Effect of 3-Hydroxyproline Residues on Collagen Stability

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Abstract: Collagen is an integral part of many types of connective tissue in animals, especially skin, bones, cartilage, and basement membranes. A fibrous protein, collagen has a triple-helical structure, which is comprised of strands with a repeating Xaa-Yaa-Gly sequence. L-Proline (Pro) and 4(R)-hydroxy-L-proline (4-Hyp) residues occur most often in the Xaa and Yaa positions. The 4-Hyp residue is known to increase markedly the conformational stability of a collagen triple helix. In natural collagen, a 3(S)-hydroxy-L-proline (3-Hyp) residue occurs in the sequence: 3-Hyp-4-Hyp-Gly. Its effect on collagen stability is unknown. Here, two host–guest peptides containing 3-Hyp are synthesized: (Pro-4-Hyp-Gly)3-3-Hyp-4-Hyp-Gly-(Pro-4-Hyp-Gly)3 (peptide 1) and (Pro-4-Hyp-Gly)3-3-Hyp-4-Hyp-Gly-(Pro-4-Hyp-Gly)3 (peptide 2). The 3-Hyp residues in these two peptides diminish triple-helical stability in comparison to Pro. This destabilization is small when 3-Hyp is in the natural Xaa position (peptide 1). There, the inductive effect of its 3-hydroxyl group diminishes slightly the strength of the interstrand 3-HypC–O···H–NGly hydrogen bond. The destabilization is large when 3-Hyp is in the nonnatural Yaa position (peptide 2). There, its pyrrolidine ring pucker leads to inappropriate mainchain dihedral angles and interstrand steric clashes. Thus, the natural regioisomeric residues 3-Hyp and 4-Hyp have distinct effects on the conformational stability of the collagen triple helix.

Introduction

Collagen is the most abundant protein in animals, comprising approximately one-third of the total protein by weight.1,2 Collagen has a unique tertiary structure, which consists of three parallel left-handed polyproline-II-type strands wound tightly around a common axis.3–6 Maintenance of this triple helix is essential for many biological functions.7 Each strand of collagen consists of the repeating sequence Xaa-Yaa-Gly, where Xaa and Yaa are often proline (Pro) residues. The post-translational hydroxylation of some of these proline residues generates 4(R)-hydroxy-L-proline (4-Hyp) residues and, to a lesser extent, 3(S)-hydroxy-L-proline (3-Hyp) residues. 3-Hyp, which is found in the natural triplet (3-Hyp-4-Hyp-Gly),8 arises from the action of the enzyme prolyl-3-hydroxylase9 rather than by regiochemical ambiguity by the enzyme prolyl-4-hydroxylase.10

In seminal work, Prockop and co-workers demonstrated that 4-Hyp residues enhance greatly the conformational stability of the collagen triple helix.11 This additional stability arises from stereoelectronic effects that preorganize a 4-Hyp residue in a conformation that befits a triple helix.12–15 In contrast to 4-Hyp, no information is available on the effect of 3-Hyp residues on collagen stability.

Here, we synthesize collagen-like peptides that contain a 3-Hyp residue. We use these peptides to assess the contribution of 3-Hyp to the conformational stability of the collagen triple helix. We find that the presence of a 3-Hyp residue, in surprising contrast to a 4-Hyp residue, destabilizes a collagen triple helix. Like the stability endowed by 4-Hyp residues, the instability imposed by 3-Hyp residues appears to arise largely from inductive effects of its pendant hydroxyl group.

