A delayed-early response nuclear gene encoding MRPL12, the mitochondrial homologue to the bacterial translational regulator L7/L12 protein

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We have characterized a new delayed-early response mRNA encoding a 21-kDa product (MRPL12) that accumulates during the G1 phase of growth-stimulated cells. MRPL12 is the mammalian homologue to the chloroplastic and bacterial 12 ribosomal proteins. Immunofluorescence microscopy and cell fractionation indicate a predominant mitochondrial localization in various mammalian cell lines. The NH2-terminal 49 amino acids are necessary and sufficient to target the protein within the mitochondria and are probably cleaved off during import. MRPL12 proteins associate in vitro and cofractionate with mitochondrial structures, as is the case for prokaryotic L12 proteins. Expression of a dominant inhibitory truncated protein leads to a severe reduction in cell growth by inhibiting mitochondrial ATP production. MRPL12 is the first mammalian mitochondrial ribosomal protein to be characterized.

Addition of growth factors to a resting cell culture elicits a wide variety of biochemical and genetic responses. The early biochemical events trigger the cytoplasmic accumulation of newly transcribed RNAs (primary or immediate-early response RNAs), which does not require de novo protein synthesis. In fibroblastic cells, a large number of genes have been characterized as being transiently induced within 4 h of growth stimulation (1, 2). They encode various types of products, such as cytokines, structural proteins, metabolic enzymes, protein phosphatases, and transcription factors (3–6). However, activation of immediate-early response genes is not sufficient per se for eliciting DNA synthesis, which requires long-term growth factor exposure and active protein synthesis for at least 10 h (7, 8). Stimulated cells may also be blocked in late G1 upon transforming growth factor-β or glucocorticoid treatment without affecting the early biochemical and genetic events (9–11). A limited number of genes activated during late G1 have been characterized as (i) early-early response mRNAs, the accumulation of which, like immediate-early response mRNAs, does not require de novo protein synthesis. They encode products such as p53 (12), cyclin genes (13), Ras-like proteins (14), and biosynthetic enzymes or secreted proteases (15, 16). A limited number of genes have also been characterized as (ii) delayed-early response RNAs, which accumulate upon growth stimulation only when protein synthesis is active. They were found to encode various types of products, such as structural proteins, non-histone chromosomal proteins, extracellular matrix proteins, and transcription factors (18, 19).

Although mitochondrial activity is not necessary for cell growth in defined cultured conditions (20), several nuclear genes encoding mitochondrial proteins have also been described as being growth-regulated. These include the mitochondrial chaperonin hsp60 (21), the Fos transformation effector (22), an ADP/ATP carrier (23), and a proton/phosphate symporter (19).

We report here the characterization of the mammalian mitochondrial ribosomal 12 protein (mitosomal) MRPL12 protein as being encoded by a delayed-early response mRNA. MRPL12 mRNA accumulation in growth-stimulated cells occurs in proportion to the mitogenic strength and is paralleled by the accumulation of the corresponding protein. MRPL12 protein is phylogenetically related to the chloroplastic and bacterial 12 ribosomal proteins, which control mRNA translation. Immunofluorescence microscopy and cell fractionation indicate a predominant mitochondrial localization of the protein in various mammalian cell lines. The amino-terminal region is necessary and sufficient to promote a mitochondrial targeting of exogenous proteins. MRPL12 proteins associate in vitro as dimers and cofractionate with ribosomal structures from mitochondrial extracts. Expression of a truncated MRPL12 protein acting as a dominant inhibitor affects cell growth and mitochondrial ATP synthesis.

MATERIALS AND METHODS

Cell Culture—CCL39, COS-7, NIH3T3, and HeLa cells were grown, respectively, in Dulbecco's modified Eagle's medium and RPMI 1640 medium supplemented with 10% calf serum (FCS). For serum starvation, confluent cells were incubated for 20 h with plain Dulbecco's modified Eagle's medium. Renewed growth was stimulated by addition of 10% FCS, α-thrombin (1 unit ml−1), or epidermal growth factor (EGF; 35 ng ml−1) in combination with insulin (10 μg ml−1). Concentrations were 1 mM for 8-bromo-cAMP and 10 μg ml−1 for cycloheximide.

