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Expression of active iron regulatory factor from a full-length human cDNA by *in vitro* transcription/translation

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ABSTRACT

Iron regulatory factor (IRF), also called iron responsive element-binding protein (IRE-BP), is a cytoplasmic RNA-binding protein which regulates post-transcriptionally transferrin receptor mRNA stability and ferritin mRNA translation. By using the polymerase chain reaction (PCR) and the sequence published by Rouault et al. (1990) a probe was derived which permitted the isolation of three human IRF cDNA clones. Hybridization to genomic DNA and mRNA, as well as sequencing data indicated a single copy gene of about 40 kb specifying a 4.0 kb mRNA that translates into a protein of 98,400 dalton. By *in vitro* transcription of a assembled IRF cDNA coupled to *in vitro* translation in a wheat germ extract, we obtained full sized IRF that bound specifically to a human ferritin IRE. *In vitro* translated IRF retained sensitivity to sulfhydryl oxidation by diamide and could be reactivated by β-mercaptoethanol in the same way as native placental IRF. An IRF deletion mutant shortened by 132 amino acids at the COOH-terminus was no longer able to bind to an IRE, indicating that this region of the protein plays a role in RNA recognition. Placental IRF has previously been shown to migrate as a doublet on SDS-polyacrylamide gels. After V8 protease digestion the heterogeneity was located in a 65/70 kDa NH_2-terminal doublet. The liberated 31 kDa COOH-terminal polypeptide was found to be homogeneous by amino acid sequencing supporting the conclusion of a single IRF gene.

INTRODUCTION

Coordinate regulation of key proteins in iron metabolism is one of the best studied cases for post-transcriptional control mechanisms of gene expression. In response to iron deprivation, the cytoplasmic stability of transferrin receptor mRNA is increased and ferritin mRNA translation inhibited (1–7). As a consequence, enhanced iron uptake and diminished iron storage tend to compensate for the lack of iron. This feedback regulation can be viewed as a protective mechanism that prevents nutritional starvation and permits the biosynthesis of essential iron- or heme-containing proteins. Under conditions of high iron supply, when cells may need to store excess iron in order to prevent adverse effects of iron overload, the regulatory balance is inversed: transferrin receptor mRNA decays more rapidly and ferritin translation is no longer inhibited.

The mechanisms affecting transferrin receptor mRNA stability and inhibiting ferritin mRNA translation are clearly distinct, but both require a highly conserved RNA structure, the iron responsive element (IRE) (3,5,6,8–10). Five IREs are located in the 3′ untranslated region of transferrin receptor mRNA and one IRE is close to the 5′ end of ferritin mRNA. Recently, additional IREs have been discovered near the 5′ end of aconitase and erythroid δ-aminolevulinic acid synthase mRNA (11–13). All these RNA structures represent specific binding sites for a cytoplasmic protein of about 95 kDa (3,9,14,15) called the iron regulatory factor (IRF) (3), also known as the IRE-binding protein (IRE-BP) (16) or ferritin repressor protein (FRP) (7). The total cellular IRF pool consists of RNA-bound molecules, an unbound active fraction, as well as the protein in an inactive state (17). Its IRE-binding affinity is modulated as a function of intracellular iron levels, and the fraction of active IRF molecules increases when iron concentration decreases (3,16,18). This post-translational change parallels precisely the *in vivo* accumulation of transferrin receptor mRNA (3), and the binding of IRF to the IRE directly prevents ribosomes from attaching to ferritin mRNA (7,19–21).

While there is no doubt that IRF activity is influenced by iron levels *in vivo*, some uncertainty prevails as to the mechanism by which this protein is modulated. Experiments with cultured cells strongly suggest a central role of chelatable iron that may directly bind to IRF. This hypothesis seems plausible since the recent isolation of an IRF cDNA clone (22) that has revealed sequence homology to pig heart aconitase (23,24). This enzyme of the citric acid cycle contains a [4Fe-4S] cluster capable of iron exchange (25). Experiments carried out *in vitro* have indicated, in addition, the involvement of redox reactions in IRF activation (16,26). Reducing agents, such as β-mercaptoethanol at unphysiologically high concentrations, activate IRF *in vitro* to the same extent as low iron levels would do *in vivo*. In contrast,

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binding of IRF to an IRE is prevented by the sulfhydryl-oxidizing agent azodicarboxylic acid bis[dimethylamide] (diamide). Hemin, itself a compound capable of inactivating IRF *in vivo*, is a strong inhibitor of IRE-IRF interactions *in vitro* (27–29) and seems to exert its effect through a reversible oxidation of IRF (our unpublished observation). It remains unclear whether the *in vitro* activation or inactivation mimics a redox reaction that is allosterically facilitated *in vivo* by iron exchange; or whether, on the contrary, iron is directly involved in an intra- or intermolecular redox step which may represent a prerequisit for IRE-binding (16).

