

SHORT REPORT

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A nuclear factor-binding domain in the 5'-untranslated region of the *amyloid precursor protein* promoter: Implications for the regulation of gene expression

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Abstract

Background: The extracellular deposition of aggregated amyloid β -protein is a neuropathological manifestation of Alzheimer disease and Down syndrome. The Amyloid β -protein is derived from a group of larger differentially spliced proteins, the amyloid protein precursors (APP). Data suggests that the level of *APP* gene expression could contribute to the pathological processes leading to amyloid depositions.

Findings: The 5' untranslated region (UTR) of the *APP* gene, encompassing 147 base pairs between the transcriptional (+1) and the translational start site, was examined for its role in *APP* expression. Deletions close to the transcriptional start site reduced expression from the *APP* promoter in part by transcriptional mechanisms. However, deletions between position +50 and +104 had no effect on transcriptional activity while significantly reducing overall expression from the promoter. A nuclear factor-binding domain designated as DAPB was identified between position +72 and +115 of the 5'-*APP*-UTR. The binding-recognition sequence was localized between position +96 and +105. The same mutations that eliminated factor-binding also reduced expression from the *APP* promoter while having no effect on *in vitro* transcription or the RNA levels transcribed from transfected constructs.

Conclusions: A nuclear factor-binding domain designated as DAPB was identified in the 5'-UTR of the *APP* gene. Elimination of factor-binding correlated with an overall decline in expression from the *APP* promoter while *in vitro* transcription and the total amount of *in vivo* transcribed RNA remained unaffected. This suggests that the binding-factor may have a function in post-transcriptional regulation, including nuclear export of mRNA.

Background

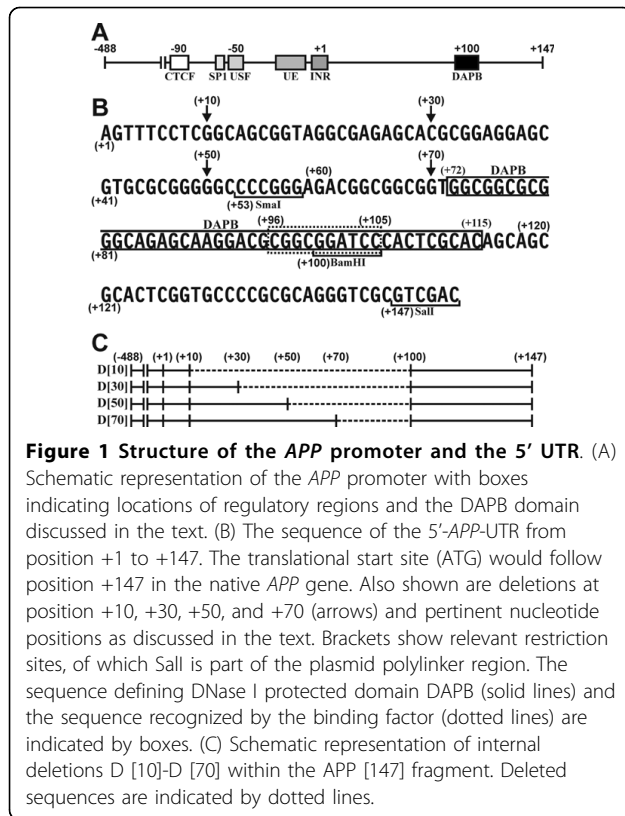
A neuropathological manifestation of Alzheimer disease and Down syndrome is the extracellular deposition of aggregated amyloid β -protein [1-3]. The Amyloid β -protein is derived from a group of larger differentially spliced proteins, the amyloid protein precursors (APP) [4]. There are three copies of the *APP* gene in Down syndrome and the level of *APP* transcript in the brains of afflicted individuals is increased about 4.5-fold [5]. A chimeric mouse model of Down syndrome shows increased *APP* transcription associated with cholinergic

neuron degeneration [6]. Promoter mutations that increase the expression of APP are associated with the development of Alzheimer disease and a duplication of the *APP* gene locus causes autosomal dominant early-onset Alzheimer disease [7,8]. These observations suggest that the level of expression of the *APP* gene could contribute to the pathological processes leading to amyloid depositions. The 5'-untranslated region (UTR) was here examined for its role in *APP* expression.

