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## Programmed stereoselective assembly of DNA-binding helical metallopeptides

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A flexible and versatile synthetic approach for the construction of water-stable DNA-binding chiral peptide helicates and that is based in the solid phase peptide synthesis (SPPS) methodology is reported.

The development of non-natural agents that can reproduce the DNA recognition properties of natural transcription factors remains a major goal in biological chemistry, as they might have a great impact in fundamental and applied biological research, and even lead to the development of gene-targeted therapies. Most of the efforts in this area have been directed towards the development of small organic binders, but in the past few years there has been a growing interest in the use of coordination and metallo-supramolecular compounds with unique structural and spectroscopic properties.

Helicates have shown promising and unusual DNA-binding properties,4 including major groove binding,5 and recognition of DNA three-way junctions.6 However, nearly 20 years after the pioneering studies by Prof. Jean-Marie Lehn, helicates are still not viable alternatives to traditional DNA-binding agents. The slow development in the biological chemistry of metal helicates ultimately derives from the lack of efficient and versatile methodologies for their enantioselective synthesis,8 which usually result in mixtures of isomers of difficult separation, insoluble or unstable species in water, 10 and above all, lack of versatility for structural and functional optimization.<sup>11</sup> Prof. Scott recently proposed a new synthetic approach to DNAbinding helicates based in the self-assembly of aldehydes and amines in the presence of M(II) ions that allows the formation of water-stable and optically pure helicates. 12 Although this method represents a great improvement over the traditional routes, it does not guarantee the straightforward access to structural variants to efficiently study the chemical and

Given our experience in the study of DNA recognition agents, <sup>13</sup> DNA-binding peptides, <sup>14</sup> metallopeptides, <sup>15</sup> and helicates, <sup>10</sup> we decided to investigate into this problem by developing an alternative approach to DNA-binding chiral

helicates. Herein we report our proposal, which potentially combines the biocompatibility, modularity and structural control of peptides with the synthetic flexibility and versatility of solid-phase peptide synthesis (SPPS) methodology, which allows the straightforward construction and modification of the helicates and, therefore, the easy optimization of their biophysical properties.

2,2'-bipyridine (Bpy) is a privileged chelator that leads to stable complexes with many metal ions that has been extensively used in coordination and supramolecular chemistry. Thus, we decided to synthesize a Bpy analog appropriately modified for its application in SPPS as the basic component of our peptide helicates. Hence, the Bpy unit was derivatized with 5-amino-3-oxapentanoic acid (O1Pen) as a Fmoc-protected achiral amino acid (Fmoc-O1PenBpy-OH (1); Scheme 1 and ESI, Scheme S1). 15

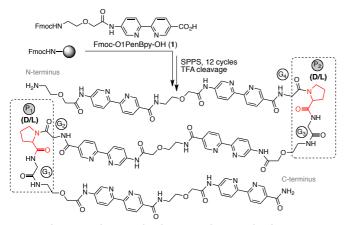
Following the synthesis of the amino acid building block, we designed a peptidic ligand capable of folding into a single-stranded dinuclear hairpin helicate; the selected peptide sequence contains six O1PenBpy units, which satisfy the coordination requirements of two octahedral metal centers, arranged in three sets (or substrands) of two consecutive Bpy residues connected through two short loops. The loops, whose structures have been previously optimized, <sup>15b</sup> are key components of this design, as they include a β-turn promoting - [(D/L)-Pro]-Gly- sequence that pre-organizes the ligand and induces the folding of the peptidic chain into discrete dinuclear species, thus avoiding the formation of higher order and polymeric complexes in the presence of metal ions (Scheme 1).

