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ARTICLE TYPE

The $\beta\beta\alpha$ fold of zinc finger proteins as a “natural” protecting group. Chemoselective synthesis of a DNA-binding zinc finger derivative†

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We report the selective modification of engineered cysteine residues in peptides derived from a Cys₂His₂ zinc finger motif. The chemoselective modification is achieved thanks to the protecting effect exerted by the zinc cation upon coordination with the native cysteines and histidines of the zinc-finger fold, and allows the straightforward bioconjugation to DNA binding zinc finger constructs.

The covalent modification of proteins is a powerful strategy to modulate their macromolecular function.¹ Nature accomplishes such alterations through a variety of post-translational modifications that modify the activity of the modified proteins.² Inspired by nature, scientists have long pursued the development of methodologies that could emulate these natural post-conjugation reactions and allow the introduction of desired groups or labels in specific sites of proteins.^{1,3} For a reaction to be of general use, it should selectively target the residue of interest in the presence of competing side chains of the unprotected polypeptide, and in aqueous environments.

Many of the strategies so far developed for the site-selective modification of proteins rely on the introduction of designed amino acids equipped with orthogonally reactive groups that can be coupled to external reactants, for instance, by using the well known click chemistry.⁴ Although this strategy allows high levels of selectivity, it requires the introduction of non-natural amino acids.⁵ Alternatively, one could pursue the modification of specific natural amino acids in proteins, but achieving a good combination of reactivity and chemoselectivity is extremely challenging. In this context, most of the successful modifications of unprotected peptides or proteins have relied on the nucleophilic reactivity window provided by the sulfur atom in cysteine side chains,⁶ which allowed a number of selective alkylations with a variety of electrophiles. A major problem of this strategy arises when the peptide or protein of interest have more than one cysteine residue, because of the competitive formation of polyalkylated products.⁷

We report the selective modification of cysteine residues incorporated into a zinc finger peptide that features two additional cysteines as part of a classical Cys₂His₂ motif. In presence of Zn(II) these cysteines are trapped in the $\beta\beta\alpha$ secondary fold and thereby exhibit a much-decreased reactivity (Fig. 1). The ligation allows a straightforward approach to bisbenzamidine-zinc finger conjugates capable of binding to designed DNA target sequences. Since the zinc finger is a natural

motive present in many transcription factors, this work opens a door for the chemoselective access to zinc finger derivatives, and for the modification and/or tagging of zinc finger proteins.

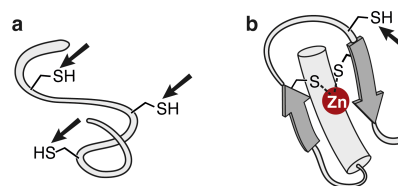


Figure 1. Schematic illustration of the approach for the chemoselective synthesis of zinc finger derivatives. a) unfolded peptide with three nucleophilic sites; b) zinc-promoted folding and cysteine coordination leaves only a single nucleophilic site for modification.

The zinc finger family is the largest among eukaryotic transcription factors, and responsible of regulating the expression of a myriad of genes controlling fundamental cellular programs.⁸ The DNA recognition by zinc finger proteins has served as inspiration for the engineering of a large variety of highly appealing artificial gene regulators.⁹ Despite the relevance of zinc finger proteins, work towards their selective chemical modification has been very scarce. There are a number of reports on the reactivity of zinc thiolates of different zinc fingers that suggest that, while the cysteines in charged Zn(Cys)₄ and Zn(Cys)₃His motifs react with electrophiles or oxidants, neutral Zn(Cys)₂(His)₂ are less reactive.¹⁰ Therefore, we reasoned that zinc finger structures might provide a natural protection for the two cysteines involved in the coordination to the metal ion, and thereby favor the selective modification of other cysteines present in the peptide, providing a rapid and versatile way of making zinc finger derivatives.

To test the approach we synthesized model peptides **1** and **2**, which exhibit the sequence of two different types of Cys₂His₂ fragments, together with an additional cysteine engineered either at the N-terminus (**1**) or in the side chain of an internal lysine (**2**). The zinc finger sequence of peptide **1** is based on a fragment of the C-terminal Cys₂His₂ unit of the trimeric Zif268 transcription factor (residues Pro¹⁶² to Arg¹⁸⁷ in the crystal structure).¹¹ Peptide **2** contains the Cys₂His₂ unit of the DNA-binding domain of the GAGA transcription factor of *Drosophila melanogaster* (from residues Ser²⁸ to Phe⁵⁸ in the reference structure).¹² Peptide **2** includes a mutation of Arg⁴⁴ to Lys to allow the selective introduction of a cysteine group in its side chain.¹³ Both peptides were assembled using standard Fmoc protocols and HBTU as

coupling agent. The Lys residue of peptide **2** was introduced as alloc derivative for its selective manipulation in the solid phase (see the ESI).