Experimental Section

General. Reagents were obtained from Aldrich Chemical (Milwaukee, WI) or Fisher Scientific (Hanover Park, IL) and used without further purification. Amino acids and their derivatives were obtained from Fisher Scientific, Bachem Bioscience (King of Prussia, PA) or Novabiochem (San Diego, CA). Dichloromethane was distilled over
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**ARTICLES**

**Scheme 2**

α-(trifluoromethyl)phenylelacetyl chloride (0.010 mL, 0.053 mmol), was added, and the resulting mixture was stirred at room temperature for 15 min. ErOAc (1 mL) was then added to the reaction mixture, followed by concentrated HCl (2 drops) and H2O (1 mL). The layers were mixed thoroughly and then separated. The aqueous layer was extracted twice more with ErOAc, and the combined organic extracts were dried over MgSO4(s), filtered, and concentrated to a colorless oil. The 19F NMR spectrum of the oil contained only a single peak at 72 ppm, indicating that compound 6 had maintained its stereochemical integrity.

**N-(13C2-Acetyl-3(S)-tert-butoxy-L-proline methyl ester (8).** Compound 7 (355 mg, 1.24 mmol) was dissolved in MeOH. Trifluoroacetic acid (0.10 mL) was added, followed by a dropwise addition of SOCl2 (1.00 mL, 13.7 mmol). The reaction mixture was heated at reflux for 1 h and then cooled to room temperature and concentrated under reduced pressure. The resulting oil was purified by chromatography on silica gel, eluting with CH2Cl2:MeOH (98:2 v/v) to yield compound 8 as a colorless oil (171 mg, 81%). 1H NMR (300 MHz, CDCl3, two rotamers) δ (ppm) major isomer 4.51 (s, 1H), 4.47 (d, J = 4 Hz, 1H), 4.07 (s, 1H), 3.65 (m, 2H), 2.20–1.80 (m, 2H), 1.96 (d, JCH = 13 Hz, 3H), 1.48 (s, 9H), 1.24 (s, 9H). 13C NMR (75 MHz, CDCl3, 8 scans) δ (ppm) 22.10, 22.25 (13C-labeled carbon).

**pk, Determinations.** The pK values of the carboxylic acid groups of 3-HypOH and 4-HypOH were determined by 1H NMR spectroscopy performed in aqueous solutions of different pH. D2O stock solutions consisted of 210 mM 3-HypOH (27.6 mg in 1.0 mL), 209 mM 4-HypOH (27.4 mg in 1.0 mL), 104 mM sodium 2,2-dimethyl-2-silapentane-5-sulfonate (DSS, 40.8 mg in 1.0 mL), 100 mM DPO4 (68.5 mL at 85% w/v D3PO4 in 10.0 mL), 100 mM DCl (156 μL of 20% DCI in 10.0 mL), and 100 mM NaOD (67.6 μL of fresh 40% w/v NaOD in 10.0 mL). Each sample contained 49 μL of the 3-Hyp or 4-Hyp stock solution, 1 μL of the DSS stock solution, and 950 μL of buffer, according to Tables S1 and S2 in the Supporting Information. The pH of each solution was measured by using a standard pH electrode calibrated in nondeuterated buffers. 1H NMR spectra were obtained from a Bruker AC 300 and Varian UNITY-500 spectrometers. Mass spectra were obtained with a Micromass LCT ESI or Perkin–Elmer Voyager MALDI-TOF instrument.
(32 scans, 24 °C), and the chemical shift of the α-proton was determined for each sample. The resulting pH and chemical shift data were fitted to eq 1 to yield the pKₐ values.

\[
\delta = \frac{\delta_{\text{low}} + \delta_{\text{high}} 10^{\text{pH} - pK_a}}{1 + 10^{\text{pH} - pK_a}}
\]  

(1)

The acidity of an aqueous solution of a molecule having a titratable group with a fraction factor near unity can be measured in D₂O by using a standard pH meter equilibrated against H₂O buffers and adding a correction factor of 0.4 units to the reading. The difference in pKₐ’s of amino acids in H₂O and D₂O is approximately 0.5 units. Thus, a correction of about 0.1 units can be applied to a pKₐ measurement obtained by measuring apparent pH values with a standard glass electrode. To determine a more precise correction factor, we measured the pKₐ’s of 3-HypOH and 4-HypOH in D₂O in the same manner and found that the 4-HypOH value was within 0.02 units of the value reported previously. Thus, we did not apply any correction factor herein to the 3-Hyp pKₐ value.