RNA and Protein Analysis—RNA extraction and analysis were carried out as described (24). The hybridization mixture contained 50% formamide, 5 × Denhard's solution, 10 μm phosphate buffer (pH 7.0), 0.75 mM NaCl, 0.1% SDS, 10% dextran sulfate, and 100 μg ml−1 denatured salmon sperm. Hybridization was at 42 °C for 12–24 h using a probe concentration of 2 × 106 cpm ml−1. Filters were washed twice in 2 × SSC, 0.1% SDS at room temperature and once in 0.2 × SSC, 0.1% SDS at 65 °C. Signals were quantified using either an image processing workstation (Bioimage, Millipore Corp.) or a PhosphorImager (Molecular Dynamics, Inc.). Proteins were prepared from cells lysed for 1 h at

1 The abbreviations used are: FCS, fetal calf serum; EGF, epidermal growth factor; HA, hemagglutinin; PCR, polymerase chain reaction; ORF, open reading frame; PAGE, polyacrylamide gel electrophoresis; PBS, phosphate-buffered saline.
4°C in radioimmune precipitation assay buffer (50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 0.5% deoxycholate, 0.1% SDS, and 1% Triton X-100). Cells extracts were cleared by centrifugation (15 min at 10,000 × g). Protein detection on Western blots was performed using the ECL detection kit (Amersham Corp.).

Isolation of Full-length cDNA Clones—The construction of cDNA libraries is described (14). Libraries from hamster CCL39 cells growth-stimulated for 5 h and exponentially growing HeLa cells were screened at low density on nylon membranes (Hybond N, Amersham Corp.). DNA was extracted from pools of colonies isolated from positive areas and restricted with BamHI and HindIII enzymes, and insert size was monitored by Southern blotting. Pools harboring inserts larger than 1 kilobase pair (kb) was determined using M13 subcloning and manual and automatic sequencing using an Applied Biosystems 373A sequencer. Data base searches and sequence analysis were worked out by using the facilities of the Centre Inter-universitaire de Traitement de l’Information (Paris) (25).

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Preparation of Specific Antibodies—Preparation of specific antibodies was immunized in rabbits. The antigen was immobilized on Western blotting of the bacterial protein. Two independently raised antibodies were used for immunoprecipitation (1). Specific antibodies were affinity-purified with glutathione S-transferase-P2A1 fusion protein immobilized by Western blotting on a nitrocellulose membrane. A nitrocellulose slice (3 × 0.2 cm) containing the fusion protein was incubated overnight at 4°C in a 5-ml test tube with 500 μl of PBS containing 0.2% gelatin and 50 μl of a180 antiserum. The membrane was washed with 30 ml with cold PBS/Tween (0.2%) and then with cold PBS, and antibodies were eluted by adding 400 μl of 100 mM glycine (pH 2.8). The antigen was immediately washed with 3 ml of Tris-HCl (pH 8.8). Antibodies to the HA epitope were prepared from the supernatant medium of the 12CA5 hybridoma cell culture and purified on a protein A-Sepharose affinity column.

Preparation of Glutathione S-Transferase-MRPL12 Fusion Proteins—The human ORF (positions +138 to +735) was amplified by PCR, subcloned in pUC18, and sequenced. It was then cloned in pMalcR1 (New England Biolabs, Inc.) and pGEX2T (Pharmacia Biotech Inc.) vectors. Maltose-binding protein-MRPL12 fusion proteins were expressed in BL21 bacteria. The monoblotting and glutatione S-transferase fusion proteins were expressed in TG1 baculovirus-infected Sf9 cells. The pellet was reprecipitated with 12CA5 antibodies, and separated by SDS-PAGE. The expression level was monitored by Western blotting of the bacterial protein. Two independent antisera were raised, termed a179 and a180. Specific antibodies were affinity-purified against 50 μg of glutathione S-transferase-P2A1 fusion protein immobilized by Western blotting on a nitrocellulose membrane. A nitrocellulose slice (3 × 0.2 cm) containing the fusion protein was incubated overnight at 4°C in a 5-ml test tube with 500 μl of PBS containing 0.2% gelatin and 50 μl of a180 antiserum. The membrane was washed with 30 ml with cold PBS/Tween (0.2%) and then with cold PBS, and antibodies were eluted by adding 400 μl of 100 mM glycine (pH 2.8). The antigen was immediately washed with 3 ml of Tris-HCl (pH 8.8). Antibodies to the HA epitope were prepared from the supernatant medium of the 12CA5 hybridoma cell culture and purified on a protein A-Sepharose affinity column.
tyrosine kinase (EGF) or G-protein-coupled receptor (α-thrombin) (26, 27). Insulin is not mitogenic on CCL39 cells, but enhances the effect of EGF. Total RNA prepared from resting CCL39 cells stimulated for 1, 6, and 12 h was analyzed by Northern blotting. Signal quantification is shown Fig. 1B.

