

N-terminal-methionylated interleukin-1 β has reduced receptor-binding affinity

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The receptor-binding affinity of recombinant-derived interleukin-1 β containing unprocessed N-terminal methionine (MAPV-) was 10-fold lower than protein containing the authentic N-terminal sequence (APV-). Structural analysis of the methionylated and non-methionylated proteins by NMR spectroscopy detected no (or minor) conformational differences. The differences in binding affinity, therefore, suggest that the additional N-terminal methionine causes a small, direct or indirect, perturbation of the receptor-binding region.

Interleukin-1; Interleukin-1 receptor; NMR; Methionine aminopeptidase; N-terminal processing

1. INTRODUCTION

The purification and characterization of recombinant-derived interleukin-1 β (IL-1 β) have been recently described [1,2]. The purified protein was found to be a mixture of 80% correctly processed protein (N-terminus = Ala) and 20% of an N-terminal-methionylated form. The presence of N-terminal Met in a mature polypeptide is not uncommon and may be due to the difficulty which the processing enzyme methionine aminopeptidase experiences in removing Met when it is followed by a residue with large radius of gyration [3]. For recombinant-derived proteins produced in *E. coli* the removal of Met may also be compromised by the very high levels of accumulated protein which may simply saturate the processing enzyme(s). For IL-1 β this is almost certainly true, since the purified protein can be readily de-methionylated *in vitro* using purified methionine aminopeptidase [4]. Partial removal of Met has also been reported

for some other recombinant-derived proteins produced in *E. coli* [5,6].

Here, we have used a competition binding assay [7,8] to compare the receptor-binding affinities of N-terminal-methionylated and non-methionylated wild-type IL-1 β and also that of a mutant in which His 30 has been replaced by an Arg residue [7]. Surprisingly, in both instances, the methionylated proteins showed 10-fold lower receptor-binding affinities compared to the corresponding non-methionylated forms.

2. MATERIALS AND METHODS

2.1. Preparation of methionylated and non-methionylated IL-1 β proteins

N-terminal-methionylated and non-methionylated IL-1 β wild-type proteins were separated by chromatofocusing as described [2]. The mutant IL-1 β His 30 \rightarrow Arg was fractionated in a similar manner except that the sample, dialysed against 20 mM Tris-HCl (pH 8.0) was applied to a fast liquid chromatography (FPLC) MonoP column equilibrated with 25 mM Bis-Tris-acetate (pH 7.3).

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Polybuffers were removed by hydrophobic chromatography using a phenyl-Superose HR 5/5 (Pharmacia) column. Protein concentrations were determined by ultraviolet absorbance: an $A_{280}^{1\%} = 0.63$ at 280 nm was used [1].

2.2. Preparation of methionine aminopeptidase and in vitro digestion of IL-1 β

Methionine aminopeptidase was purified from *Salmonella typhimurium* and used for the in vitro processing of N-terminal-methionylated IL-1 β as in [4].

2.3. NMR spectroscopy

Sample preparation and measurements were made as detailed elsewhere [7,8].

2.4. Analytical measurements

Isoelectric focusing on thin-layer polyacrylamide gels and SDS-polyacrylamide gel electrophoresis (SDS-PAGE) were performed according to [1,2].

2.5. IL-1 receptor-binding assay

The assay procedure has been described in detail elsewhere [7,8].

3. RESULTS AND DISCUSSION

As reported in [2], purified N-terminal-methionylated and non-methionylated wild-type IL-1 β exhibit single bands on SDS-PAGE ($M_r = 17500$) and the methionylated protein has an isoelectric point ($pI = 6.55$) approx. 0.25 pH units lower than the non-methionylated protein. Similar results were obtained with the corresponding IL-1 β mutant proteins (not shown).

The methionylated wild-type IL-1 β had an approx. 10-fold lower receptor-binding activity compared to the non-methionylated protein (fig.1A). To show that the reduced receptor binding was specifically due to the presence of N-terminal Met, N-terminal-methionylated IL-1 β was digested with an N-terminal-specific peptidase, methionine aminopeptidase, purified and utilized as described by Miller et al. [4]. As expected, removal of N-terminal Met resulted in a pI increase of 0.25 pH units with a concomitant 10-fold increase in receptor-binding affinity (fig.1A). Enzyme treat-

ment of the non-methionylated IL-1 β had no effect on binding affinity (fig.1A).

