

Designed Molecular Switches: Controlling the Conformation of Benzamido-diphenylacetylenes

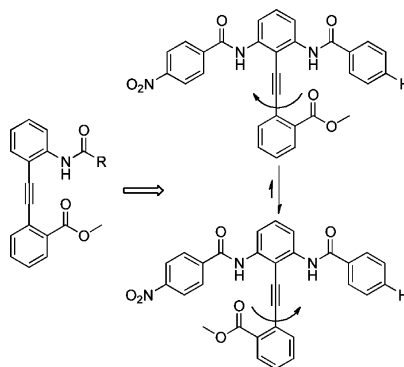
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Received June 16, 2010

ABSTRACT



With the goal of creating a molecular switch, the hydrogen-bonded diphenylacetylene structure has been modified such that an equilibrium now exists between two intramolecular H-bonded states. Through X-ray crystallography and ^1H NMR analysis it is shown that this equilibrium can be biased in a predictable manner by modulating the relative acidity of the amide NH's.

Molecules that can change conformation in a stimulus-dependent fashion are valued synthetic targets due to their potential use as logic gates,^{1–3} information storage systems,^{4,5} sensors,⁶ and as stepping stones toward the design of angstrom scale machines.⁷ In light of the myriad applications

for switches, many structural motifs have been pursued in the past 15 years that exhibit a conformational change based upon a variety of stimuli.^{7–17}

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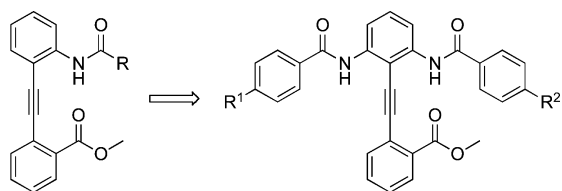


Figure 1. Conceptual transformation of the classical hydrogen bonded diphenylacetylene into a molecular switch.

Our interest in the design of β -strand mimetics stabilized by an intramolecular hydrogen bond across an alkyne spacer¹⁸ prompted us to investigate the use of this system as a new switching entity. The key feature of this scaffold is the 10-membered H-bonded ring first described by Kemp^{19,20} (Figure 1), which increases the rotational barrier around the phenyl-alkyne bond from 0.6 to 7.19 kcal/mol.^{21,22} The utility of this intramolecular interaction has been established in the stabilization of helical foldamers,^{22–24} molecular wires,²⁵ a proteomimetic,¹⁸ and an ion sensor.²⁶

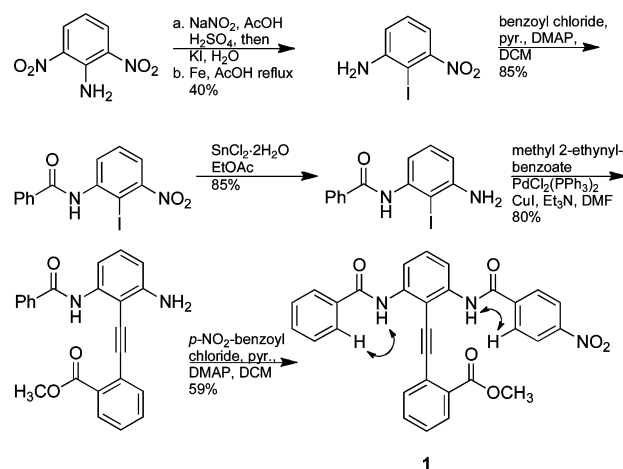
Transforming the H-bonded diphenylacetylene unit into a switch requires that we (i) set up a conformational equilibrium between two forms, (ii) demonstrate that the equilibrium can be biased in a predictable fashion, and (iii) show that this bias can be altered through the application of a stimulus. Herein we report our synthetic and analytical stratagem for accomplishing parts i and ii.