α-Thrombin led to a 3.5-fold increase in P2A1 mRNA 9 h after stimulation, whereas a combination of EGF and insulin led to a 2.5-fold induction. To ensure that P2A1 mRNA accumulation correlated with the mitogenic response induced by growth factors, we tested the antimitogenic effect of 8-bromo-cAMP on α-thrombin stimulation. The accumulation of P2A1 mRNA was inhibited 80% when 8-bromo-cAMP was added in conjunction with α-thrombin, indicating that biochemical pathways associated with DNA synthesis are responsible for the increase in the P2A1 RNA level. Identical cAMP-mediated inhibition was observed in cells treated with EGF or EGF + insulin (data not shown).

To demonstrate that P2A1 activation also occurs at the protein level, Western blots of proteins prepared from cells in various physiological states were incubated with affinity-purified rabbit polyclonal antibodies (a183) to the bacterially expressed human protein. As observed in Fig. 1C, a single 21-kDa peptide was revealed, whose level decreased in resting versus exponentially growing cells (compare lanes E and Q) and increased when cells were stimulated to grow.

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The size of the insert in the original clone was 0.5 kilobase pair. Full-length cDNAs were then isolated from hamster and human libraries, and complete sequences were determined (data not shown). Searching for homologous sequences in the GenBank™ Data Bank revealed no match with known DNA sequences except for several randomly sequenced cDNAs (GenBank™ accession numbers H51431, H69197, H51739, R10227, and R10550). The largest ORFs contained in hamster and human cDNAs encode proteins of 203 and 198 amino acids, respectively. Two additional AUG initiator codons were found upstream of the human ORF, at positions 19 and 63 (Table I). The codon at position 63 is in frame with the main ORF (starting at position 138). Both codons are included within a 34-nucleotide-long tandem repeat (positions 13–47 and 57–91) and are followed by stop codons (positions 40 and 84). Protein sequences derived from hamster and human main ORFs were compared against NBRF, GenPro, and SwissProt data bases using the BLAST program, which revealed that their carboxyl-terminal ends displayed a significant similarity to chloroplastic and bacterial L7/L12 proteins (smallest Poisson probability ranging from 10^{-12} to 10^{-3}) (Fig. 1D). We investigated more precisely the relationships between P2A1 and L7/L12 proteins from different sources: chloroplasts from Arabidopsis thaliana (ear cress) (28), Spinacia oleracea (spinach) (29), Nicotiana tabacum (common tobacco) and Nicotiana sylvestris (wood tobacco) (30, 31), and prokaryotes (Bacillus steaerotherophilus and Bacillus subtilis (32), Escherichia coli (33), Salmonella typhimurium (34), and Synechocystis sp. (35)). Sequences were first aligned with the TREEALIGN package (36). Multiple sequence alignments were then used to compute identity and distance scores between members of each pair and to trace the evolution of L7/L12 proteins, presented in Fig. 1E. Proteins from Gram-positive and Gram-negative bacteria are correctly clustered, as are chloroplastic proteins. The tree consists of three main distinct stems, corresponding to prokaryotic, chloroplastic, and P2A1 proteins, the latter having diverged earlier from chloroplastic proteins than from prokaryotic proteins. In addition to primary sequence similarity, secondary structures (37) of human and hamster putative proteins exhibit features very close to those of prokaryotic L7/L12 proteins (38): a helical region spanning amino acids 45–100 and a highly flexible glycine alanine-rich hinge region (amino acids 100–113), followed by two large helical α- and β-segments separated by a "turn" region, constituting a globular domain. The amino-terminal regions (amino acids 1–45) of mammalian and chloroplastic proteins also share common features, i.e. two short helical segments separated by coiled structures.