In order to gain some information about the structural viability of our design, molecular modeling was performed on the Fe(II) helicate derived from the peptide ligand LL-H (Scheme 1).<sup>17</sup> The system was optimized following a hierarchical protocol that consists in: 1) Molecular Dynamics simulation on the loops of an initial structure of the metallopeptide candidate; 2) clustering of the resulting MD, and 3) refinement by QM/MM geometry minimization of the

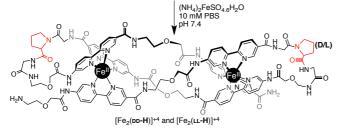
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most populated cluster representatives [see ESI (figure S1)]. The final calculation was performed with solvent and electronic embedding effects. The lowest energy model presents a helical geometry (Scheme 1) with both Fe(II) ions in octahedral configurations and the six bipyridine rings ordered around the metal centers. The first coordination sphere of the metal ions is barely constrained by the entire peptide framework, indicating that an excellent complementarity between organic and inorganic moieties is achieved in this design.

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 $\begin{array}{l} \textbf{DD-H} = H-(O1PenBpy)_2\text{-}Gly-(D)Pro\text{-}Gly-(O1PenBpy)_2\text{-}Gly-(D)Pro\text{-}Gly-(O1PenBpy)_2\text{-}NH_2\\ \textbf{LL-H} = H-(O1PenBpy)_2\text{-}Gly-(L)Pro\text{-}Gly-(O1PenBpy)_2\text{-}Gly-(L)Pro\text{-}Gly-(O1PenBpy)_2\text{-}NH_2\\ \end{array}$ 





**Scheme 1.** Solid-phase synthesis of the peptide ligands LL-H and DD-H. The L-Pro or D-Pro residues in the loops select a particular supramolecular chirality in the final helicates ( $\Lambda\Lambda$  – or  $\Delta\Delta$  –, respectively). Below, molecular representation of the most stable  $\Lambda\Lambda$  –[Fe<sub>2</sub>(LL-H)]<sup>4+</sup> helicate highlighting the interaction of the ammonium group of the N-terminal end with the C-terminal loop.

Supported by the computational results, we synthesized the two enantiomeric peptide ligands, each of them equipped with two L-Pro (LL-H) or D-Pro residues (DD-H) in their loops (Scheme 1). Both peptidic strands were obtained following standard Fmoc/tBu solid-phase protocols, <sup>18</sup> and purified by reverse-phase HPLC (see ESI). Incubation of  $\approx 4.0 \, \mu M$  solutions of LL-H and DD-H in PBS buffer (pH = 7.4, 298 K) with increasing concentrations of Fe(II) resulted in a bathochromic shift of the bipyridine absorption band from 304 to 322 nm, as well as in the appearance of a new band centered at 545 nm, typical of octahedral trisbipyridine Fe(II) complexes

[see ESI (figures S2 and S4a)]. <sup>19</sup> The increase in the absorption intensity of the d-d band was used to calculate the binding constants, which were the same within the experimental error for both **LL-H** and **DD-H**, <sup>20</sup> thus for the first association  $\beta_{1,1}(\text{LL-H}) \approx \beta_{1,1}(\text{DD-H}) \approx 12.9 \, \mu\text{M}$ , and the overall formation constants  $\beta_{2,1}(\text{LL-H}) \approx \beta_{2,1}(\text{DD-H}) \approx 18.9 \, \mu\text{M}.^{21,22}$  The successful assembly of the helicate, which can be considered as quantitative, was further confirmed by MALDI-TOF mass spectrometry showing a major peak at 2337.9 (see ESI). To our knowledge, SPPS has never been used for the preparation of helicates. Moreover, fully-peptide ligands have not been used before as precursors of metal helicates, and there are only a handful of examples of organic strands equipped with oligopeptides as spacers or functional appendages. <sup>23</sup>

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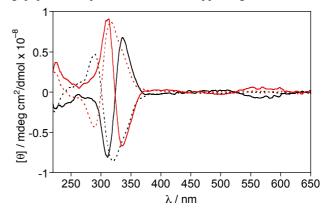


Figure 1. CD spectra of the μ-H and pd-H peptide ligands (50 μM) and their helicates. μ-H before (black dashed line) and after (black solid line,  $\Lambda\Lambda$ –[Fe<sub>2</sub>(μ-H)]<sup>4+</sup>) addition of 2 eq. of Fe(II) and pd-H before (red dashed line) and after (red solid line,  $\Delta\Delta$ –[Fe<sub>2</sub>(pd-H)]<sup>4+</sup>) addition of 2 eq. of Fe(II). All measurements were made in PBS buffer pH = 7.4, 298 K.