Addition of a second amide, *ortho* to the alkyne spacer (Figure 1), opens up the required equilibrium providing two donors for intramolecular H-bonding. We can potentially bias the benzoate H-bond acceptor to prefer one amide over the other by conjugating electron-withdrawing and -donating groups to the amide carbonyls. If the carbonyl is electron-rich, the NH bond should be less acidic thus making the amide a weaker H-bond donor. Conversely, an electron-poor carbonyl will increase the acidity of the NH making it a stronger H-bond donor.

para-Substituted benzoic acids are ideal electron-modulating groups because of the range of available derivatives with well characterized σ -Hammett values.²⁷ These values can be used to quantify the effect of substitution on acidity and, in 4-substituted benzamides, the strength of H-bond dona-

tion.^{28,29} Accordingly, we should be able to use the $\Delta\sigma$ between the two benzamides in our system to predict which NH is the preferred H-bond donor.

Scheme 1. Synthesis of **1**



To test this idea, compound **1**, which balances *p*NO₂-benzamide with benzamide, was assembled from 2,6-dinitroaniline according to Scheme 1. The *p*NO₂-amide has less electron density than benzamide, as described by $\Delta\sigma = 0.78$, and so the *p*NO₂-amide should be the preferred H-bond donor.

Single crystal X-ray diffraction of **1** (Figure 2) shows that the preferred H-bond donor is indeed the *p*NO₂-benzamide with a NH...OC distance of 2.23 Å. There is also a steric clash between the methyl ester and the *p*NO₂-phenyl that creates a 50° dihedral angle between the ring and the amide carbonyl.

With this result in hand, we expanded our analysis to the solution phase using ¹H NMR. The spectrum of **1** shows the *p*NO₂-NH at 9.43 and the benzamide NH at 9.07 ppm (4 mM, CDCl₃). These resonances are assigned by the NOE between these peaks and the aryl protons *ortho* to each carbonyl (Scheme 1).

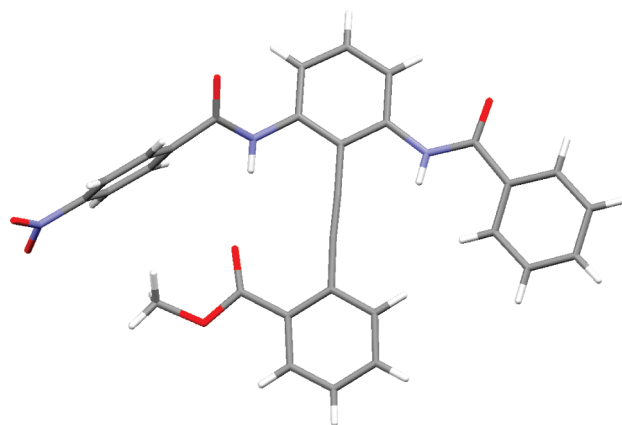


Figure 2. Single crystal X-ray structure of **1**.

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Kemp-type diphenylacetylenes show proton spectra with non-H-bonded amide resonances around 8 ppm and H-bonded amide resonances from ~9 to 9.2 (CDCl₃).^{22,24} That both amides in our compound resonate around this latter range suggests that each could be involved in a hydrogen bond. Intermolecular H-bonding, a concentration-dependent phenomenon, is ruled out by the fact that the NH shifts of **1** stay constant as the solution is diluted from 16 to 0.063 mM (CDCl₃). Thus, the downfield shift of both NH's must be due to an equilibrium between the conformations of the benzoate acceptor.

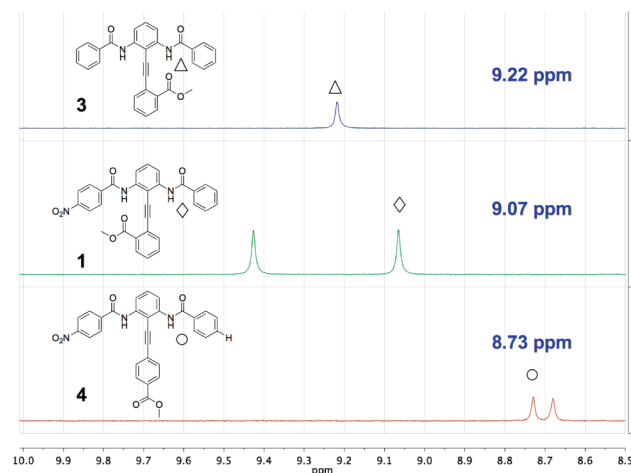


Figure 3. ¹H NMR amide resonances of compounds **3**, **1**, and **4** from top to bottom (4 mM in CDCl₃). The benzamide resonances are denoted by Δ, ◇, and ○ for **3**, **1**, and **4**, respectively, and the chemical shifts are also reported.