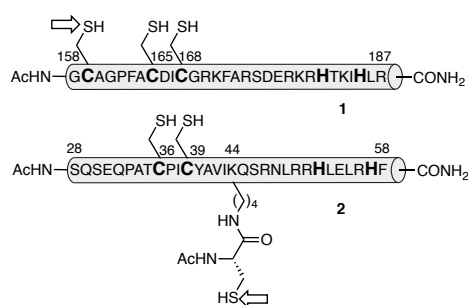


Figure 2. Structure of model peptides derived from Zif268 (**1**) and GAGA (**2**). Arrows point to the thiols to be selectively modified.

We tested the selectivity in the alkylation of the sulfur side chains in the peptides with benzyl bromoacetate, a very good electrophile that is commercially available. The reactions were carried out in parallel, in the absence and in the presence of 1.5 equiv of ZnSO_4 , and in a desoxygenated phosphate buffer (pH 7.5) under argon atmosphere. The reactions were monitored by RP-HPLC and the identity of the products was confirmed by mass spectrometry. For peptide **1** the alkylation was carried out at rt in presence of 4 equiv of benzyl bromoacetate. After 10 min, LC-MS analysis of an aliquot of the reaction carried out in the absence of Zn(II) showed a mixture of several products, the major being the trialkylated adduct (retention time 22.36 min). The HPLC peak at 19.45 min corresponds to a monoalkylated derivative (Fig. 3 left, and ESI). Interestingly, when the reaction was carried out in presence of ZnSO_4 we observed a different outcome, with the exclusive formation of a monoalkylated derivative (retention time 18.42 min). The other peaks correspond to the starting peptide **1** (16.73 min) and benzyl bromoacetate (Fig. 3, right).

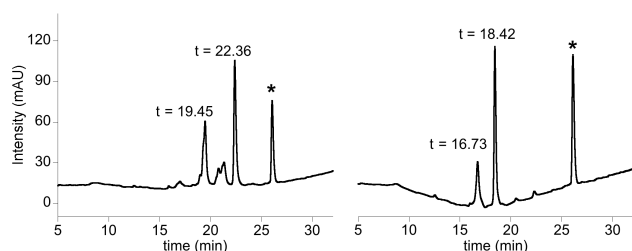


Figure 3. HPLC traces of the reactions of peptide **1** (200 μM) with benzyl bromoacetate (4 equiv), in the absence (left) and in the presence (right) of 1.5 equiv of ZnSO_4 , after 10 minutes of reaction at rt, in a desoxygenated phosphate buffer (pH 7.5). Peaks with asterisk: benzyl bromoacetate.

For the full identification of the monoalkylated product of the Zn containing reaction we did a MS/MS study of the fragments obtained after digestion of the modified peptide with trypsin. After 2h of digestion, HPLC of the mixture showed two peaks with double-charged signals at 851.36347 and 787.31604 (see ESI), which correspond to fragments cleaved at Lys¹⁷¹ (*y*/14 fragment) and Arg¹⁷⁰. The deconvoluted MS/MS spectra of the first peak shows signals corresponding to the *y* ion series of the partial sequence $\text{GC}^{159}\text{AGPFAC}^{165}\text{DIC}^{168}\text{GRK}$, where Cys¹⁵⁹ is the cysteine alkylated with benzyl bromoacetate, and Cys¹⁶⁵ and

Cys¹⁶⁸ are carbamidomethyl cysteines,¹⁴ which are formed during the treatment of the sample before digestion (see the ESI). The mass difference of 251.04275 between the signals at 1602.68829 (*y*/13) and 1351.62554 (*y*/12) can only be accounted for if the cysteine alkylated with benzyl bromoacetate is next to the acetylated glycine. Interestingly, the monoalkylated derivatives obtained in presence or in absence of Zn(II) are different, which suggests that the intrinsic reactivity of the terminal cysteine is lower than that of the internal ones.

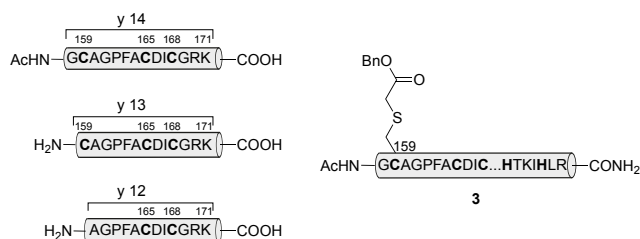


Figure 4. Left: schematic representation of the fragmentations of the *y* ion. Right: structure of the monoalkylated peptide **3**.