Further progress on the biochemistry of IRF will require the isolation of large amounts of IRF and the testing of IRF mutants. Thus far, IRF has been purified in relatively small quantities from liver and placenta (20,30,31), and its analysis has not yet revealed an iron-sulfur cluster. However, since isolation procedures were carried out in the presence of oxygen, where iron-sulfur clusters become unstable, it is possible that the cluster exists, but has remained undetected for technical reasons. It obviously would be of importance to express the protein *in vivo* or *in vitro* from its cDNA. In the present study, we isolated human IRF cDNA clones with a PCR probe based on a previous sequence determined by Rouault et al. (22). A reconstructed full-length cDNA has allowed us to obtain active IRF by *in vitro* transcription coupled to *in vitro* translation in a wheat germ extract.

MATERIALS AND METHODS

Cloning and Sequencing of IRF cDNA clones

Screening of libraries was carried out with a PCR-probe that was amplified from a human placenta cDNA library. The opposite oligonucleotide primers corresponded to position 210 to 235 and 446 to 472 in the sequence published by Rouault et al. (22). The reaction mixture contained 20 mM Tris-HCl pH 8.8, 10 mM KCl, 10 mM $(NH_4)_2SO_4$, 2 mM $MgSO_4$, 0.1% Triton X-100, 100 μg/ml BSA, 200 μM dNTP and 1 U Vent^{TM}-polymerase (New England Biolabs, Beverly, MA). The amplification was carried out at 67°C for annealing and 72°C for the polymerase reaction. The amplified product was cloned into pGEM-3zf(−) (Promega, Madison, WI) and confirmed by sequencing. This probe was used to screen two different cDNA libraries, one from human placenta in λgt11 (Clontech, Palo Alto, CA) and the other one from the fibroblast cell line EK4 (32) in λgt10 (gift of Dr. R. Tyrrell, ISREC, Epalinges, Switzerland). In both cases about 4×10^5 phages were plated. Duplicate filters (GeneScreen Plus, Du Pont, Boston, MA) were hybridized at 42°C with a random-primed probe (3×10^5 cpm/ml) in 5×SSPE, 0.3% SDS and 1% milkpowder and washed after 15 h with 5×SSPE, 0.1% SDS at 52°C twice for 15 min. Positive plaques were picked and rescreened 4 times. Finally, among five positive clones with overlapping restriction sites, we analysed in further detail two from the placenta library and one from the fibroblast library. These clones were digested with EcoRI and the fragments from inserts subcloned into pGEM-3zf(−)

Sequencing was carried out according to the dideoxynucleotide chain termination method of Sanger et al. (33), using Sequenase version 2.0 (United States Biochemical, Cleveland, OH). Single-stranded DNA from subclones of EcoRI-fragments in pGEM was prepared by using the helper phage VCS13 (Stratagene, Heidelberg, Germany). The inserts of λIRF2 and λIRF4 were entirely sequenced, where necessary with the help of internal sequencing primers. The part of the sequence matching exactly the one of Rouault et al. (22) was verified only on one strand, but any mismatches and new sequences were ascertained on both strands.

Reconstruction of a full-length IRF cDNA clone

The overlapping inserts of λIRF2 and λIRF4 (Fig.1) were used to reassemble a larger cDNA clone. The 5′ EcoRI-DraIII fragment from λIRF2 (previously subcloned as an entire EcoRI-fragment into pGEM-3zf(−)) and the central DraIII-KpnI fragment from λIRF4 were ligated together into the EcoRI/KpnI sites of pGEM-7zf(−). This new clone was linearized with KpnI in order to insert a KpnI-KpnI fragment containing the 3′ KpnI-EcoRI region of λIRF4 and polylinker sequences between the EcoRI and KpnI sites of pGEM-3zf(−). This plasmid will be referred to as pGEM-hIRF.

Northern and Southern blot analysis

Total cytoplasmic RNA from the fibroblast cell line EK4 was isolated according to the procedure of Chomczynski and Sacchi (34). 25 μg of RNA was loaded on a 1.2% agarose gel containing 6.6% formaldehyde in 20 mM morpholinoethane sulfonic acid pH 7.0, 1 mM sodium acetate, 1 mM EDTA. After migration, the RNA was blotted onto a GeneScreen membrane (Du Pont, Boston, MA). A random-primed IRF cDNA probe (10^6 cpm/ml) from bases 143 to 3040 (Fig.2) was hybridized to the RNA in 5×SSPE, 100 mM sodium phosphate pH 6.5, 5×Denhardt's solution, 50% formamide, 10 mM EDTA, 1% sarcosyl and 125 μg/ml tRNA for 16 h at 42°C. Random priming was done with a kit from Boehringer (Mannheim, Germany) which yielded a specific activity of 0.5 to 1×10^9 cpm/μg DNA. The blot was washed in 6×SSC, 0.1% SDS for 30 min at room temperature, followed by one wash in 2×SSC, 0.1% SDS for 15 min at 55°C.