P2A1 Protein Colocalizes with the Mitochondria—The topology of the evolutionary tree suggested that P2A1 might be the mitochondrial homologue of L12 proteins. To address this hypothesis, α180 antibodies were used in Western blotting of in vitro translated human products on SDS-PAGE. Proteins were translated in vitro from the full-length cRNA or from RNA corresponding to the largest ORF and separated by SDS-PAGE. Size markers are indicated on the right (lane M). B, detection of the unprocessed MRPL12 product. Extracts from HeLa cells transected with the p(FT)L12 construct (lane T) or from control cells (lane C) were analyzed by Western blotting using the α180 antibodies. C, immunolocalization of Δ(L(FT)L12 and L(FT)Rh0G proteins. HeLa cells were transiently transected with pL(FT)L12 and pl(FT)Rh0G (see "Materials and Methods" and Fig. 4). 24 h after transfection, cells were fixed and incubated in the presence of immunopurified 12CA5 antibodies or affinity-purified α180 antibodies. D, in vitro translation of Δ(L(FT)L12 protein. RNA was synthesized and translated in vitro in the presence of [35S]methionine. Labeled products were separated by SDS-PAGE. Lane wt, (FT)L12 protein; lane Δ, Δ(L(FT)L12 protein.

**Fig. 2. A,** subcellular fractionation of MRPL12. Nuclei and membranes (lane N.E.) were separated from cytoplasmic extracts (lane C) by low speed centrifugation of mechanically broken CCL39 cells. The cytosolic extracts (lane C-M) were depleted of mitochondria (lane M) by high speed centrifugation. Aliquots of either fraction were separated by SDS-PAGE, and the amount of MRPL12 protein was detected by immunostaining of Western blots using the affinity-purified α180 antibody. B, immunolocalization of MRPL12. Exponentially growing CCL39 cells (panel 1), COS-7 cells (panel 2), HeLa cells (panel 3), and NIH3T3 cells (panel 4) were incubated for 30 min with rhodamine 123, and mitochondria were observed under confocal microscopy (row b). Alternately, cells were fixed and incubated in the presence of the affinity-purified α180 antibodies (row a).

**Fig. 3.** A, comparison of electrophoretic mobilities of in vitro translated human products on SDS-PAGE. Proteins were translated in vitro from the full-length cRNA or from RNA corresponding to the largest ORF and separated by SDS-PAGE. Size markers are indicated on the right (lane M). B, detection of the unprocessed MRPL12 product. Extracts from HeLa cells transected with the p(FT)L12 construct (lane T) or from control cells (lane C) were analyzed by Western blotting using the α180 antibodies. C, immunolocalization of Δ(L(FT)L12 and L(FT)Rh0G proteins. HeLa cells were transiently transected with pL(FT)L12 and pl(FT)Rh0G (see “Materials and Methods” and Fig. 4). 24 h after transfection, cells were fixed and incubated in the presence of immunopurified 12CA5 antibodies or affinity-purified α180 antibodies. D, in vitro translation of Δ(L(FT)L12 protein. RNA was synthesized and translated in vitro in the presence of [35S]methionine. Labeled products were separated by SDS-PAGE. Lane wt, (FT)L12 protein; lane Δ, Δ(L(FT)L12 protein.
ies (Fig. 2B, row a) were carried out in hamster CCL39 cells (panel 1), monkey COS-7 cells (panel 2), human HeLa cells (panel 3), and murine NIH3T3 cells (panel 4). In all cell lines studied, most of the fluorescence appeared as cytoplasmic punctations or short filaments, reminiscent of mitochondrial distribution. This was further confirmed by specific mitochondrial staining of living cells with rhodamine 123 (Fig. 2B, row b). No signal was obtained with the preimmune serum (data not shown).

Taking into account its similarity to the bacterial and chloroplastic L12 proteins and its mitochondrial localization, this protein will be termed MRPL12 for mitochondrial ribosomal protein L12.