Results and discussion

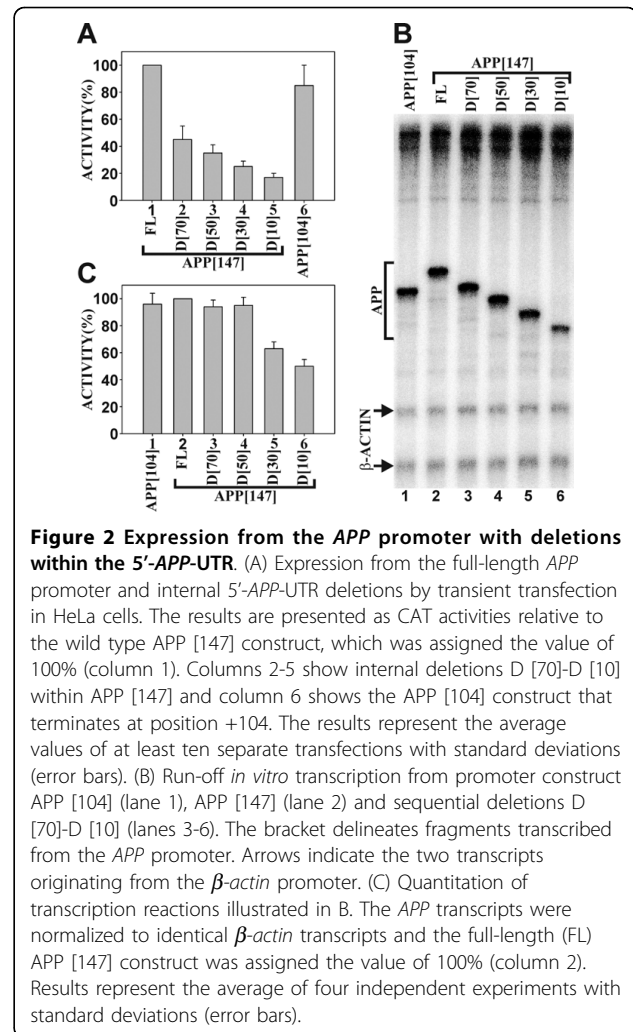
Deleting 5'-APP-UTR sequences between position +10 and +104 decreases expression from the APP promoter
Four incremental internal deletions within 5'-*APP*-UTR construct APP [147], designated as D [10], D [30],

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D[50], and D [70] were analyzed by transient transfection (Fig. 1B and 1C). The deletions resulted in stepwise reductions of CAT activity from 48% (D [70]) to 18% (D [10]) of the wild type value (Fig. 2A, columns 1-5).