Genomic DNA from human placenta was prepared as previously described (35). 20 μg of DNA was digested with 50 U EcoRI or HindIII and loaded on a 0.8% agarose gel in 1×TBE. After migration, the gel was treated for 15 min first in 250 mM HCl and then for 15 min in 0.4 M NaOH. The DNA was transferred overnight to a nylon membrane (ZETA-PROBE, BioRad, Richmond, CA) according to the manufacturer's instructions. The membrane was sequencially hybridized with several random-primed probes. In each case hybridization was carried out in 0.5 M sodium phosphate pH 7.2, 7% SDS, 1 mM EDTA and 1% BSA at 68°C for 16 h with a probe concentration of 10^6 cpm/ml. The membrane was washed twice for 30 min at 65°C in 40 mM sodiumphosphate pH 7.2, 1 mM EDTA, 0.5% BSA and 5% SDS. Prior to re-hybridization the previous probe was stripped with 0.1×SSC and 0.5% SDS.

In vitro transcription and translation of IRF

The plasmid pGEM-hIRF, which contains the IRF full-length cDNA, was linearized by various restriction enzymes and transcribed *in vitro* with T7 polymerase (Promega) in the presence of $m^7G(5')ppp5'G$ (Pharmacia, Uppsala, Sweden) (36) according to the supplier's instructions. 100 ng of capped RNA was translated *in vitro* in 25 μl reaction volume using a wheat germ extract (Promega). The reaction was carried out according to the manufacturer's protocol in the presence of ^{35}S-methionine for SDS-polyacrylamide gel-analysis or unlabelled methionine for gel retardation assays. The length of translated polypeptides in amino acids (aa) depended on the restriction site at which pGEM-hIRF was linearized: 889aa (HindIII or ClaI), 757aa

(KpnI), 682aa (PvuII), 559aa (NdeI), 546aa (SmaI), 392aa (StyI). Radiolabelled translation products were analysed on a 8% SDS-polyacrylamide gel. The gel was fixed with 10% TCA and treated with enhancer (EN^{3}HANCE, Du Pont), prior to drying and exposure for autoradiography.

RNA-protein bandshift assays

To analyse the biological activity of *in vitro* translated IRF, a 5 μl aliquot of the *in vitro* translation reaction was incubated at room temperature with a molar excess of [^{32}P]CTP-labelled RNA transcript from plasmid pSPT-fer as previously decribed (3,14). This plasmid contains the sequence corresponding to the IRE from the 5′ untranslated region of human ferritin H chain mRNA. After 20 minutes, RNase T_1 (1 U) was added for 10 min, followed by an incubation with heparin (5 mg/ml final) for another 10 min. RNA-protein complexes were analysed on a 6% non-denaturing polyacrylamide gel as described (3). Where indicated, *in vitro* translated IRF was preincubated for 10 min with 1.5 mM diamide on ice or with 2% β-mercaptoethanol. For measurements of specificity, RNA-protein bandshifts were performed in the presence of an excess of unlabelled pSPT-fer RNA or 4F2 antigen heavy chain RNA (37).

IRF isolation, partial protease digestion and peptide sequencing

Affinity-purified IRF from human placenta (31) was digested with V8 protease or trypsin sequencing grade protease (Boehringer Mannheim). V8 protease was added to IRF at a ratio of 1:20 (w/w), and digestion was carried out in 25 mM NH_4HCO_3 pH 7.8 at room temperature. For trypsin, the protease to IRF ratio was 1:100 (w/w), and digestion was done in 100 mM Tris-HCl pH 8.5 at 37°C. Partially digested IRF was analysed on a 7.5% SDS-polyacrylamide gel. For peptide sequencing V8 protease digestion products were transferred electrophoretically onto Immobilon P transfer membrane (Millipore, Bedford, MA) in 10 mM 3-(cyclohexylamino)-1-propanesulfonic acid pH 11 and 10% methanol. After transfer, the membrane was stained with 0.5% Ponceau S (Sigma) in 1% acetic acid and washed several times with water. The bands corresponding to the digestion products were exised, rinsed with water, air dried and submitted to automated amino acid sequencing.