As expected, LL-H and its enantiomer DD-H give rise to mirror image CD spectra with two bands of opposite signs at approximately 290 and 324 nm (Figure 1, and ESI). The intensity of these bands decreases upon addition of Fe(II), while at the same time they display a bathochromic shift to 302 and 333 nm, respectively. The sign of the Cotton effect of the helicates is consistent with a  $\Lambda$ - configuration on each metal center for the LL-H derivative  $(\Lambda \Lambda - [Fe_2(LL-H)]^{4+})$ , and a  $\Delta$ configuration for the **DD-H** analog  $(\Delta \Delta - [Fe_2(\mathbf{DD-H})]^{4+})$ .<sup>24</sup> These data confirm that the enantiomeric peptide ligands give rise to the chiral helicates.<sup>25</sup> This means that the chiral proline residues do not only direct the folding of the peptide chain into a discrete dinuclear helicate, but also encode its chirality, which is selected under thermodynamic control at room temperature in water media upon incubation with Fe(II) ions. Controlling the metal center configuration in helicates usually requires demanding synthetic procedures for obtaining chiral organic ligands,26 which complicates the access to multiple structural variants that are required for the systematic studies involved in the optimization of their biological properties. In our approach, however, the chirality of the peptide helicates arises naturally from two single Pro residues located in the loops connecting the three bisBpy substrands (Scheme 1).

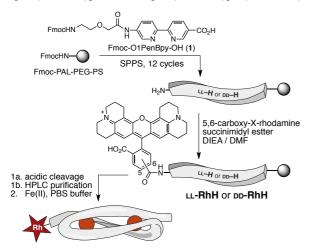
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The chiral peptide helicates are very stable in water at room temperature, and no degradation or racemization was detected even after several weeks. Additionally, thermal denaturation experiments produced sigmoidal melting profiles for both helicates that were consistent with cooperative transitions in the decomplexation of the Fe(II) ions (see ESI, Table S1, Figures S5, S6 and S7). Both melting curves were qualitatively similar; with a  $T_m$  temperature of  $\approx 80.5$  °C. Van't Hoff analysis showed that the unfolding process displays a positive entropic variation  $(\Delta S \approx 447.1 \text{ J/mol})$ , consistent with the increase in molecular disorder resulting from the disassembly of the complexes; the unfolding process is also highly endothermic ( $\Delta H \approx 157.9$ kJ/mol), in agreement with the large association constants obtained in the UV/Vis titrations and reported studies of related supramolecular metal complexes.<sup>27</sup> Alternatively, global analysis of the unfolding process using the Gibbs-Helmholtz equation provided qualitatively similar results.<sup>28</sup>

Having at hand the methodology for the efficient assembly of water-stable and optically pure peptide helicates, we decided to explore the DNA binding properties of these species. In particular, we were interested in studying the affinity and chiral selectivity of their binding to three-way DNA junction, <sup>29,30</sup> data that remain unknown until now.

Towards this end, we synthesized the N-terminal rhodamine labeled derivatives of the previously described LL-H and DD-H peptide ligands. In short, once the core peptide sequences were fully assembled, and still attached to the solid support, their N-terminal amines were reacted with 5-(and 6)-carboxy-X-rhodamine succinimidyl ester to yield the fluorescent peptidic ligands LL-RhH and DD-RhH, which were then cleaved from the resin and purified as described before, and incubated with 2 eq. of Fe(II) to form the corresponding fluorescent helicates  $\Delta\Delta$ -[Fe<sub>2</sub>(LL-RhH)]<sup>4+</sup> and  $\Delta\Delta$ -[Fe<sub>2</sub>(DD-RhH)]<sup>4+</sup> (Scheme 2).