Characterization of MRPL12 Mitochondrial Targeting Sequences—To confirm the efficient use of the third AUG codon, the human ORF was selectively PCR-amplified, and in vitro translated products were compared with those synthesized from the complete cDNA by SDS-PAGE (Fig. 3A). Proteins translated from both substrates displayed an identical apparent molecular mass of 29 kDa, indicating that the third AUG codon is efficiently used. However, the in vitro translated peptide exhibited a SDS-PAGE mobility 7–8 kDa higher than that of the MRPL12 protein (21 kDa) extracted from hamster or human cells. To rule out any artifactual modifications during in vitro translation, we first transiently transfected human 293 cells with the p(FT)L12 plasmid (Fig. 4A), a construct expressing the complete human MRPL12 protein fused to the HA epitope. A single product was specifically detected in transfected cells (Fig. 3B), whose apparent mobility (29 kDa) was identical to that of the in vitro translated peptide. We next examined the amino-terminal sequence of both hamster and human proteins, which revealed classical features of a mitochondrial sequence leader (39, 40): (i) absence of acidic residues; (ii) a high content of arginine, leucine, and serine residues (34% (man) and 44% (hamster)); (iii) a high content of positively charged amino acids (23% (man) and 18% (hamster)); and (iv) a high hydrophobic helical moment. A potential cleavage site (R^{X}Z^{X}2(S/T/G)^{X}4R, where Z is any hydrophobic residue) for mitochondrial processing peptidase (39, 40) was found at positions 45 (man) and 47 (hamster), as shown in Fig. 1B. To address the role of the amino-terminal sequence, we transiently transfected human HeLa cells with the pDL(FT)L12 construct (Fig. 4B), expressing a HA-tagged truncated version of the human MRPL12 protein lacking 48 amino acids in its amino-terminal part. In vitro translation yielded a product of 21 kDa, in agreement with the size of the endogenous protein (Fig. 3D). Immunolocalization of the DL(FT)L12 protein with both anti-HA monoclonal 12CA5 antibodies and anti-MRPL12 polyclonal antibodies revealed a distribution throughout the cytoplasm (Fig. 3C), indicating that at least part of the targeting signal has been deleted from the protein. We next transiently transfected the plDL(FT)RhoG construct (Fig. 4C), which drives the expression of a HA-tagged mutated version of RhoG protein, normally localized in the perinuclear endoplasmic reticulum (41), fused to the first 49 amino acids of MRPL12 leader sequence. At variance with the pDL(FT)L12 construct, staining of cells transfected with the pl(FT)RhoG construct
with 12CA5 antibodies showed a typical mitochondrial distribution. These data establish that the NH2-terminal 49 amino acids are necessary and sufficient for mitochondrial targeting and suggest that the leader peptide is cleaved off during translocation.

Expression of MRPL12Δ, a Truncated Version of MRPL12 Protein—Prokaryotic L7/L12 proteins are associated with ribosomes as structures made of two homodimeric complexes bound to a single molecule of L10 protein (42). The protein segments involved in homodimer formation span the amino-terminal helix, corresponding to amino acids 46–91 in the human sequence, while the region spanning amino acids 119–198 displays a basic helix-turn-helix structure, required for binding to ribosomal RNA (43–45). To inhibit the activity of endogenous MRPL12, we expressed a MRPL12 protein lacking its RNA binding activity upon deletion of 76 amino acids in its carboxy-terminal tail (pL12Δ(FT) construct) (Fig. 4D), but retaining its ability to be targeted to the mitochondria and to interact with the endogenous protein. The correct processing and targeting of the exogenous protein were monitored by analyzing the apparent mobility and the localization of the truncated protein in transiently or stably transfected HeLa cells (Fig. 5A). 18-kDa (i.e. the same size as the in vitro translated product) lane C) and 15-kDa peptides were detected with 12CA5 antibodies in cellular extracts from transiently transfected cells (lane T), while a single band of 15 kDa was observed in extracts from stably transfected cells (lane S). Although the mobility shift approximates 3 kDa, this indicates that stably transfected cells express prominently the processed protein. We next isolated six independent stably transfected clones and compared the subcellular distribution of the truncated protein with that of endogenous MRPL12 by immunofluorescence analysis. All cell clones elicited a strong signal for the truncated construct, corresponding to a mitochondrial distribution, as illustrated in Fig. 5B.

