Cloning, expression in *Escherichia coli*, and reconstitution of human myoglobin

(gene expression/heme protein)

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**ABSTRACT** A full-length cDNA clone for human myoglobin has been isolated from a human skeletal muscle cDNA library. The clone as isolated has a cDNA insert approximately one kilobase long and has 5' and 3' untranslatable regions of approximately 80 and 530 base pairs, respectively. The sequence of the translated region corresponds exactly to that predicted for human myoglobin. The cDNA was expressed in high yield in *Escherichia coli* as a fusion protein consisting of the first 31 amino acids of the phage λ cII gene, the tetrapeptide Ile-Glu-Gly-Arg, and the myoglobin sequence by following the approach of Nagai and Thogersen [Nagai, K. & Thogersen, M. C. (1984) *Nature* (London) 309, 810–812]. The fusion product was isolated, reconstituted with heme, cleaved with trypsin, and purified to generate a protein whose properties are indistinguishable from those for authentic human myoglobin. Myoglobin can be readily prepared on a gram scale by using these methods.

In the present communication we report the cloning of the cDNA for human myoglobin (Mb), the expression of this gene in high yield in *Escherichia coli*, simple procedures for purification of the gene product and reconstitution with heme, and limited comparisons of the isolated human Mb with Mbs from natural sources. This sets the stage for detailed physical and biochemical studies of Mbs modified by site-directed mutagenesis.

Mb is among a handful of the most studied proteins (1). Sperm whale Mb was the first protein to be characterized by x-ray crystallography (2–4), and the structures of several other Mbs and hemoglobins have been reported as well (5, 6). All Mbs studied to date have very similar secondary and tertiary structures. Because of their physiological importance, abundance, stability, and high-resolution structural characterization, these proteins have been subjected to characterization by essentially all tools available to protein chemists, biochemists, and biophysicists. Their features serve as paradigms for many aspects of globular protein structure, folding and dynamics, and ligand binding. It is straightforward to remove the heme group from Mb and reconstitute the apoMb with native heme (7), modified hemes (8), dye molecules (9), and even chlorophyll derivatives (10).

Recently Jeffrey’s co-workers have isolated the genes for seal and human Mb (11–13). In each case the gene is in excess of 9 kilobase pairs (kb) long, whereas the coding regions total about 500 base pairs (bp). Because of the high level of homology between exon II of the seal and the human gene (87%), our strategy for isolating the cDNA for human Mb was to use a convenient restriction fragment containing exon II from the seal gene to probe a cDNA library from human skeletal muscle. By using the technique recently introduced by Nagai and Thogersen (14), this cDNA was fused to a piece of the phage λ cII gene via a dodecamer linkage, leading to high-level expression in *E. coli* of a fusion protein. This gene product is readily isolated, combined with heme, and cleaved to produce high levels of human Mb.

**MATERIALS AND METHODS**

Unless mentioned otherwise, all DNA manipulations were as described elsewhere (15). Plasmid DNA preparation was by the method as described in ref. 16. Minilysates were prepared by the alkaline lysis method (17). DNA restriction fragments were separated by electrophoresis on agarose gels in Tris/acetate buffer. DNA fragments were recovered from low-melting agarose gels by using either Elutip-d columns (Schleicher & Schuell) or extraction with phenol and precipitation with ethanol. Authentic human Mb was obtained from Rockland Co. All enzymes were from New England Biolabs except for mung bean nuclease (P-L Biochemicals), lysozyme (Boehringer Mannheim), and trypsin ( Worthington). DNA sequencing was performed according to the method of Maxam and Gilbert (18). *E. coli* strain MZ1 was a gift from M. Zuber. N99cII1 wild-type lysogen and the expression vector pAS1 were from Allan Shatzman. The β-globin expression system consisting of the vectors M13mp11FX and pLcIIFXβ was generously provided by K. Nagai.

**cDNA Clone Isolation.** Plasmid pSM19.5 (12) containing the seal Mb gene was a generous gift from A. J. Jeffrey’s. The plasmid was digested with EcoRI (see Fig. 1), and the 2-kb EcoRI/EcoRI fragment containing exon II was isolated. One microgram of this fragment was nick-converted with [α-32P]dATP (3000 Ci/mmole; 1 Ci = 37 GBq) to a specific activity of 2 × 107 cpm/µg and was used as a probe.