Fig.2 shows a comparison of the 500 MHz $^1\text{H-NMR}$ spectra from the methionylated form of IL-1 β and from the protein without the N-terminal Met. As can easily be appreciated both spectra are very similar, thus demonstrating that no gross conformational differences exist between the two forms of IL-1 β . The resonances arising from the additional Met are indicated at the top of the figure. The new methyl resonance is clearly visible in the one-dimensional spectrum, whereas the other resonances belonging to the additional Met were identified in a two-dimensional HOHAHA spectrum (not shown). A comparison of the two-dimensional spectra confirmed that only very small differences exist between the two protein forms. We could identify two shifts in α -proton resonances and two in the methyl region; both are, however, extremely small (<0.05 ppm). Incidentally, one of the residues experiencing a shift is a

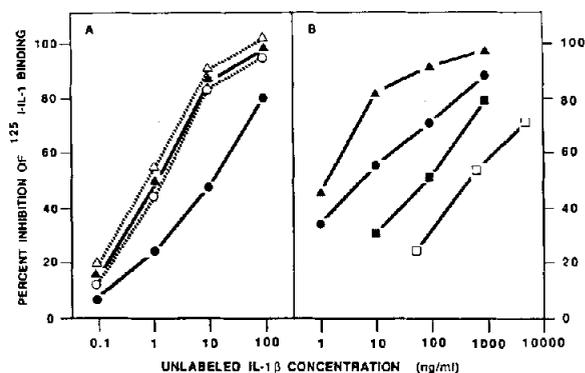


Fig.1. Competition binding assay of N-terminal-methionylated and non-methionylated IL-1 β . The indicated concentrations of unlabeled IL-1 β proteins were mixed at 4°C with ^{125}I -IL-1 α (1 ng/ml) prior to addition of EL4-6.1 cells (5×10^5 /tube). After 4 h at 4°C, bound radioactivity was evaluated by centrifugation of cells through an oil gradient. Data are expressed as percent inhibition of ^{125}I -IL-1 binding compared to untreated controls. (A) N-terminal non-methionylated IL-1 β treated (Δ) and non-treated (\blacktriangle) with methionine aminopeptidase are compared with N-terminal methionylated IL-1 β treated (\circ) and non-treated (\bullet) with protease. (B) N-terminal non-methionylated IL-1 β with a His 30 \rightarrow Arg substitution (\blacksquare) and N-terminal-methionylated mutant IL-1 β (\square) are compared with the corresponding wild-type proteins.