In Vitro Interaction between MRPL12 and MRPL12Δ—We then examined whether wild-type MRPL12 and MRPL12Δ proteins were able to associate. mRNAs transcribed from a wild-type MRPL12 cDNA and the pL12Δ(FT) construct were co-translated in vitro in the presence of [35S]methionine, and translation products were immunoprecipitated using 12CA5 antibodies (Fig. 6A). Equal amounts of nonimmunoprecipitated (lanes C) and immunoprecipitated (lanes IP) reactions were analyzed by SDS-PAGE. Under these conditions, ~19% of the 18-kDa MRPL12Δ protein immunoprecipitated (MRPL12Δ, lane IP versus lane C), while 12CA5 antibodies gave a background of 0.05% with the untagged 29-kDa complete protein (MRPL12, lane IP versus lane C). After cotranslation, addition of 12CA5 antibodies led to the immunoprecipitation of 5% of the untagged 29-kDa protein (MRPL12+MRPL12Δ, lane IP versus lane C). According to the relation described under “Materials and Methods” and given that the relative amounts of the proteins synthesized during cotranslation were 68% (29 kDa) and 32% (18 kDa) (MRPL12+MRPL12Δ, lane C), this indicates that ~60% of the translated proteins have interacted, probably as heterodimers, as shown for the bacterial L7/L12 proteins (42).

Cofractionation of Wild-type and Mutant MRPL12 Proteins—The previous experiments showed that the truncated version of MRPL12 protein was processed and targeted to the mitochondrion and could associate in vitro with the wild-type protein. As bacterial L12 proteins were shown to associate with ribosomes, we next examined the submitochondrial localization of both endogenous and truncated proteins in stably transfected HeLa cells. Lysates from purified mitochondria were fractionated on a 15–30% sucrose gradient, and aliquots of the collected fractions were analyzed by Western blotting for their content in MRPL12 and MRPL12Δ proteins, by Northern blotting for their content in 16 S ribosomal RNAs, and by spectrophotometry for their content in nucleic acids (Fig. 6B). The overall distribution of nucleic acids (upper panel, dashed line) is in agreement with published data (46), exhibiting three peaks corresponding to 35–45 S (ribosomal subunits), 60 S (monomeric ribosome), and 74 S (polysomal structures). 16 S rRNA is mainly distributed within all ribosomal structures (filled squares). Western analysis of MRPL12 proteins shows a loose distribution of the endogenous protein centered at 35–45 S (Fig. 6B), while the truncated protein exhibits a much tighter distribution on the same ribosomal structure (Fig. 6B). This establishes that both endogenous and truncated MRPL12 proteins cofractionate with ribosomal subunits. As the truncated protein has lost its basic helix-turn-helix RNA-binding domain, this also suggests that both wild-type and truncated proteins are present in the same protein complex. To address this latter issue, mitochondrial extracts were immunoprecipitated using anti-HA 12CA5 antibodies. Immunoprecipitated products were analyzed by Western blotting using anti-MRPL12 a180 anti-
bodies (Fig. 6C). Two peptides of 21 and 15 kDa were detected, indicating that both proteins are associated with the same structures.

Expression of MRPL12Δ Inhibits Cell Growth and Mitochondrial ATP Production—We next examined transfected HeLa clones for their physiological properties. We first compared the growth kinetics of six independent transfected clones. Cells transfected with wild-type pcDNAI/Neo were included as a control. Cells were seeded at 20 × 10^3 cells ml^-1 in RPMI 1640 medium supplemented with 10% FCS, and cell populations were estimated up to 172 h after seeding. As observed in Fig. 7, all transfected clones exhibit a reduced growth rate (average doubling times ranging from 26 to 28 h for clone 2 to 34 to 36 h for clones 1 and 5) compared with the control cells (average doubling time of 18–20 h). As the mitochondrial genome codes exclusively for proteins involved in oxidative phosphorylation, we analyzed the transfected clones for their mitochondrial ATP production. Three clones exhibiting different ranges of growth inhibition were compared for their behavior with regard to the absence of glycosylation by incubating cells in glucose-free medium and with regard to mitochondrial ATPase inhibition upon addition of 10 μg ml^-1 oligomycin (Fig. 7B). In the presence of oligomycin, the doubling time of control cells increased moderately (20–22 h), while the doubling times of MRPL21-transfected cells remained similar to those observed in Fig. 7A, indicating that inhibition of mitochondrial ATPase in the transfected clones has no effect on their growth properties. At variance, glucose starvation led to an expected reduction in the growth rate of control cells (doubling time of 28–30 h), but to a rapid death of the transfected clones, confirmed by trypan blue staining (data not shown). Identical cell death was observed in control cells upon inhibition of both pathways. These data demonstrate that mitochondrial ATPase activity is inhibited or severely reduced in the transfected clones and that their ATP supply derives exclusively from glycolysis.