A human skeletal muscle cDNA library (20) was linearized with both EcoRI and HindIII. One microgram of each digest was run on a 0.7% agarose gel. Blotting onto nitrocellulose and subsequent hybridization of the probe were carried out as described in ref. 21. A single band appeared on the autoradiogram, indicating the presence of a cDNA insert approximately 1 kb long.

One microgram of the library was used to transform *E. coli* HB101; 5000 ampicillin-resistant colonies were picked and screened according to the method of Grunstein and Hogness (22). One positive clone was obtained. Plasmid DNA from this clone (pMbO, see Fig. 2) was isolated, a restriction map was prepared as shown in Fig. 1a, and the region from the distal Ava I site to the message start codon was sequenced.

**Construction of pMbI.** Twenty micrograms of the expression vector pAS1 (23) was linearized with BamHI and then digested with 75 units of mung bean nuclease under conditions described in ref. 23. Twenty micrograms of pMbO partially digested with *Nco* I was treated with 60 units of mung bean nuclease. These digested plasmids were both

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**Abbreviations:** kb, kilobase(s) or kilobase pair(s); bp, base pair(s).
Further digested with Sph I. The 637-bp Nco I/Sph I fragment from pMB0 was ligated to the 5.69-kb BamHI/Sph I fragment from pAS1 and used to transform N99c1'. Transformants were selected on L broth ampicillin plates, and plasmid from one such transformant was isolated to ensure that the first glycine codon of the Mb cDNA was preceded by the ATG codon from pAS1.

**Construction of pMB3.** As outlined in Fig. 2, the 993-bp HindIII/Sph I fragment from pMB0 was ligated to the 3.83-kb HindIII/Sph I fragment from pAS1 to give pMB2. pMB2 was partially digested with Nco I and then with mung bean nuclease as described above. The resulting fragments were further digested with Sal I. The 726-bp Nco I/Sal I fragment was then ligated to Sal I/Sal I-cleaved M13mp11FXB (14). The ligation mixture was used to transform *E. coli* strain JM101 (24). Cells were plated in the presence of isopropyl β-D-thiogalactopyranoside and 5-bromo-4-chloro-3-indoly β-D-galactopyranoside (BMB). Six colorless plaques were picked and the double-stranded replicative form of the recombinant phage was isolated. Double digestion with HindIII and BamHI confirmed the presence of the desired insert. The replicative form from one such plaque was selected for further use and was named M13mp11FXMb. The 759-bp BamHI/HindIII fragment from M13mp11FXMb was ligated to BamHI/HindIII-cleaved pl.LcIFX8 (14) and used to transform N99c1'. Plasmid from one recombinant clone was sequenced to ensure that the first glycine codon of Mb was preceded by the DNA sequence coding for Ile-Glu-Gly-Arg. This plasmid was named pMB3.

**Expression.** Plasmids pMB1 and pMB3 were used to transform the *E. coli* strain MZ21 as follows. One hundred nanograms of plasmid in buffer (10 mM Tris-HCl, pH 8.0/1 mM EDTA) was added to 200 µl of competent MZ21 cells (prepared as described in ref. 15). The mixture was incubated on ice for 30 min and then heat shocked at 34°C for 5 min. Then 2.5 ml of warmed L broth was added, and the mixture was incubated at 28°C for 60 min, then plated on L broth/ampicillin plates and incubated at 28°C. Ampicillin-resistant colonies were picked and grown in L broth to an OD$_{600}$ of 0.75. The temperature was then rapidly elevated to 42°C by adding an equal amount of 65°C L broth with rapid swirling, and the culture was grown at 42°C. After a 2-hr induction the cells were spun down and frozen at ~70°C. Cells were lysed by keeping them at room temperature for 1–2 min and then adding 100 µl of 2× Laemmli buffer (25). Samples were then heated to 90°C for 5 min and analyzed by NaDodSO$_4$/PAGE. Protein was detected by either Coomassie blue staining (Fig. 3) or immunoblotting using horseradish peroxidase coupled with antiserum to human Mb (Cappel Laboratories, Cochranville, PA) (26).