RESULTS AND DISCUSSION

Molecular cloning and structure of IRF cDNA clones

Previous purification of IRF from human placenta by affinity chromatography on an IRE-containing RNA-column has revealed two bands with molecular weights of about 95 and 100 kDa (31). Both proteins showed similar biochemical properties, and were capable of binding IREs from different sources *in vitro* (3,31). However, IRF purified from liver has been reported without such a heterogeneity and with a single molecular mass of 90 kDa (20, 30). Thus, there existed the possibility for tissue-specific variations among IRE-binding proteins. Particularly in view of the large number of mRNAs that contain IREs and are regulated by IRF, it was of interest to examine whether the observed IRF heterogeneity reflects distinct gene products or rather variants from a single gene. We, therefore, decided to isolate IRF cDNA clones from a human placenta library. For screening we amplified a PCR-probe encompassing bases 210 to 472 in the sequence published by Rouault et al. (22). This probe was chosen close to the 5′ end in order to select for rare full-length cDNAs. The

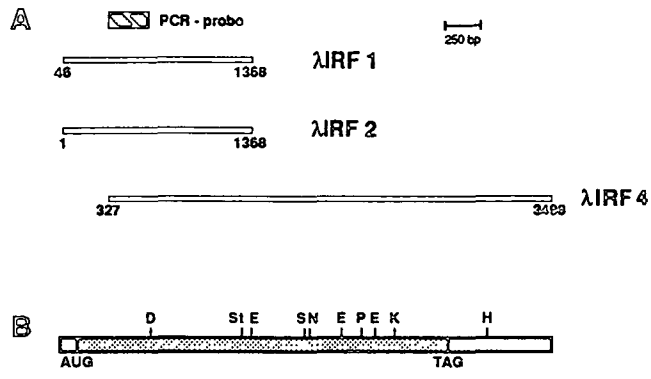

Figure 1. Isolation and assembly of human IRF cDNA clones. A PCR-probe was amplified according to the published sequence of Rouault et al. (17) (between positions 210–472). This probe was used to isolate phages with inserts λIRF1 and λIRF2 from a human placenta cDNA library and λIRF4 from a human EK4-fibroblast cDNA library (panel A). The inserts of clones λIRF2 and λIRF4 (Fig.1) were assembled to provide a full-length cDNA of IRF, which is 3498 bases in length (panel B). The start of translation is at position 108, the stop codon ends at nucleotide 2778. Restriction sites indicated are D, DraIII, E, EcoRI; H, HindIII; K, KpnI; N, NdeI; P, PvuII; S, SmaI, St, StyI.

PCR-probe was used to screen two independent cDNA libraries, a random primed one from human placenta and an oligo-dT primed library from the human fibroblast cell line EK4. In each case about 4×10^5 λ-phages were screened, and plaque hybridization yielded three clones in the placenta library (λIRF1, 2, and 3) and two clones in the fibroblast library (λIRF4 and 5) that were consistently positive after four rounds of re-screening. When the size and restriction sites of inserts were determined, we noticed in all three placenta clones a divergent pattern towards the 5′ end as compared to the reported clone of Rouault et al. (22). We did not continue to analyse λIRF3 and 5, because these two clones had similar inserts as λIRF1 and 4, respectively. EcoRI-fragments from λIRF1, 2 and 4 were subcloned into pGEM-vectors and entirely sequenced by the method of Sanger et al. (33).

Sequence data showed that the different clones are overlapping (Figs 1 and 2), and that the longest one from the placenta library contains a new sequence of 318 bases diverging from Rouault's clone (22) at their position 174. Due to this difference, our cDNA clones code for additional 99 amino acids upstream of the previously assumed initiation codon. We also found several other sequences to be different in λIRF4 compared to the originally published data (22). These changes concern sequences located at amino acids 532 to 543 and 712 to 727 (Fig.2) that have since been corrected by the authors (23). New sequences were verified on both strands.

The different 5′ end in our cDNA might have been due to alternative splicing or the existence of a second gene, but both assumptions seem unlikely. To test for the first possibility, we tried to amplify the 5′ end sequence of Rouault et al. by PCR in different cDNA libraries, but failed to obtain an amplification product. The second possibility is improbable due to the fact that our clones are identical over most of the remaining sequence with the one published by Rouault et al. (22). Therefore, we consider it likely that our IRF cDNAs and the IRE-BP clone from Rouault et al. are representative of the same gene. It is interesting, that our new NH_2-terminal amino acid sequences (Fig.2) as well as internal corrections improve the alignment to a related protein,