DISCUSSION

To get a better understanding of the molecular events associated with cell proliferation, several groups have initiated an overall survey of mRNAs that accumulate in late G1 of serum-stimulated cells. We previously characterized a subset of cDNA clones complementary to serum-inducible RNAs, derived from hamster CCL39 fibroblastic resting cells stimulated with serum for 5 h. Three of them were shown to participate in the delayed-early response (19). Sequence analysis showed that two delayed-early response mRNAs encoded the plasminogen activator inhibitor (type I) (19) and the immunophilin-binding FKBP59 protein (41). We report here the characterization of the third delayed-early response mRNA, originally termed P2A1 (19), as well as its human counterpart.

This represents the first cloning and characterization of a mammalian mitochondrial ribosomal protein encoded by the nucleus. Previous reports led to the identification of various mammalian L12 ribosomal proteins related to prokaryotic L11 and yeast L15 proteins (47–49) that were shown to bind 28 S rRNA and to be cross-linked to elongation factors 1α and 2 (50–52). Although attempts were made to relate these proteins to prokaryotic L12 (30), our data unambiguously demonstrate that P2A1 is the mitochondrial homologue of prokaryotic L7/L12 ribosomal protein, which will now be termed MRPL12. Although sharing a low level of identity in their primary structures, MRPL12 and bacterial L12 proteins exhibit a conserved overall secondary structure (two helical structures separated by a flexible hinge region). In bacteria, the NH₂-terminal helix is involved in dimerization, while the COOH-terminal helix displays a helix-turn-helix structure, involved in binding to...
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...ribosomal RNA. Assuming similar properties for MRPL12 protein, we showed that the expression of a protein potentially devoid of RNA binding activity impairs the normal function of the protein complex, probably due to reduced translation, leading to inhibition of oxidative phosphorylation.

Mitochondria are organelles whose main function is ATP production, but that also contribute to the biosynthesis of many metabolites such as pyrimidines, amino acids, and phospholipids. Although not essential for in vitro cell cultures (20), the mitochondrial activity is regulated at developmental and physiological levels (53, 54), and its failure is probably involved in numerous degenerative diseases (55–57). Several nuclear genes activated by growth factors or hormones were shown to encode proteins controlling various aspects of mitochondrial metabolism: energy production (the adenine nucleotide translocator ANT2 (23), a proton/phosphate symporter (19), or cytochrome c (58)), lipid biosynthesis (the p90 glycerol-3-phosphate acyltransferase (59) or the uncoupling protein (60)), and protein import (the chaperonin hsp60 (61) or Fos effector protein-1, similar to a yeast mitochondrial protein import (22)).

In mammalian cells, the mitochondrial genome encodes a limited number of proteins involved in oxidative phosphorylation. Mitochondrial RNAs are transcribed as polycistronic primary transcripts from a unique bidirectional promoter, implying that regulation of gene expression mainly relies on post-transcriptional mechanisms such as RNA or protein turnover and translational control (62–64). As L7/L12 proteins have been shown to control the efficiency of mRNA translation in E. coli, it is tempting to speculate a similar function for MRPL12 in the mitochondria. Our data establish that MRPL12 mRNA and protein accumulate in response to growth factor stimulation and that mRNA induction is inhibited when cells are treated with antimitogenic agents such as cAMP. Growth regulation of MRPL12 protein could then represent a direct regulatory mechanism for increasing the amount of proteins involved in mitochondrial metabolic pathways in response to external stimulation.

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