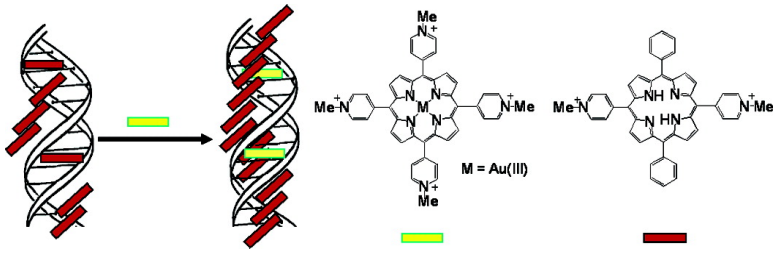
Communication

Tuning Porphyrin/DNA Supramolecular Assemblies by Competitive Binding

Luigi Mons Scolaro, Andrea Romeo, and Robert F. Pasternack

J. Am. Chem. Soc., **2004**, 126 (23), 7178-7179• DOI: 10.1021/ja049669m • Publication Date (Web): 22 May 2004



More About This Article

Additional resources and features associated with this article are available within the HTML version:

- Supporting Information
- Links to the 2 articles that cite this article, as of the time of this article download
- Access to high resolution figures
- Links to articles and content related to this article
- Copyright permission to reproduce figures and/or text from this article

View the Full Text HTML

J|A|C|S
COMMUNICATIONS

Published on Web 05/22/2004

Tuning Porphyrin/DNA Supramolecular Assemblies by Competitive Binding

Luigi Monsù Scolaro,[†,‡] Andrea Romeo,[†,‡] and Robert F. Pasternack*,[§]

Dipartimento di Chimica Inorganica, Chimica Analitica e Chimica Fisica, Università di Messina, Salita Sperone 31, 98166 Vill.S.Agata, Messina, Italy, INFM, Unità di Messina, Messina, Italy, and Department of Chemistry, Swarthmore College, Swarthmore, Pennsylvania 19081

Received January 19, 2004; E-mail: rpaster1@swarthmore.edu

The identification of both photosynthetic light harvesting antenna complexes and reaction centers has inspired considerable effort to mimicking such organized assemblies of chromophores. In addition to the insights such systems provide to fundamental issues concerning photosynthesis, the interest in such organized arrays reflects their potential for applications in molecular electronics,[1,2] nonlinear optics,[3] and solar energy storage and conversion.[4] Porphyrins are attractive compounds for these studies because they are relatively easy to synthesize and their photophysical properties can be tuned through careful choice of peripheral substituents and inserted metal ions. Conventional synthetic approaches have been developed to obtain well-defined assemblies with sizes spanning from nano- to mesoscopic scale.[5] Less conventional approaches to obtaining such organized arrays are based on noncovalent interactions between a templating scaffold and properly selected chromophores.[6−11] In these cases, the thermodynamics and kinetics of the supramolecular assembling process are governed by absolute and relative concentrations of the building blocks and by several medium parameters (e.g., pH, ionic strength, temperature).[12−15]

Here we describe a convenient method to control the size and extent of supramolecular porphyrin assemblies on a nucleic acid matrix by exploiting competitive binding toward the biological scaffold between two chromophores having different aggregating properties. In particular, we selected (i) a nonaggregating porphyrin, tetrakis(*N*-methylpyridinium-4-yl)porphinegold(III) (AuT4), able to bind mainly by intercalation into the double helix of nucleic acids[16] and (ii) *trans*-bis(*N*-methylpyridinium-4-yl)diphenylporphine (*t*-H_2P_{agg}), which binds intercalatively to DNA at low ionic strength, but forms extended ordered chiral assemblies on the nucleic acid backbone with increasing ionic strength.[10]

At low ionic strength conditions ($I < 5$ mM), both porphyrins, AuT4 and *t*-H_2P_{agg}, interact similarly with DNA, exhibiting a series of spectroscopic features—in particular, small negative-induced circular dichroism (ICD) signals in the relative Soret regions (408 and 420 nm, respectively)—that unambiguously point to an intercalative monodispersed binding mode.[17] At higher ionic strength, *t*-H_2P_{agg} behaves very differently. Addition of sodium chloride to a preformed intercalated adduct of this porphyrin triggers a process that leads to large bisignated ICD features and very intense resonance light scattering in the Soret region. These spectroscopic features have been reported as specific markers for the formation of large aggregates of porphyrins having long-range chiral order, in which the chromophores are strongly coupled electronically and behave as an antenna system.[18] Figure 1 displays the dependence of the negative signal on the concentration of *t*-H_2P_{agg} porphyrin at fixed DNA concentration and ionic strength ($I = 0.05$ M). The value of the ionic strength has been selected to ensure that the porphyrin assemblies grow on the surface of the polyelectrolytes with little dissociation into the solvent.

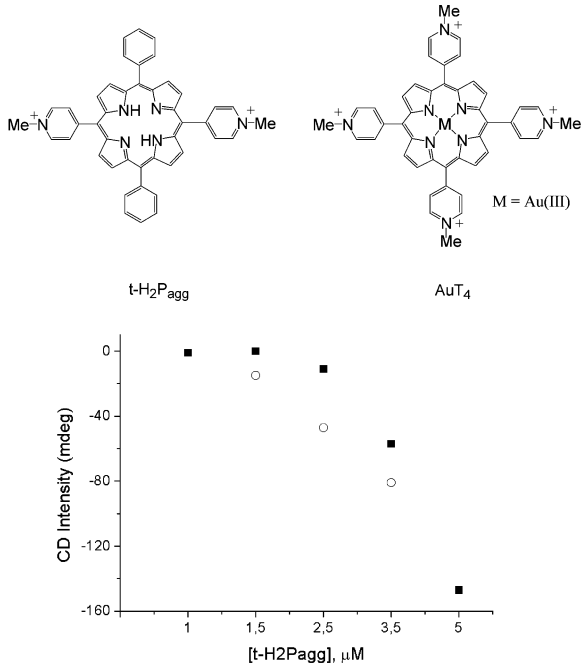


Figure 1. Induced circular dichroism intensity for *t*-H_2Pagg/DNA supramolecular assemblies as function of porphyrin concentration. (■) *t*-H_2Pagg at [DNA] = 25 μM, [NaCl] = 0.05 M in 1 mM phosphate buffer pH 6.7, $T = 298$ K. (○) Mixture with AuT4 at [porphyrin]$_{tot}$ = 5 μM ($\lambda = 450$ nm).