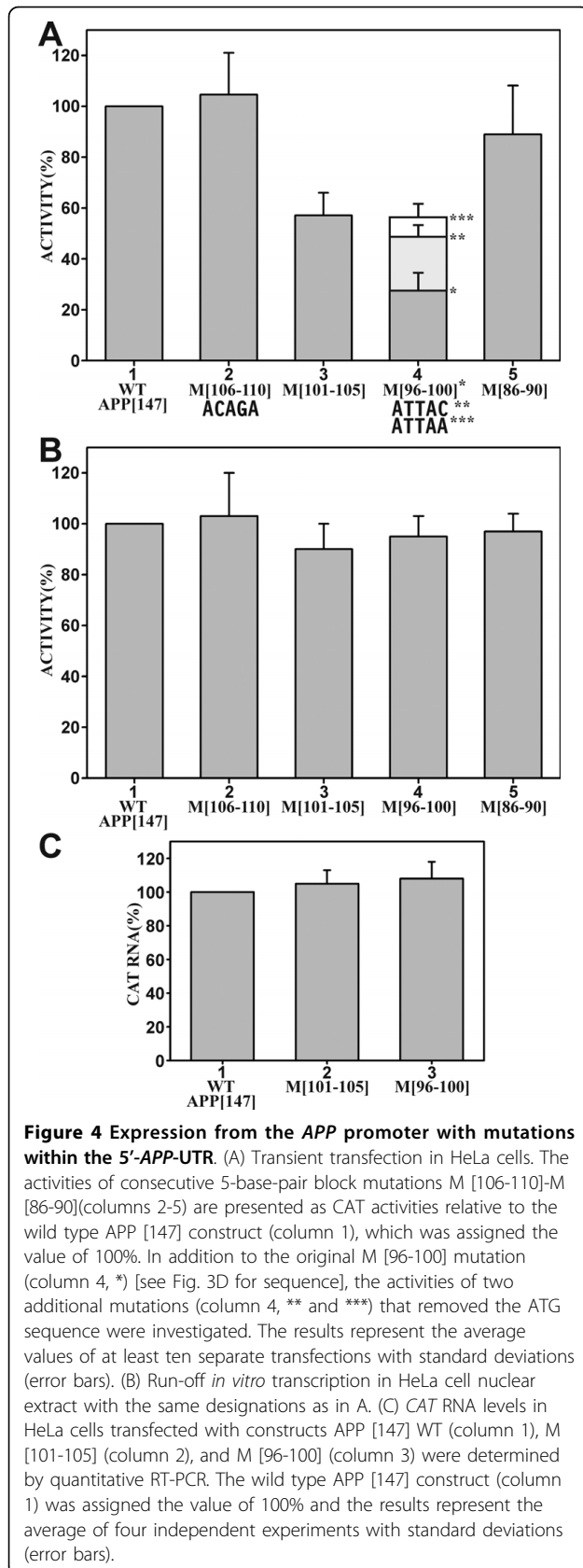
The deletion constructs were further analyzed by run-off *in vitro* transcription. The constructs with deletions in the 5'-APP-UTR region resulted in run-off fragments of correspondingly smaller size (Fig. 2B, lanes 1-6). Transcription from deletions D [30] and D [10] was reduced to 68% and 50% of the wild type value, respectively (Fig. 2C, columns 1-6). Since the deleted sequences in D [30] and D [10] are close to the transcriptional start site, they may be considered components of the core promoter. Downstream core promoter sequences such as DPE [9], DCE [10] or MTE [11] that are located within the first 35 nucleotides 3' to the transcriptional start site are often required for efficient transcription. However, the downstream region of the APP promoter does not match the consensus sequences for any of these elements. This may imply the existence of a non-conventional proximal downstream element in the APP core promoter. The remaining deletions D [50] and D [70] had no effect on *in vitro* transcriptional activity, while they did diminish *in vivo* expression from the APP promoter (Fig. 2A and 2C). In contrast, a 3'-deletion terminating at position +104 (APP [104]) had no significant effect on APP promoter expression (Fig. 2A-C).



A nuclear factor displays sequence specific binding to the 5'-APP-UTR

The APP sequence from position -40 to +147 was analyzed by DNase I footprinting with HeLa cell nuclear extract (Fig. 3A). A prominent DNase I protected domain that extended from position +72 to +115 was designated as DAPB.

The factors that interact with the DAPB sequence were further examined by mobility shift electrophoresis with nuclear extract fractionated on SP-Sepharose. The major DNA binding activity eluted in fractions 10-14 (Fig. 3B, lanes 2-6). Fractions 11 and 12 were combined and used for further experiments. The binding complex was effectively competed with 5- and 20-fold molar excesses of unlabeled wild type [60-120] sequence (Fig. 3C, lanes 1-3). Transverse mutations within the [60-120] double stranded oligonucleotide were introduced from positions +71 to +85 (M [71-85]) and +86 to +100 (M [86-100]). Factor-binding was not effectively competed with a 100-fold molar excess of unlabeled M [86-100]



for DAPB binding (not shown). Furthermore, the transverse mutations that eliminate DAPB complex formation on the [60-120] fragment are actually located outside the postulated TR recognition sequence and the SP1 binding site. The observation that DAPB binding was non-specifically competed by RNA (not shown) may suggest a role in nuclear export of nascent mRNA.