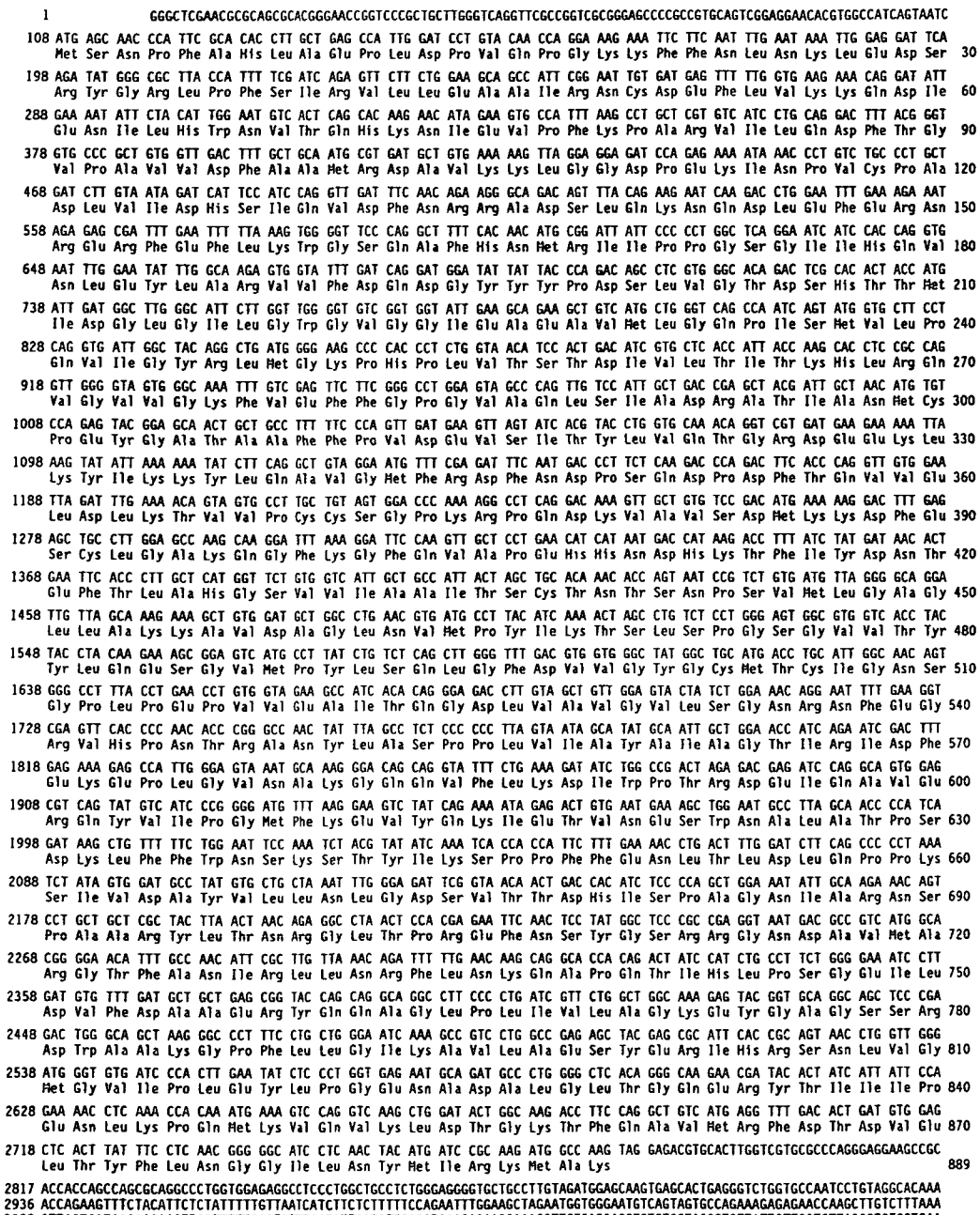

Figure 2. Nucleotide and protein sequences of the human IRF cDNA. The cDNA inserts from clones λIRF2 and λIRF4 were fully sequenced by the method of Sanger et al. (33). The number of nucleotides (left side) and amino acids (right side) are indicated.

clone 10.1 published by Rouault et al. (22). No cross-hybridizing clones were found in our screening.

The overlapping inserts of clones λIRF2 and λIRF4 were assembled into a larger cDNA for IRF (Fig.1) according to the description in Materials and Methods. The complete sequence is 3498 nucleotides in length with an open reading frame coding for 889 amino acids (Fig.2). The first initiation codon is located at position 108 and matches the second most frequent sequence found for mammalian translation start sites (38), and the stop codon ends at position 2778. The deduced amino acid sequence specifies a protein of 98,398 Da (Fig.2), a value close to the size of our previous determinations for purified placental IRF (3,31). Computer calculation estimates the pI of this protein at 6.21, close to the experimental pI of 6.45 to 6.55 found for purified IRF from human placenta (31). As pointed out by Rouault et al. (23), the IRF protein sequence shows homology to pig aconitase. The new NH_2-terminal region, however, does not improve the sequence similarity between the two proteins.