Crytalization of N⁴(C⁵-Acetyl)-3(S)-hydroxy-L-proline Methyl Ester (8). Equal portions of a solution of amide 8 (67 mg) in 3.0 mL of dichloromethane were placed in six half-dram vials. Approximately 15 drops (Pasteur pipet) of a different cosolvent (hexanes, ethyl acetate, diethyl ether, tetrahydrofuran, tert-butyl methyl ether) or no cosolvent was added to each vial. The vials were then capped loosely and allowed to sit at room temperature undisturbed for several days. The vial with ethyl acetate as a cosolvent contained the crystals most suitable for X-ray diffraction analysis.

X-ray Diffraction Analysis. A colorless crystal with approximate dimensions 0.50 × 0.50 × 0.41 mm³ was selected under oil under ambient conditions and attached to the tip of a glass capillary. The crystal was mounted in a stream of N₂(g) at (173 ± 2) K and centered in the X-ray beam by using a video camera. Crystal evaluation and data collection were performed on a Bruker CCD-1000 diffractometer with Mo Kα (λ = 0.71073 Å) radiation and a diffractometer-to-crystal distance of 4.9 cm.

Initial cell constants were obtained from three series of ω scans at different starting angles. Each series consisted of 20 frames collected at intervals of 0.3° in a 6° range about ω with an exposure time of 10 s per frame. A total of 102 reflections were obtained. The reflections were indexed successfully by an automated indexing routine built into the SMART program. The final cell constants were calculated from a set of 1508 strong reflections from the actual data collection.

Data were collected by using the hemisphere data collection routine. The reciprocal space was surveyed to the extent of a full sphere to a resolution of 0.80 Å. A total of 2911 data sets were harvested by collecting one set of frames with 0.3° scans in ω with an exposure time of 10 s per frame. This redundant data set was corrected for Lorentz and polarization effects. The absorption correction was based on fitting a function to the empirical transmission surface as sampled by multiple equivalent measurements. All software and sources of the scattering factors were contained in the SHELXTL (version 5.1) program library (G. Sheldrick, Bruker Analytical X-ray Systems, Madison, WI).

Synthesis of Peptides 1 and 2. Peptide synthesis was performed on an Applied Biosystems Synergy synthesizer using standard Fmoc/tBu methodology and HBTU as the coupling reagent. 3-Hyp residues were incorporated by using compound 6.

Peptide 1, which was (Pro-4-Hyp-Gly)₃-3-Hyp-4-Hyp-Gly-(Pro-4-Hyp-Gly)₃, was purified by reverse-phase HPLC on a C-18 column, eluting with a linear gradient (5–60% v/v) of solvent B, where solvent A was H₂O containing TFA (0.1% v/v) and solvent B was CH₃CN containing TFA (0.1% v/v). MALDI MS (mlc) [M + H]⁺ calculated, 1905; found, 1906. Peptide 2, which was (Pro-4-Hyp-Gly)-(Pro-3-Hyp-Gly)-(Pro-4-Hyp-Gly), was purified likewise. MALDI MS (mlc): [M + H]⁺ calculated, 1889; found, 1890.

Thermal Denaturation Experiments. Values for Tm for each triple helix were determined in triplicate by thermal denaturation experiments monitored by CD spectroscopy on an Aviv 202 SF instrument equipped with an automated temperature controller. A 0.2 mM solution of peptide 1 or 2 in 50 mM HOAc was incubated at 4 °C for >24 h. Aliquots of 300 μL were placed in 0.1-cm path length quartz cuvettes that had been equilibrated at 5 °C. Wavelength scans were performed from 200 to 260 nm at 50 and 50 °C, with a slit width of 1 nm and an averaging time of 3 s. Thermal denaturation experiments were performed by raising the temperature from 5 to 50 °C in 3 °C steps, equilibrating for 5 min at each temperature, and monitoring at 225 nm with a 20-s averaging time. Values of Tm, which is the temperature at the midpoint of the thermal transition, were determined by fitting the data to a two-state model using the software package NLREG v. 4.0 (Philip Sherwood).