**Isolation of Fusion Product, Cleavage, and Purification.** Purification of the fusion product was essentially as described by Marston et al. (27). Cultures were grown as described and cells were isolated by centrifugation. Cells were lysed and fusion protein-containing inclusion bodies were isolated and solubilized as described in ref. 27. The solubilized denatured protein was dialyzed against 50 mM Tris-HCl, pH 8.0/100 mM NaCl/1 mM CaCl$_2$. Approximately 10 equivalents of heme dissolved in a minimal amount of 0.01 M NaOH was added to reconstitute the fusion protein. This product was then subjected to 12-hr digestion by trypsin (18 mg of trypsin per g of protein) at 25°C, followed by dialysis against 10 mM Tris-HCl, pH 8.0. The resulting moderately pure human Mb was concentrated, loaded onto a DEAE-Sepharose column (Pharmacia), and eluted with 50 mM Tris-HCl, pH 8.0. Mb-containing fractions were pooled and applied to a Seph-
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acryl S-200 column in 10 mM Tris·HCl, pH 8.0, for final purification.

Electronic Absorption Spectra. Cyanometmyoglobin was prepared by adding a small crystal of potassium cyanide to a cuvette containing the metaco form. Reduction to the ferrous deoxygenated form was accomplished by adding a few crystals of sodium dithionite to the cyanometmyoglobin. Carbonmonoxymyoglobin was prepared by slowly bubbling carbon monoxide into the cuvette containing the deoxy- genated form prepared above. All absorption spectra (Fig. 4) were obtained on a Varian 2300 spectrophotometer.

RESULTS AND DISCUSSION

The human Mb cDNA clone isolated had an insert of approximately 1 kb and has 5′ and 3′ untranslated regions of approximately 80 and 530 bp, respectively. The entire coding region was sequenced and found to be identical with the sequence derived from the exons of the human Mb gene (13). This in turn is consistent with the known protein sequence (28).

Several different approaches were taken to express human apoMb in E. coli. To this end the human Mb cDNA was cloned in the expression vector pAS1 (23), which has been shown to give relatively high yields of a number of eukaryotic proteins. In the desired recombinant, pMb1, the Gly-1 codon of human Mb was preceded by the initiation codon of the cI1 gene, as demonstrated by sequence analysis. Expression was under the control of the λ P L promoter. pMb1 was used to transform the defective λ lysogen MZ1, which has a temperature-sensitive mutation (cI857) in the λ cI gene. When these cells are grown at 30°C the repressor synthesized by this gene is active, and transcription from the P L promoter is repressed. At 42°C, however, the repressor is no longer active and transcription from the P L promoter is possible.

MZ1 cells containing pMb1 were induced as described in Materials and Methods, and protein expression was analyzed by NaDodSO4/PAGE. No apoMb was detectable by Coomassie blue staining above the background of native E. coli proteins of comparable molecular weight. Immunoblotting experiments with antibodies to human Mb revealed a band at apparent molecular mass 17 kDa, demonstrating that apoMb was expressed in induced cells at a low level (no more than 0.2% of total protein estimated crudely from the sensitivity of immunoblots using known quantities of sperm whale Mb). No fragments of lower molecular weight were detected. Although this experiment demonstrates that human apoMb itself can be expressed in E. coli, the levels of expression in our hands were not sufficient for biophysical studies, and this approach was not optimized or pursued further.

Very recently Nagai and Thogersen (14) reported an ingenious approach to the expression of β-globin in E. coli. It has often been observed that eukaryotic gene expression in E. coli can be enhanced considerably by fusing the gene of interest to a portion of an E. coli or phage λ gene (29). Nagai and Thogersen have generalized this approach by inserting a linker between a fragment of the cI1 gene (DNA coding for the first 31 amino acids of cI1) and the gene of interest. The linker codes for the tetrapeptide sequence Ile-Glu-Gly-Arg, which serves as the recognition site for the protease factor Xa. Many previous workers have been frustrated in their attempts to express β-globin at high levels in E. coli. However, Nagai and Thogersen demonstrated both expression of the fusion product and cleavage by factor Xa to β-globin by NaDodSO4/PAGE (yields and reconstitution were not reported).