Southern and Northern blot hybridizations were carried out in order to determine whether the IRF cDNA would hybridize

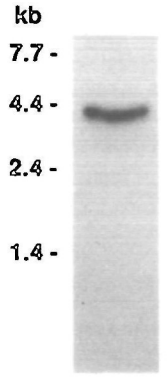

Figure 3. Northern blot analysis of IRF mRNA. Total RNA (25 μg) from human fibroblast cell line EK4 was separated on a 1.2% agarose gel containing 6.6% formaldehyde and transferred to nylon filters. The blot was hybridized to a probe corresponding to base positions 143 to 3040 of the human IRF cDNA.

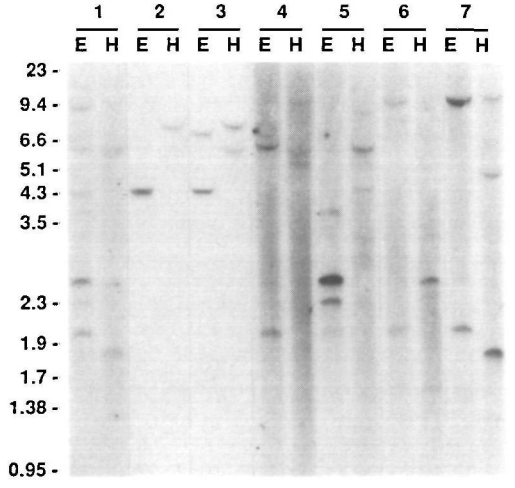

Figure 4. Southern blot hybridization of IRF cDNA fragments to human DNA. Genomic DNA from human placenta was digested with EcoRI (E) or with HindIII (H), separated on a 0.8% agarose gel and transferred to a nylon membrane. The blot was sequencially hybridized with various IRF cDNA probes at base positions 143–3040, (lane 1), 44–344 (lane 2), 210–472 (lane 3), 644–1368 (lane 4), 1368–2015 (lane 5), 2015–2220 (lane 6), and 2220–3040 (lane 7). Fragments of λ-DNA digested with HindIII/HindIII-EcoRI were used as molecular weight markers.

to a single gene or mRNA species. The radio-labelled cDNA probe recognized a single mRNA species of about 4.0 kb in a Northern blot with total RNA from the human fibroblast cell line EK4 (Fig.3). For Southern blot analysis, human genomic DNA from placenta was digested to completion with EcoRI or HindIII. The restriction fragments were resolved in an agarose gel, blotted and sequencially probed with a series of cDNA fragments (Fig.4). The results show that the IRF gene is at least 40 kb in size and represents a single copy gene. This is particularly evident in lanes 2 and 3 of Fig.4, where a short cDNA probe hybridizes with a single genomic restriction fragment, or two adjacent fragments, respectively.

From Southern hybridizations and sequence data it was not possible to decide whether the observed protein doublet of affinity-purified human placental IRF (31) is derived from a single

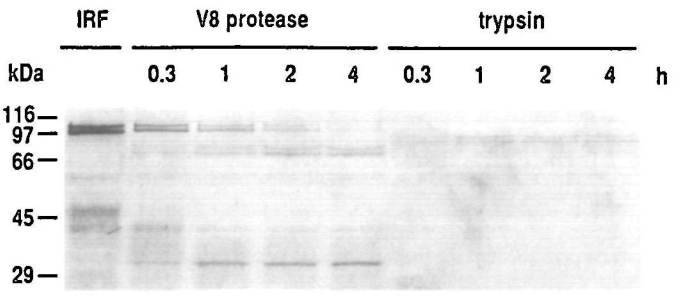

Figure 5. Partial digestion with V8 protease or trypsin of native IRF from human placenta. IRF was purified by affinity chromatography from human placenta (31), and 1 μg aliquots were partially digested for different lengths of time as indicated with V8 protease (1:20 w/w) or trypsin (1:100 w/w). The products were analysed on a 7.5% SDS-polyacrylamide gel and stained with Coomassie blue.

gene or two non-crosshybridizing genes. Therefore, we took a biochemical approach with proteases to analyse this heterogeneity. Highly enriched IRE-binding proteins from human placenta were partially digested with V8 protease or trypsin for different lengths of time (Fig.5). IRF was cleaved by both enzymes resulting in large sized protein doublet and, in the case of V8 protease, an apparently homogeneous fragment of 31 kDa. In order to determine the V8 protease cleavage site, both the large and the small fragments were sequenced by automated Edman degradation. The NH_2-terminus of the large doublet, as previously observed for the entire protein, was found to be blocked. The NH_2-terminus of the small 31 kDa-V8 protease fragment, however, gave a homogeneous sequence: XXNALATPSDKLFFXN. From this result it was concluded that partial digestion with V8 protease cuts native IRF at position 621. We deduced that the fragments of 65 and 70 kDa (Fig.5) correspond to the NH_2-terminal region of IRF and carry the observed heterogeneity of the placental protein. Since the COOH-terminal fragment did not show any heterogeneity in the sequenced amino acids , it is likely that the two proteins in the placental IRF doublet are encoded by a single gene. This is consistent with the above results from genomic Southern blots (Fig.4) and the previous identification of a single locus on chromosome 9 (22,39). The heterogeneity of the placental IRF doublet could be due to alternative splicing, a post-translational modification or allelic forms of IRF.