Molecular Modeling. Molecular models of triple-helical 1 and 2 were created by modifying the structure of crystalline collagen (PDB entry 1CAG)™. The atomic coordinates were imported into the program SYBYL (Tripos, St. Louis, MO). The side-chain methyl group of the three alanine residues were replaced with a hydrogen atom, and a section of the (Pro-Hyp-Gly) triple helix was excised from the C-terminus. This section was subjected to energy minimization with the Tripos force field. A hydroxyl group was added to C⁵ of the proline residue in the Xaa position of the central triplet in each strand (to mimic peptide 1) or moved from C⁵ to C³ in the Yaa position of the central triplet in each strand (to mimic peptide 2). The dihedral angles of the 3-Hyp residues were then altered to match those of the structure of crystalline amide 8. The resulting structures were not subjected to further minimization.

Results and Discussion

Synthetic collagen mimics have been effective in dissecting the basis for the conformational stability of the collagen triple helix. In particular, host–guest studies have revealed important insights on the contribution of individual amino acid residues, both natural and nonnatural. To reveal the effect of 3-Hyp residues on triple-helical stability, we synthesized two host–guest peptides in which the central triplet of (Pro-4-Hyp-Gly)₃ was replaced with one containing 3-Hyp. These peptides were (Pro-4-Hyp-Gly)₃-3-Hyp-4-Hyp-Gly-(Pro-4-Hyp-Gly)₃ (1) and (Pro-4-Hyp-Gly)₃-3-Hyp-4-Hyp-Gly-(Pro-4-Hyp-Gly)₃ (2). Peptide 1 was designed to elucidate the role of the 3-Hyp-4-Hyp-Gly triplet as is found most often in natural collagen. Peptide 2 was designed to reveal the effect of the regiochemistry (3-Hyp versus 4-Hyp) of the pendant hydroxyl group. These peptides were synthesized by standard Fmoc/tBu coupling strategies using compound 6 (Scheme 1) to introduce 3-Hyp residues.

Conformational Stability. The unfolding of triple helices of peptides 1 and 2 was monitored by CD spectroscopy. The
resulting $T_m$ values, along with those of triple helices of (Pro-4-Hyp-Gly)$_3$ (3) and (Pro-4-Hyp-Gly)$_3$-Pro-Pro-Gly-(Pro-4-Hyp-Gly)$_3$ (4), are listed in Table 1. The values confirm that, in its natural (i.e., Xaa) position, 4-Hyp provides more conformational stability to a triple helix than does Pro. In contrast, 3-Hyp provides less conformational stability than does Pro in either its natural (i.e., Xaa) or a nonnatural (i.e., Yaa) position. The additional stability endowed by 4-Hyp is known to arise from stereoelectronic effects.14,15 What is the origin of the detrimental effect of 3-Hyp on collagen stability?

Peptide Bond Isomerization. All of the peptide bonds in triple-helical collagen are in the trans (i.e., Z) conformation. The 4-hydroxyl group of a 4-Hyp residue increases the trans/cis ratio of an Xaa-4-Hyp peptide bond by approximately 50% compared to that of a Xaa-Pro bond.28 We used NMR spectroscopy to determine the effect of the 3-hydroxyl group of a 3-Hyp residue on its trans/cis ratio. We found that the trans/cis ratios of amide 8 and Ac-Pro-OMe in D$_2$O were 4.9 and 4.6, respectively. These similar values indicate that peptide bond isomerization makes a negligible contribution to the instability of triple-helical 1 and 2.