The construction of pMb3 outlined in Fig. 2 replaces the cDNA for β-globin with that for human Mb in the expression vector pLcIIFXβ. The region of the sequence in the vicinity of the Gly-1 codon was sequenced, demonstrating that the cI1 gene fragment and the ATC-GAG-GGT-AGG sequence coding for the cleavage site (abbreviated FX) were as desired. pMb3 was introduced into MZ1 by transformation as described above and whole cells were analyzed by NaDodSO4/PAGE (Fig. 3) revealing the presence of a new, intense band at apparent molecular mass about 21 kDa. As shown in the second and third lanes in Fig. 3, this band was present in cells that had been induced and not in those kept at 30°C. In addition to being at the correct molecular mass for the fusion product, this band was shown by immunoblotting to react with antibodies to human Mb. From these gels we estimate that on the order of 10% of total cell protein is the fusion product.

When induced cells were lysed by using a French press and spun down the desired protein was found to be in the pellet. This suggests that the protein aggregates and inclusion bodies are formed, so we followed the isolation procedure recently described in ref. 27. As shown in the fourth lane of the gel in Fig. 3, this procedure leads to isolation of the fusion protein at quite a high level of purity, and NaDodSO4/PAGE analysis of the supernatant (not shown) demonstrates that very little of the fusion product is not sedimented. Reconstitution of the partially purified fusion product with heme was successful, as demonstrated by characteristic features in the electronic absorption spectrum (see below). It is well known that reconstituted Mbs are insensitive to proteolytic enzymes, whereas the apoproteins are rapidly degraded (1). Thus, we chose to use trypsin in place of factor Xa, as it will also cleave at the arginine residue preceding Gly-1 of human Mb and is much less expensive. As shown in lane 5 of Fig. 3, treatment of the reconstituted fusion protein with trypsin produces a protein of apparent molecular mass 17 kDa and digests essentially all other protein impurities as a bonus, minimizing the need for further purification. This protein (predicted molecular mass without heme = 17,053 Da) was mixed with sperm whale Mb (17,199 Da), horse heart Mb (16,951 Da), or authentic human Mb and subjected to NaDodSO4/PAGE. The human protein migrated as if it had a slightly higher apparent molecular mass than the horse heart protein and about the same apparent molecular mass as the sperm whale protein, and it was indistinguishable from authentic human Mb (data not shown). From the amino acid sequence the closest undesirable tryptic fragments are predicted to have molecular masses of 17,936 or 14,982 Da, far outside the range observed. Thus, we are confident that the correct protein has been produced. All of the procedures described

![Fig. 3. Expression of human apoMb in E. coli. NaDodSO4/PAGE (17.5%) of the following: Lane 1, protein molecular mass standards (kDa); lane 2, whole MZ1 cells containing pMb3 before induction; lane 3, whole cells after induction at 42°C for 2 hr, showing fusion protein at apparent molecular mass 21 kDa that cross-reacts with antibodies to human Mb; lane 4, precipitated fusion protein resolubilized in 8 M urea; lane 5, final product after reconstitution with heme, 12-hr digestion with trypsin, and purification; lane 6, sperm whale apoMb (17,199 Da).](image-url)
The electronic absorption spectrum of Mbs provides a very sensitive measure of the integrity of the heme–apoprotein interaction and specific interactions with ligands. The absorption spectrum of the purified protein was examined under a variety of conditions, including the cyanmet, deoxy, and carbonmonoxy forms, as shown in Fig. 4. The absorption maxima and relative band intensities are identical to those of authentic human Mb and other related myoglobinins (1). The $^1$H NMR spectra at 500 MHz of the cyanmet forms of authentic Mb and that produced in E. coli were compared (data not shown). These spectra were identical for both hyperfine shifted heme and resolvable protein resonances and will be the subject of subsequent communications. These results demonstrate that the protein is fully functional with respect to ligand binding, the electronic structure of the heme, and the protein tertiary structure, setting the stage for detailed biophysical studies.

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