Expression of IRF by *in vitro* translation and its binding to an IRE

Several questions concerning the structure and function of IRF remain to be solved, in particular, the modulation of its activity by iron levels and the physical features of its interaction with IREs. Studying these questions would be facilitated by expression of IRF from cloned cDNA sequences. Since there are no previous reports of a successful expression, we decided to investigate IRF made in an *in vitro* transcription/translation system. The IRF cDNA was assembled (Fig.1) and subcloned behind the T7-promoter into pGEM-7zf(−). This plasmid, pGEM-hIRF, was linearized downstream of the cDNA insert and transcribed *in vitro* with T7-polymerase to obtain a capped RNA of 3.5 kb. The RNA was translated *in vitro* in a wheat germ translation reaction in the presence of ^{35}S-methionine. When the synthesized polypeptides were analysed by SDS-polyacrylamide gel electrophoresis, the major band migrated at about 97 kDa

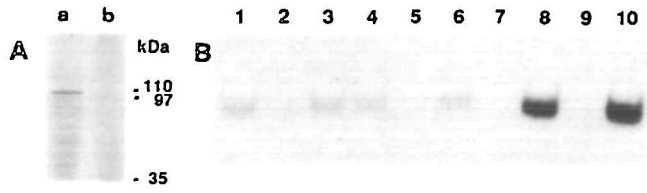

Figure 6. Expression of active IRF in a wheat germ translation system. In panel A, *in vitro* translated proteins were analysed on a 8% SDS-polyacrylamide gel. The translation was either with a full-length IRF RNA transcribed from the reassembled cDNA behind a T7 promoter (a) or without any RNA (b). A translation of Brome Mosaic Virus RNA was used for molecular weight markers. In panel B, a gel retardation-assay with the ^{32}P-labelled IRE of human ferritin H chain (transcript of pSPT-fer (3)) and aliquots from an *in vitro* transcription/translation reaction of IRF (lanes 1–6) or from a human placenta extract (lanes 8–10). Lane 1: incubation of *in vitro* translated IRF with 0.1 ng IRE RNA; lane 2: as in lane 1, but after pre-incubation of IRF with the sulfhydryl oxidizing reagent diamide at 1.5 mM; lane 3: as in lane 2, but followed by the reduction of oxidized IRF with 2% β-mercaptoethanol; lane 4: same as lane 1, after reduction with 2% β-mercaptoethanol only; lane 5: like lane 4, reduced IRF in the presence of 60 ng unlabelled competitor pSPT-fer RNA; lane 6: reduced IRF, as in lane 4, in the presence of 60 ng 4F2 antigen heavy chain RNA; lane 7: aliquot of a translation reaction without IRF RNA; lane 8: incubation of probe with human placenta extract (1 μg); lane 9; as in 8, but in the presence of 60 ng unlabelled pSPT-fer RNA; and lane 10: in presence of 60 ng 4F2 antigen heavy chain RNA.

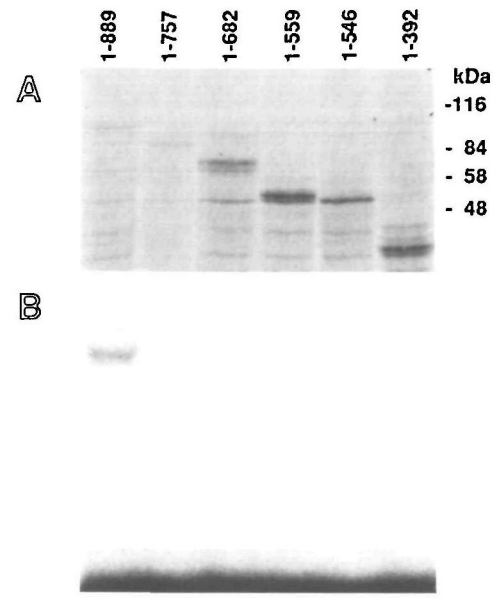

Figure 7. Requirement of the COOH-terminal part of *in vitro* translated IRF for the RNA-protein interaction. The assembled IRF cDNA plasmid pGEM-hIRF was linearized by different restriction enzymes and transcribed *in vitro* with T7 polymerase (see Materials and Methods). Each transcript was translated *in vitro* by the wheat germ extract. In panel A, the various COOH-terminal deletion mutants of IRF were analysed on a 8%-SDS-polyacrylamide gel. Numbers above the panel indicate the first and last amino acids of translated polypeptides. Prestained proteins were used as molecular weight markers. In panel B, a gel retardation assay with an aliquot of each translation reaction and 0.1 ng of ^{32}P-labelled pSPT-fer probe.

as expected for the open reading frame of the IRF cDNA (Fig.6A, lane a). No protein was translated in the absence of RNA (Fig.6A, lane b).