Structure of a 3-Hyp Residue. We used X-ray diffraction analysis to determine the structure of crystalline amide 8 (Figure 1A).29,30 The pyrrolidine ring of crystalline amide 8 is puckered such that its $N-C^\alpha-C^\beta-O^\gamma$ bond has a dihedral angle of $-81.46 \pm 0.16^\circ$, as would be expected from the manifestation of a gauche effect.14,15 The ring puckers in crystalline Ac-3-Hyp-OMe (8) differs significantly from the ring puckers in crystalline Ac-4-Hyp-OMe (Figure 1B). The conformation of the pyrrolidine ring in amide 8 is intermediate between a $1^E$ envelope and $1^E_2$ twisted conformation.31 In the envelope conformation, the flap atom is $C^\beta$. In the twisted conformation, atoms $N_1, C^\alpha, C^\beta,$ and $C^\gamma$ form the base plane. Atom $C^\beta$ resides 0.456 ± 0.004 Å above that plane, and atom $C^\gamma$ resides 0.153 ± 0.005 Å below that plane. The phase angle $\phi_2 = 9.6 \pm 0.3^\circ$, and the puckering amplitude is $\rho_2 = 0.378 \pm 0.002$ Å.

The structure of crystalline Ac-4-Hyp-OMe contains two symmetry-independent molecules.33 (Thus, there are two numbers herein for each parameter.) In both molecules, the pyrrolidine ring is in the $\gamma_T$ (that is, $\gamma_T(C^\beta_1)$) twisted conformation with a characteristic phase angle of $\phi_2 = 129.8 \pm 0.7^\circ$ (127.8 ± 0.7$^\circ$) and puckering amplitude of $\rho_2 = 0.354 \pm 0.004$ Å (0.389 ± 0.006 Å).32 The base plane is determined by atoms $N_1, C^\beta_1,$ and $C^\gamma_1$. Atom $C^\beta_1$ resides 0.28 ± 0.01 Å (0.22 ± 0.01 Å) above that plane, and atom $C^\gamma_1$ resides 0.35 ± 0.01 Å (0.36 ± 0.01 Å) below the plane. The ring puckers of 3-Hyp and 4-Hyp (Figure 1B) serve to preorganize the $\phi$ ($C^\gamma_1-C^\beta_1-N_1-C^\alpha$) and $\psi$ ($N_1-C^\beta_1-C^\gamma_1-N_1+1$) dihedral angles in a conformation that is appropriate for the Yaa position of a collagen triple helix.34–36 Likewise, a 3-Hyp

<table>
<thead>
<tr>
<th>peptide</th>
<th>Xaa-Yaa-Gly</th>
<th>$T_m(\degree C)^\alpha$</th>
</tr>
</thead>
<tbody>
<tr>
<td>3</td>
<td>Pro-4-Hyp-Gly</td>
<td>36 ± 2$^b$</td>
</tr>
<tr>
<td>1</td>
<td>3-Hyp-4-Hyp-Gly</td>
<td>32.7 ± 0.9</td>
</tr>
<tr>
<td>4</td>
<td>Pro-Pro-Gly</td>
<td>30.5 ± 2.2$^b$</td>
</tr>
<tr>
<td>2</td>
<td>Pro-3-Hyp-Gly</td>
<td>21.0 ± 2.2</td>
</tr>
</tbody>
</table>

$^a$ Values of $T_m$ were determined by CD spectroscopy for peptides (0.2 mM) in 50 mM acetic acid and are the average ($\pm$SE) of at least three determinations. $^b$ From ref 27.
residue would be stabilizing in the Xaa position relative to Pro because its main-chain dihedral angles are favorable for that position, whereas a 3-Hyp residue would be destabilizing in the Yaa position because its dihedral angles differ significantly from the optimal (Table 2). Although 3-Hyp is destabilizing in both positions (Table 1), the preorganization that arises from the gauche effect does favor a triple helix with 3-Hyp in the Xaa rather than the Yaa position. Unlike 3-Hyp and 4-Hyp residues, a Pro residue is not constrained by a gauche effect to adopt a particular pucker and can, therefore, accommodate the different \( \phi \) and \( \psi \) angles of the Xaa and Yaa positions in a triple helix (Table 2).