To determine the position of that equilibrium, two reference compounds were designed. The first reference positions an unsubstituted benzamide on both sides (**3**, Figure 3) and has a $\Delta\sigma = 0$. As such, the methyl ester must partition equally between the amides, providing a definition of the benzamide NH chemical shift in a system where no conformational preference exists (50/50 definition). The second reference compound (**4**, Figure 3) juxtaposes *p*NO₂-benzamide with benzamide; however, in this molecule the ester is *para* to the acetylene linker. Because the ester cannot influence the amide chemical shifts (again intermolecular association is ruled out by the same dilution assay), these values represent the resonances of **1** if they are not H-bonded (100/0 definition).

We expect that if the *p*NO₂-NH is preferred in solution, then the other NH will be more shielded, as the result of a decrease in H-bonding, and will resonate between our two definitions. Figure 3 shows that the benzamide resonance for **1** does appear between that of **3** and **4**, demonstrating

that the conformational equilibrium is biased toward the *p*NO₂-benzamide.

This analysis also determines the magnitude of the conformational bias from the degree to which the benzamide NH has shifted upfield. Dividing the difference in chemical shift between **3** and **1** by the difference in chemical shift between **3** and **4**, we find that this initial system has a preference of 30.6% for the NO₂-NH.

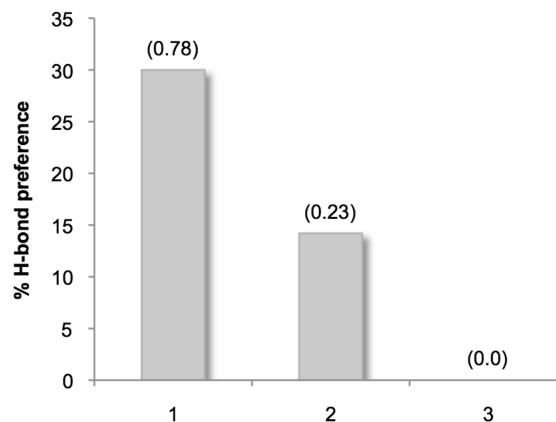


Figure 4. Comparison of the % H-bond preference for compounds **1–3**. The $\Delta\sigma$ values appear at the top of each bar.

Having shown that the solid-state and solution-phase conformations can be biased in a predictable manner, we next investigated the sensitivity of conformational preference toward a varying $\Delta\sigma$. Toward this end, compound **2** (Figure 1, R¹ = H, R² = Cl) was prepared and analyzed in the same fashion as **1**. Comparison of **2** with its appropriate control molecules (Figure S2 in Supporting Information) shows that decreasing $\Delta\sigma$ from 0.78 to 0.23 attenuates the H-bond preference from 30.6% to 14.2% (Figure 4).

In summary, we have shown (i) evidence of a conformational equilibrium in these bis(benzamido)-diphenylacetylene molecules and (ii) that electronic modulation can be used to attenuate or enhance benzamide H-bond donation strength, resulting in a measurable conformational bias. Indeed, the sensitivity of the conformational equilibrium toward a varying $\Delta\sigma$ suggests the utility of this scaffold for dynamic switching, and we are currently working to develop this facet.

Acknowledgment. The authors would like to thank Dr. Christopher D. Incavito at Yale University for X-ray crystallographic analysis, Drs. Marc Adler and Andrew Jamieson at Oxford University for helpful insights, and the NSF (CHE-0750357) and Oxford University for funding.

Supporting Information Available: General experimental methods, procedures, NMR spectra, and X-ray crystallographic data in CIF format. This material is available free of charge via the Internet at <http://pubs.acs.org>.

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