In order to test whether the translated protein corresponded to active IRF, a parallel unlabelled batch of the same protein was made and examined in gel retardation assays. An aliquot of the translation reaction was incubated with a ^{32}P-labelled RNA transcript of pSPT-fer containing the human ferritin H chain IRE (Fig.6B). The translated protein bound to this probe (lane 1), and the RNA-protein complex migrated at the same position as a complex between the IRE and IRF from a human placenta extract (lane 8). However, no complex could be detected with a translation reaction carried out in the absence of IRF RNA (lane 7). When the translated protein was pre-incubated with the sulfhydryl-oxidant diamide, binding to the IRE was inhibited (lane 2), but could be restored after reduction with β-mercaptoethanol (lane 3). Thus, *in vitro* translated IRF had the same properties as those described for affinity-purified IRF from human placenta (31). This was also true for the specificity of its interaction with the IRE. Binding could be entirely inhibited by an excess of unlabelled pSPT-fer RNA (lanes 5 and 9), but not with an unrelated RNA (lanes 6 and 10).

The addition of β-mercaptoethanol to the translated products without prior oxidation did not increase the IRE-binding activity (lane 4) compared to an untreated aliquot (lane 1). Therefore, *in vitro* translated IRF is synthesized immediatly with features of an active RNA-binding protein. In the case of IRF, this finding is not trivial. Recent evidence from sequence comparisons have revealed homology to iron-sulfur cluster containing isomerases (23,24), suggesting that IRF is most likely also an iron-sulfur cluster protein. IRF activity could be controlled as aconitase by iron exchange in such a cluster. This postulate is supported by the *in vivo* data indicating that chelatable iron has a central role in the final setting of IRF activity (3,14,15). Other lines of evidence mainly based on *in vitro* data suggest, however, that the modulation of IRF involves also the oxidation and reduction of sulfhydryl groups (16). Therefore, if *in vitro* translated IRF is inherently fully active, this might be due to the presence of 5 mM DTT in the translation reaction. It should be noted, however, that such a concentration of DTT has little or no effect on the activity of native IRF (17). Alternatively, *in vitro* translated IRF may actually represent an apoprotein, and the redox effects observed in Fig.6B could be independent of a putative iron-sulfur cluster. In support of this hypothesis, we and others found that changes in the redox state of the sulfhydryls on IRF are less permanent than changes induced *in vivo* by iron levels (17, our unpublished observation). In addition, it is known that [4Fe-4S] clusters are unstable in an aerobic environment (40). This makes it highly unlikely that such a cluster is incorporated into the nascent polypeptide during the *in vitro* translation. As a consequence, it would seem that apo-IRF can still bind to IREs.

A COOH-terminal region of IRF is required for interaction with IREs

To examine how IRF interacts with the IRE-element and which sites of the protein are necessary for this activity, deletions were made in the full-length cDNA. We shortened IRF at its COOH-terminus in order to analyse polypeptides of various length for their RNA-binding activity. pGEM-hIRF was linearized at particular restriction sites located in the open reading frame of the cDNA (see Fig.1). Each linearized plasmid was transcribed and translated *in vitro* creating deleted versions of IRF (Fig.7A). These polypeptides were incubated with the labelled probe of pSPT-fer in a gel retardation assay (Fig.7B). Interestingly, only the wild type form of IRF bound to the RNA (lane 1), whereas a deletion of just 132 amino acids abolished the binding entirely (lane 2). This means that the COOH-terminal region is required for the interaction of IRF with the IRE.

The present results leave open how other parts of IRF are involved in the RNA binding. In preliminary experiments with ultra-violet crosslinking, we observed complexes between the NH_2-terminal 65/70 kDa V8 protease fragments (Fig.5) and an IRE probe (unpublished results). This suggests, that both NH_2- and COOH-terminal regions of IRF participate in the RNA-protein interaction. Thus, unlike certain transcription factors (41) or hnRNA-binding proteins (42) IRF does not seem to contain a restricted domain for its binding activity. It will be of interest to mutagenize IRF in order to precisely locate which regions are necessary for its interaction with IREs and its activation by iron levels. Expression *in vitro*, as described in this paper, will provide a fast method to analyse such mutants.

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