To discern whether hydroxyproline residues have similar conformations in small molecule and collagen-related peptides, contexts, we compared the dihedral angles of Ac-4-Hyp-OMe with those of a 4-Hyp residue in crystalline collagen (PDB entry 1CAG20) by pseudorotational analysis.37 We found that the two rings were essentially superimposable (data not shown), indicating that Hyp ring puckers are not dependent on context and providing validity to our assumption that 3-Hyp would have the same pucker in a peptide context as in amide 8.

Steric Effect on Collagen Stability. Could steric effects contribute to the instability imparted by 3-Hyp? In a collagen triple helix, residues in the Xaa position are more solvent-exposed than are those in the Yaa position23 and are, therefore, less likely to introduce unfavorable steric interactions. Indeed, residues with bulky side chains are found only rarely in the Yaa position of natural collagen.23 A steric clash between 3-Hyp in the Yaa position with residues in neighboring strands (Figure 2, bottom) is likely to diminish the stability of triple-helical 2. This steric clash is absent in triple-helical 1 (Figure 2, top).

Effect of Hydrogen Bonds on Collagen Stability. In a collagen triple helix, the C=O of the residue in the Xaa position accepts a hydrogen bond from the glycine N—H of another strand (Figure 3). The carboxyl \( pK_a \) of XaaOH is a measure of the ability of the Xaa residue to accept such a hydrogen bond.39 The \( pK_a \) values of the carboxyl groups of 3-HypOH and 4-HypOH were determined by monitoring the effect of pH on the \(^1\)H NMR chemical shift of their \( \alpha \)-protons. The carboxyl \( pK_a \) of 4-HypOH was found to be 1.80, which is close to the value of 1.82 reported previously,18 and that of ProOH is 1.95.18 In contrast, the \( pK_a \) of 3-HypOH is 1.62, making the 3-Hyp residue a weaker hydrogen bond acceptor than Pro. This attribute is likely to contribute to the instability conferred by a 3-Hyp residue in the Xaa position.

Biological Implications. 3-Hyp only decreases the \( T_m \) value of triple-helical 2 by \( 3 \) °C compared to \( \geq 5 \) °C for other residues in the Xaa position of (Pro-Hyp-Gly)-based host–guest triple helices.38 Thus, the insertion of 3-Hyp could serve to modulate the local stability of triple helices. This idea is supported by the 10-fold increase in 3-Hyp residues in basement-membrane collagens as compared to fibrillar collagens.8,40 Collagen triple helices in basement membranes interact with each other, as well as with other biomolecules, in a more varied and complex manner than do those in fibrils. This network of interactions could require regions of finely tuned conformational stability, and 3-Hyp residues could provide that tuning.

### Table 2. Main-Chain Angles of Proline and Hydroxyproline Residues in Crystalline Amides and Triple Helices

<table>
<thead>
<tr>
<th>angle</th>
<th>Ac-4-Hyp-OMe</th>
<th>[^{13}\text{CH}_3\text{Ac}-3\text{Hyp-OMe}]</th>
<th>triple helix</th>
</tr>
</thead>
<tbody>
<tr>
<td>( \phi )</td>
<td>–50.9</td>
<td>–79.5</td>
<td>–75</td>
</tr>
<tr>
<td>( \psi )</td>
<td>145.2</td>
<td>163.7</td>
<td>164</td>
</tr>
</tbody>
</table>

From ref 33. a From ref 35. b From ref 41.
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Supporting Information Available: Data for pH titration of 3-HypOH and 4-HypOH, thermal denaturation of triple-helical peptides 1 and 2, and X-ray diffraction analysis of amide 8. This material is available free of charge via the Internet at http://pubs.acs.org.