Conclusion

The 5'-APP-UTR was analyzed for its effect on promoter expression by transient transfection. Deletions close to the transcriptional start site reduced expression from the APP promoter in part by transcriptional mechanisms. Deletions between position +104 and +50 had no effect on transcriptional activity while significantly reducing overall expression from the promoter. A nuclear factor-binding domain designated as DAPB from position +72 to +115 within the 5'-APP-UTR was identified with a recognition sequence located between position +96 and +105. The same mutations that eliminated factor-binding also reduced expression from the APP promoter while having no effect on *in vitro* transcription or RNA levels transcribed from transfected constructs. These results suggest that the nuclear binding-factor exert its effect through post-transcriptional mechanism. The nuclear localization of the binding factor and its affinity for RNA may suggest a function in RNA transport. A review of the literature of related studies suggested that the DAPB binding-factor is distinct from those previously described.

Materials and methods

Cell cultures, promoter constructs, and enzyme assays

Cell cultures, transient transfections, enzyme assays, and oligonucleotide preparations were carried out as previously described [23,24].

Plasmid pCAT2bGAL [25] contains the bacterial genes *CAT* and *LacZ*, which are both transcribed in the same direction. The *LacZ* gene is transcribed from the β -actin promoter and serves as an internal control for experimental variations. The polycloning site on the 5'-end of the *CAT* transcriptional unit was the recipient for the various APP promoter constructs. The 5'-end of the full-length APP promoter (APP [147]) construct extended from position -488 upstream from the transcriptional start site (+1)[24]. This upstream promoter region contains all nuclear factor-binding sites relevant for efficient APP expression (Fig. 1A). The 3'-end extended to position +147, which in the endogenous APP gene transcript would have been followed by the translational start site (Fig. 1B). Mutations and deletions within wild type APP [147] were generated by *in vitro* mutagenesis [26,27].

Nuclear extracts, mobility shift electrophoresis, and DNase I footprinting

Nuclear extracts were prepared from HeLa cells grown in suspension to a density of $5-8 \times 10^5$ cells/ml [23,24]. The final protein concentration in extracts was 10-15 mg/ml in buffer D [23,24]. For fractionation, a 10 ml SP-Sepharose Fast Flow column (GE Healthcare) was equilibrated with buffer D. Ten ml of nuclear extract was loaded on the column, washed with 15 ml of buffer D, and eluted with a 50 ml linear gradient of 200 mM-700 mM KCl in buffer D. Fractions of 2 ml were collected and analyzed by mobility shift electrophoresis.

For mobility shift electrophoresis, binding reactions were assembled in a total reaction volume of 16 μ l and processed as described [23]. In competition assays, labeled and unlabeled oligonucleotides were premixed at indicated molar ratios before adding them to the binding reaction.

DNase I footprinting was conducted on *APP* DNA fragments extending from position -40 to +147. The fragments were amplified by PCR with the [32 P] end-labeled reverse primer complementary to the 5'-*APP*-UTR from position +142 to +113 and unlabeled forward primer from position -40 to -29 [24]. The resulting double stranded DNA fragment was purified by polyacrylamide gel electrophoresis in $0.5 \times$ TBE. Binding reactions were preincubated with 8 μ l of HeLa cell nuclear extract and 50×10^3 cpm of labeled fragment under the same conditions as described above for mobility shift electrophoresis, except that the total reaction volume was adjusted to 32 μ l, and processed as described [23].