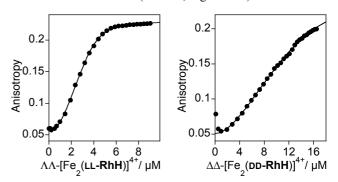
 $\Lambda\Lambda$ -[Fe<sub>2</sub>(LL-**RhH**)]<sup>4+</sup> or  $\Delta\Delta$ -[Fe<sub>2</sub>(DD-**RhH**)]<sup>4+</sup>

Scheme 2. Synthesis of the rhodamine-labeled peptide ligands LL-RhH and DD-RhH by solid phase modification of the core peptides, and their corresponding helicates  $(\Lambda\Lambda-[Fe_2(LL-RhH)]^{4^+}$  or  $\Delta\Delta-[Fe_2(DD-RhH)]^{4^+}$  respectively). See Scheme 1 for complete sequences of LL-H and DD-H.

Incubation of 1  $\mu$ M solutions of the rhodamine-labeled helicates with increasing concentrations of the DNA three-way junction  $\mathbf{Y_1Y_2Y_3}^{31}$  (see ESI) produced a concentration-dependent increase in the fluorescence anisotropy that could be fitted to a modified 1:1 binding mode, including higher order aggregates resulting from non-specific interactions (Figure 2). The  $\Lambda\Lambda$ -[Fe<sub>2</sub>(LL-RhH)]<sup>4+</sup> peptide helicate displayed significantly higher affinity—almost 150 fold—for the  $\mathbf{Y_1Y_2Y_3}$  DNA junction than the enantiomeric  $\Delta\Delta$ -[Fe<sub>2</sub>(DD-RhH)]<sup>4+</sup>, with apparent dissociation constants for the 1:1 complexes of  $0.25 \pm 0.04 \ \mu$ M and  $37.6 \pm 1.0 \ \mu$ M, respectively. 32,33

The structure of the peptide helicate obtained by molecular modeling is comparable to that of the simpler helicates previously described by Hannon *et. al.* Specifically, the three-fold symmetry of the peptide strands folding around the metal ions that create a compact structure with the right diameter for insertion into the cavity at the center of the three-way junction. These similarities, together with the tight binding constants observed in the fluorescence titrations support a similar binding model with the DNA junction (see ESI, Figure S9).<sup>6</sup>

Once we characterized the basic properties of the peptide helicates, we decided to exploit the presence of the fluorescent rhodamine dye to study their cell-internalization. Thus, we incubated Vero cells with  $\Delta\Delta$ -[Fe<sub>2</sub>(LL-RhH)]<sup>4+</sup> for 12 h, washed them with PBS, and observed the preparations without fixation. Gratifyingly, we found that the compound was efficiently internalized into the cells, concentrating in endocytic vesicles in the cytoplasm, which is consistent with the internalization pathway observed with other metal complexes,<sup>34</sup> and luminescent helicates (see ESI, Figure S10).<sup>35</sup>



**Figure 2.** Fluorescence anisotropy titrations of 1 μM solutions of peptide helicates with a DNA three-way junction ( $Y_1Y_2Y_3$ ) in 10 mM PBS buffer, NaCl 10 mM; pH: 7.3, 20 °C. ΛΛ–[Fe<sub>2</sub>(LL-RhH)]<sup>4+</sup> (left) and ΔΔ–[Fe<sub>2</sub>(DD-RhH)]<sup>4+</sup> (right). Lines represent the best fit to 1:1 binding models including the contribution of nonspecific complexes. DNA oligo sequences:  $Y_1$ : 5′–CAC CGC TCT GGT CCT C–3′;  $Y_2$ : 5′–CAG GCT GTG AGC GGT G–3′;  $Y_3$ : 5′–GAG GAC CAA CAG CCT G–3′.

In summary, we present a simple and versatile methodology for the enantioselective assembly of water-stable DNA-binding helicates. This novel approach relies in the modularity and synthetic flexibility of SPPS and in the preorganization of the peptide ligands provided by two single proline residues, which also encode the chirality of the helicates formed under thermodynamic control. We demonstrated the potential of this approach by synthesizing fluorescently-labeled helicates that

show chiral discrimination and high selectivity for three-way DNA junctions and promising cell-internalization properties.

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Electronic Supplementary Information (ESI) available: synthetic procedures and characterization of peptide ligands and helicates, computational details, spectroscopic studies (UV, CD, melting). See DOI: 10.1039/c000000x/

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