Peptide **2** is analog to one previously used by us to construct DNA binding peptide conjugates containing a zinc finger fragment and a minor groove binder,¹³ and seemed particularly appropriate to apply the chemoselective strategy for the preparation of DNA binders. Previous synthesis of this—and related—conjugates required the solid phase modification of the peptide chain with the minor groove binder, which represented an important drawback in terms of efficiency and versatility.¹⁵ Therefore we first analyzed the reactivity of peptide **2** with benzyl bromoacetate, and found that, after only 5 min at 5 °C in absence of Zn(II) it was fully converted into the trialkylated adduct (25.09 min, Fig. 5, left). However, in the presence of ZnSO_4 the reaction resulted mainly in the formation of a monoalkylated product (22.17 min, for details see the ESI).

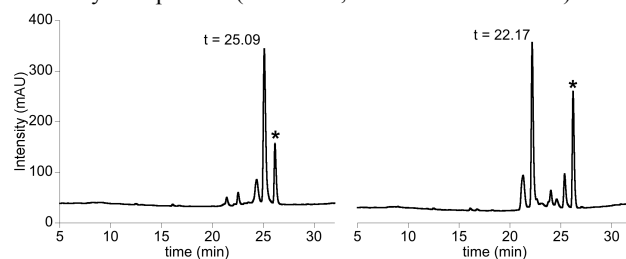


Figure 5. HPLC chromatograms, after 5 minutes at 5 °C, of the reactions of peptide **2** (200 μM) with benzyl bromoacetate (4 equiv), in the absence (left) and in the presence (right) of 1.5 equiv of ZnSO_4 and in a desoxygenated phosphate buffer (pH 7.5).

The reaction outcome is consistent with the folding of the peptide precursor **2** in the presence of Zn(II) , as shown by the increase in the negative ellipticity at 208/222 nm measured by circular dichroism (see ESI).¹⁶ Moreover, the spectral changes displayed by the monoalkylated product in the presence of zinc are similar to those observed for the precursor peptide, and are therefore consistent with the exclusive modification of the cysteine in the side chain of Lys⁴⁴, since alkylation of either of these cysteines would prevent such conformational changes.

More importantly, when the reaction was carried out with a more challenging electrophile equipped with a bisbenzimidine DNA binder (**bb-Br**),¹⁷ it also took place efficiently at rt, in the

presence of 1.5 equiv of ZnSO₄. Moreover, the resulting conjugate is an efficient and selective DNA binder, as demonstrated by EMSA (Figure 6).¹⁸ Therefore, the chemoselective ligation provides a very simple approach to functional zinc finger peptides, and opens the possibility of running related reactions with recombinant zinc fingers.

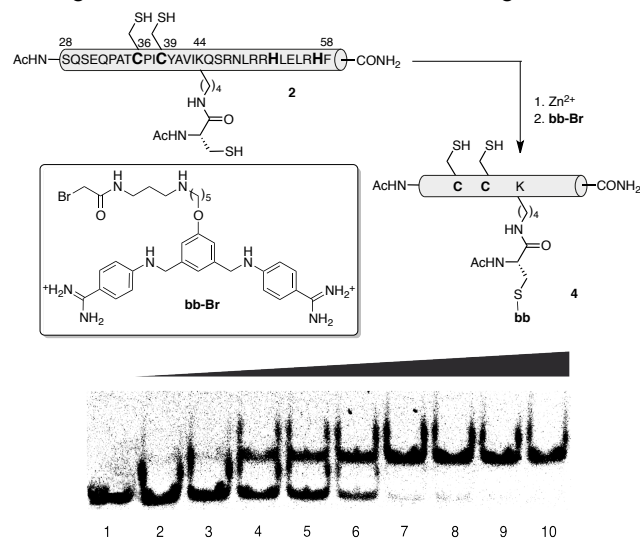


Figure 6. Top: Synthesis of conjugate 4. Bottom: EMSA results; Lanes 1-10: [4] = 0, 100, 200, 300, 400, 500, 600, 800, 900, 1000 nM with 50 nM of AT•GAGA dsDNA (SYBR gold staining). Oligonucleotide sequence (binding site underlined, only one strand shown): AT•GAGA: 5'-GACGGAATTTGAGAGCGTCG-3'.

Conclusions

The Zn(II) cation can be exploited both as a folding agent and as a protecting group. This double role allows the selective modification of cysteines present in zinc finger peptides that are not involved in the formation of the Cys₂His₂-Zn fold. The strategy provides a direct approach to functional DNA binding zinc finger conjugates, and promises to be useful for the post-transcriptional modification of zinc finger proteins.

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† Electronic Supplementary Information (ESI) available: Peptide synthesis, full experimental procedures and analytical data of the peptides and products obtained. See DOI: 10.1039/b000000x/

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