Run-off in vitro transcription

Plasmid pCAT2bGAL containing the wild type or mutated *APP* [147] constructs were digested with restriction enzymes *EcoRI* and *Acc65I*. *In vitro* transcription reactions were assembled in a volume of 8 μ l containing 2.5 μ l of nuclear extract, 0.5 μ l (1 μ g) of plasmid template, and 5 μ l of a buffer containing 40 mM Hepes, pH 7.6, 75 mM KCl, 2 mM $MgSO_4$, 0.1 mM EDTA, 1 mM DTT, and 10% glycerol. Thereafter, 0.5 μ l of 10 mM GTP, 10 mM CTP, 3.3 mM ATP, 3 mM UTP and 0.3-0.7 μ l (10^6 cpm) of α -[32 P]-UTP (PerkinElmer) was added and reactions were incubated at 30°C for 30 min. Transcribed RNA was purified with the RNeasy (Qiagen) RNA isolation kit.

Quantitative RT-PCR of RNA from transfected cells

Total RNA was prepared from transfected cells with the RNeasy Mini kit, digested with 10 units of RNase free DNase I (Roche), and repurified. One μ l of purified RNA (0.3-0.6 μ g) was combined in 10 μ l annealing buffer containing 300 mM NaCl, 10 mM Tris, pH 7.5, 1 mM EDTA with 10 pmol each of primers Gal-R (5'-GGTTACG-TTGGTGTAGATGGGCG) complementary to the *LacZ* transcript, and CAT-R (5'-TGAGCATTCAT-

CAGGCGGGC) complementary to the *CAT* transcript. The solution was heated to 99°C for 5 minutes, incubated at 61°C for 5 min, at 57°C for 10 min, and at 48°C for 5 min. To each annealing mixture was added 40 μ l of a reverse transcriptase reaction mixture containing 12.5 mM Tris, pH 8.0, 10 mM $MgCl_2$, 12.5 mM DTT, 1.25 mM each of the dNTPs, 20 units of AMV reverse transcriptase (CHIMERx), and 10 units of RNasin (Invitrogen). The reaction was continued at 48°C for 90 min.

PCR amplification of 4 μ l aliquots of the reverse transcription reaction products was assembled in 40 μ l of Mg + PCR buffer (Roche) supplemented with 0.2 mM of each dNTP, 0.4 pmol each of 5' end-labeled (50-100 \times 10^3 cpm) CAT-R, Gal-R, unlabeled CAT-F (5'-TTTCAG-GAGCTAAGGAAGCTAAAATGGAG) and Gal-F (5'-CTGAGCCGCGATATTGCCAG) primers. Amplification was carried out for 18 cycles. PCR products were separated on 5% polyacrylamide gels. The amount of *CAT* RT-PCR product was normalized to the amount of *LacZ* RT-PCR product. To establish that the RT-PCR procedure was quantitative, different amounts of RNA and different numbers of PCR cycles were used. Lack of plasmid contamination in RNA preparations was confirmed by amplifying aliquots of reverse transcription reaction mixture prior to reverse transcription.

Abbreviations

APP: amyloid precursor protein; UTR: untranslated region; CAT: chloramphenicol acetyltransferase; DTT: dithiothreitol; CHAPS: 3 [(3-cholamidopropyl)dimethylammonio]-propanesulfonic acid; Hepes: N-2-Hydroxyethylpiperazine-N'-2-ethanesulfonic acid; Tris: Tris-(hydroxymethyl) aminomethane; EDTA: ethylenediamine tetraacetic acid; TBE: tris-borate-EDTA; cpm: counts per minute; RT: reverse transcriptase; PCR: polymerase chain reaction; IRE: iron response element; IRP: iron regulatory protein; TRE: thyroxin response element; C: cytidine; T: thymidine; A: adenosine

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Authors' contributions

MT, WQ, and NI carried out molecular cloning, transfections, and *in vitro* mutagenesis. AV performed DNase I footprinting, mobility shift electrophoresis, and *in vitro* transcription. All authors contributed to data analysis. WQ and AV wrote the manuscript. All authors read and approved the final manuscript.

Competing interests

The authors declare that they have no competing interests.

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