 amino acids and has an estimated molecular weight of 14.5 kDa. The deduced amino acid sequence indicate that human rpL17 is a basic protein of 140 residues, and has a molecular weight of 15 kDa. Comparative analyses of protein sequences show 97% identity between the human and the rat S12 protein (3) whereas the 140 residues long L17 protein displays 78% identity with its yeast counterpart (4). Consistent with this fact, the nucleic acid sequences diverged poorly except for the non coding region (88.4% between human and rat rpS12 and 64% for human and yeast rpL17). For vertebrates, homology deduced from available ribosomal protein gene sequences, range from 82 to 92% identity in the different species. Differences are restricted to the wobble position of anticodons. The codon usage for the human rpS12 and rpL17, similar to the situation of other known ribosomal proteins, is typical of that of abundant proteins.

Surprisingly, the structure of the 5′ untranslated region (UTR) of these two human ribosomal proteins are very short (79 nt for rpS12 and 25 nt for rpL17). And for both, the 5′ UTR starts with the run of pryrimidines, typical of all vertebrates r-protein mRNAS. It has been proposed that these structural features could be involved in the regulation of dependent expression of r-protein mRNAS.

These results suggest that accumulation of transcripts of the genes coding for the translation machinery is a prerequisite for cells to achieve high rates of proliferation. It is likely that coordinated control of r-protein mRNA is also mediated by common promoter regulatory mechanisms, suggested by previous studies on the yeast(5) and mouse rp-genes (6).

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