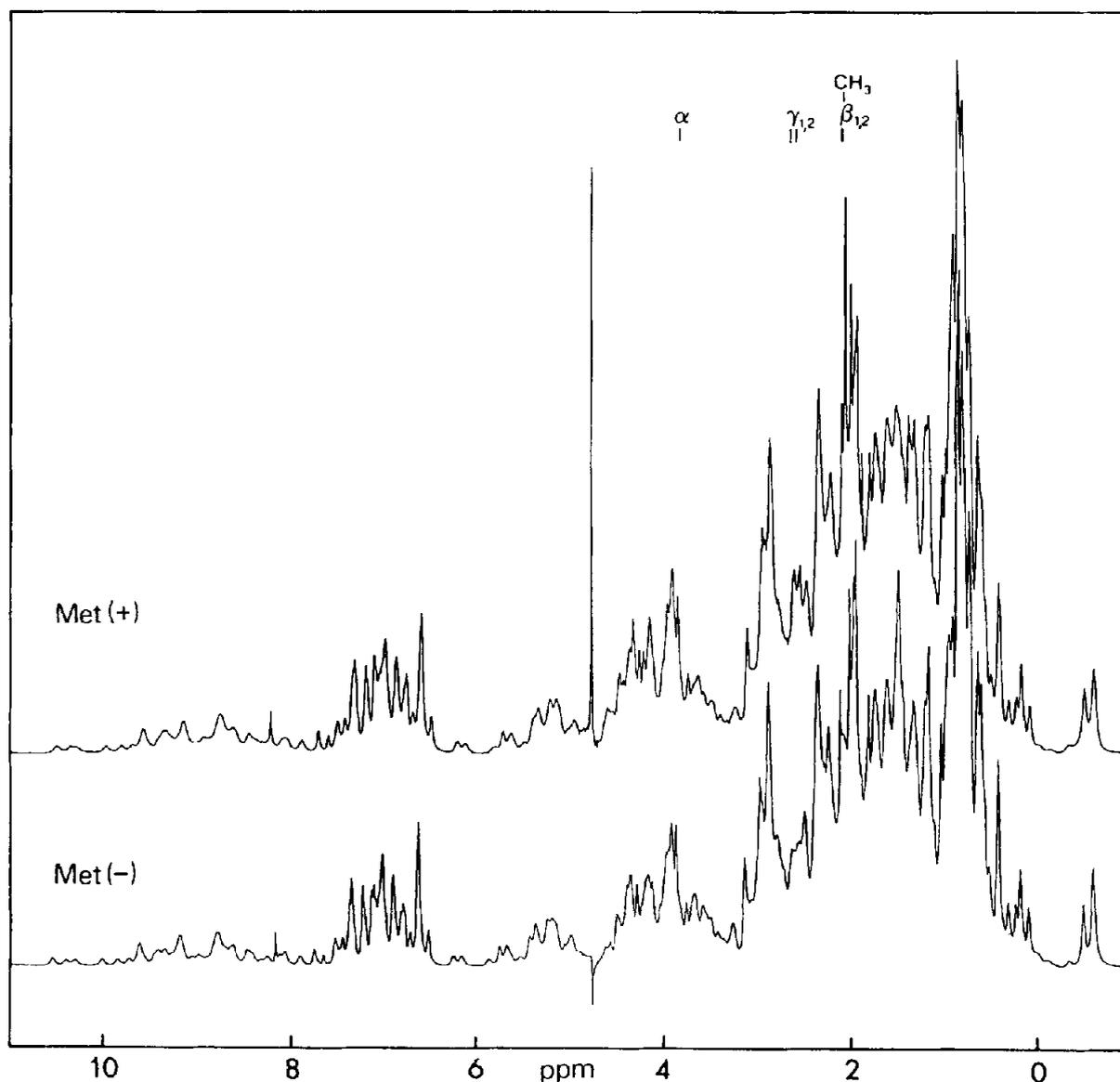


Fig.2. 500 MHz ^1H -NMR spectra of N-terminal-methionylated [Met(+)] and N-terminal non-methionylated [Met(-)] IL-1 β at 25°C.

threonine (Thr b), whose spin system was identified in an earlier study [8].

In a previous report it was shown that the IL-1 β mutant His 30 \rightarrow Arg has a 100-fold lower receptor-binding affinity compared to wild-type protein [7]. Furthermore, analysis by NMR spectroscopy indicated that this activity difference was not due to gross conformational changes [7]. The mutant protein used in the aforementioned study,

similar to wild-type IL-1 β , consisted of approx. 20% N-terminal-methionylated and 80% non-methionylated protein. It was, therefore, of interest to see whether the presence of N-terminal Met also affected receptor binding of this protein. The result obtained, which indicated a 10-fold reduction in receptor-binding affinity (fig.1B), was similar to that obtained with the corresponding wild-type proteins. The methionylated IL-1 mutant

has, therefore, almost a 1000-fold lower receptor-binding affinity compared to the wild-type non-methionylated protein. This simple additive decrease in binding affinity may indicate that the two protein modifications are producing independent, and probably indirect, perturbations of the receptor-binding region. If both N-terminal Ala and His 30 were directly involved in receptor binding, we might have expected larger, i.e. synergistic, rather than additive decreases in binding affinity as a result of modifying both residues.

Obviously, in the absence of real structural information on IL-1 β and its receptor, we can only speculate on the mechanism by which modification of the N-terminus of IL-1 β perturbs receptor binding. However, several recent reports are relevant to this issue. Schrader et al. [10] have drawn attention to the N-terminal sequence homologies among several cytokines, including IL-1 β and interleukin-2 (IL-2). The N-terminal sequence of IL-1 β , namely Ala-Pro, is the most common sequence, and the conservation of N-terminal Ala is suggested to have functional and/or structural significance. The results described herein would seem to support this prediction, at least for IL-1 β . In the case of IL-2, however, Yamada et al. [5] have reported that there is no difference in biological activity between N-terminal-methionylated and non-methionylated protein. In this context, Wingfield et al. [1] also saw little difference in biological activity between methionylated and non-methionylated IL-1 β . (Although the methionylated IL-1 β was consistently at least 2-fold less active than the non-methionylated protein, this was not considered significant in view of the inherent variability in the assay used.) In the case of IL-2, it would be of interest to compare the receptor-binding affinities of the methionylated and non-methionylated proteins.

Various biologically active N-terminal deletion analogues of IL-1 have been reported [11,12], suggesting that the N-terminal region has no direct functional role. Since these reports were of a somewhat preliminary nature and since the chemical and physical properties of neither the control nor deletion analogues used were described, one must say that the structural and/or functional role of the N-terminal region remain to be established.

4. CONCLUSIONS

Recombinant-derived proteins produced in *E. coli* may contain N-terminal Met as a result of incomplete processing of initiating *N*-formylmethionine (see [13] for discussion). The presence of this additional residue on the N-terminus would be a concern if the protein in question were to be used in clinical studies [14,15]. Although there is no immediate clinical application envisaged for IL-1 β , the reduced receptor-binding affinity of the N-terminal-methionylated protein would make it seem worthwhile to use only the purified non-methionylated protein for detailed structural/function studies. The methods and procedures outlined here and in the cited references provide routes to pure recombinant-derived IL-1 β with the chemical, and presumably the biological, properties of the authentic protein.

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