

The renaissance of myoglobin: dynamics, structure and oxygen binding control

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Abstract

Myoglobin as a prototype of a globular protein has been widely employed in advanced studies on the dynamics, folding and evolution of proteins. The advent of fast and super-fast lasers, the expression of site-directed mutants, and the application of advanced analytical and spectroscopic techniques have provided new insights into the structure-function relationships in proteins.

The work carried out by the Rome group has focussed on the mechanisms of control and discrimination of ligand binding in myoglobin. It is known¹ that bound oxygen is stabilised by H-bonding to the distal His(E7), and that substitution of this residue is generally associated to a large (or very large) increase in the oxygen dissociation rate constant². We have attacked the problem of engineering into the sperm-whale 3-D framework alternative distal residues that would exert a control on bound oxygen even in the absence of His(E7)³. Of particular interest in this context is the synthesis of a new mutant⁴ which is expected (on the basis of molecular modelling) to make H-bonds with bound oxygen, one with Gln(E7) and the other with Tyr(B10), mimicking therefore the structure of the active site of *Ascaris* Hb⁵.

The functional properties of this new myoglobin mutant (see table 1) can be accounted for by the new H-bonding network, and provide a clue to a possible strategy for engineering a distal site suitable for a blood substitute, given that a low oxygen dissociation rate constant (which reduces the rate of autoxidation, see ref. 6) is associated in this mutant to a lowered oxygen association rate constant, thereby moderating oxygen affinity.

Mini-myoglobin has been prepared in our group by limited proteolysis of horse Mb as a model for the central exon of the globin gene in order to test theories on the role of introns in molecular evolution. This myoglobin fragment binds heme stoichiometrically, acquires a high degree (~63%) of α -helical secondary structure and (more importantly) binds oxygen with equilibrium and kinetic parameters very similar (within a factor of 2) to those of native myoglobin (see table 2)^{7,8}; therefore it is a valuable model for a possible ancestor of the modern-day oxygen carriers.

Table 1. O₂ Binding data on mutant myoglobins.

| | | k_{off} (s ⁻¹) | k_{on} (M ⁻¹ s ⁻¹) | P _{1/2} (mmHg O ₂) |
|---------------|-----------------|--|---|--|
| Wild type | Leu(29) His(64) | 17 | $1.6 \cdot 10^7$ | 0.6 |
| Single mutant | Leu(29) Gln(64) | 100 | $2.0 \cdot 10^7$ | 1.8 |
| Double mutant | Tyr(29) Gln(64) | 1 | $1 \cdot 10^6$ | 0.6 |

Table 2. Functional properties of horse heart mini-Mb.

| | CO | O ₂ | |
|---------|---|---|------------------------|
| | l' (M ⁻¹ s ⁻¹) | k' (M ⁻¹ s ⁻¹) | k (s ⁻¹) |
| Mini-Mb | $4.5 \cdot 10^5$ | $5 \cdot 10^6$ | 20 |
| Mb | $5.0 \cdot 10^5$ | $1 \cdot 10^7$ | 11 |

Laser photolysis of the CO-derivative of Mini-myoglobin, and extensive analysis of its temperature and wavelength dependence⁹, have indicated that Mini-myoglobin is likely to be the domain responsible for the ligand-linked conformational transition, while the two polypeptides corresponding to the terminal exons of the globin gene would stabilise the protein by damping the conformational fluctuations of the central exon, a novel view on the relationships between the dynamics at the heme site and the overall mass of the protein.

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