As is evident from Figure 1, after a threshold concentration the ICD intensity follows an almost linear dependence on *t*-H_2P_{agg} concentration. The occurrence of a "critical assembly concentration" (cac) has been proposed in the formation of such porphyrin assemblies,[13,14] and from Figure 1 we can estimate a value of 2.4 μM as the lower limit below which aggregation does not occur. This value is in good agreement with a value of 2.7 μM for the cac calculated for these conditions using a previously published equation.[14] When the nonaggregating AuT4 porphyrin is added to a preformed intercalated adduct of *t*-H_2P_{agg} (low ionic strength conditions), a slight *decrease* in the magnitude of the ICD bands of the latter porphyrin can be detected, concomitant with the appearance of a new negative component around 410 nm due to intercalated AuT4. This observation suggests that the gold(III) derivative, bearing five positive charges, competes effectively with *t*-H_2P_{agg} (which is a dicationic species) for binding sites in the double helix, partially displacing the latter species.

Upon addition of NaCl, aggregation is fostered and large bisignated ICD signals are detected in the Soret region. The ICD spectra are extremely similar to those observed in the absence of

[†] Università di Messina.
[‡] INFM, Unità di Messina.
[§] Swarthmore College.

10.1021/ja049669m CCC: $27.50

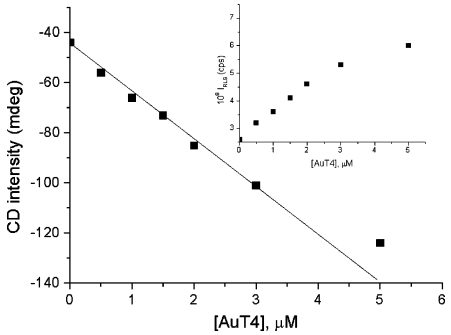


Figure 2. Induced circular dichroism intensity for *t*-H_2Pagg/AuT4/DNA supramolecular assemblies as function of porphyrin AuT4 concentration. The inset shows the RLS intensity for the same samples. [*t*-H_2Pagg] = 3.5 μM, [DNA] = 25 μM, [NaCl] = 0.05 M in 1 mM phosphate buffer pH 6.7 (λ = 450 nm).

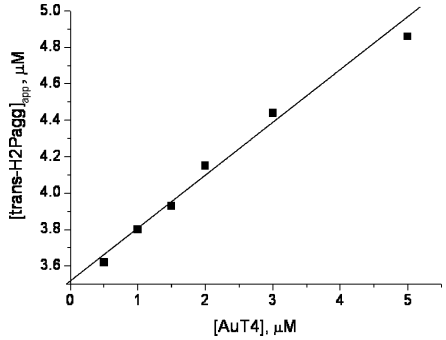


Figure 3. Apparent *t*-H_2Pagg concentration as a function of AuT4 porphyrin concentration (the solid line is the linear fit of the data; see text for details). [*t*-H_2Pagg] = 3.5 μM, [DNA] = 25 μM, [NaCl] = 0.05 M in 1 mM phosphate buffer pH 6.7 (λ = 450 nm).

AuT4, but their intensities are somewhat larger with respect to the same experiments performed on the *t*-H_2P_{agg}/DNA binary system (open circles in Figure 1).

Interestingly, the same experimental procedure involving *t*-AuP_{agg}, the gold(III) metal derivative of *t*-H_2P_{agg} as the nonaggregating component,[10] leads to qualitatively similar results, but with somewhat reduced signals, suggesting a further potential control of the aggregation process by the *charge* of the competing species. Because both *t*-AuP_{agg} and AuT4 coordinate the same metal ion, we are inclined to think that the overall charge plays a substantial role. At a fixed concentration of *t*-H_2P_{agg}, the intensity of the ICD signal and the corresponding RLS intensity depend linearly on the concentration of the added AuT4. Figure 2 shows that this linear behavior is maintained up to a maximum concentration of $\sim$5 μM. Above this limiting concentration value, the ternary system is unstable, even at low ionic strength, and precipitation of red fibers occurs.

As has been reported in previous studies on the *t*-H_2P_{agg}/DNA binary system,[10] the size of the ICD and RLS signals at equilibrium for the ternary system depends also on the concentration of DNA. At fixed porphyrin ratio ([AuT4]/[*t*-H_2P_{agg}] = 0.43), on increasing the DNA concentration, both ICD and RLS intensities decrease, leveling to virtually zero when the ratio $[\text{porphyrin}]_{tot}/[\text{DNA}] < 0.08$. This effect reflects the increase in potential binding sites along the polyelectrolyte, which in turn, leads to a de facto dilution of the porphyrins and a decreased tendency for them to cluster and aggregate.

The ellipticity data in Figures 1 and 2 allow for an evaluation of the *apparent* concentration of *t*-H_2P_{agg} porphyrin, $[t\text{-}H_2P_{agg}]_{app}$; that is, the concentration in the binary system that gives the same ICD intensity as that measured in the ternary system. Figure 3 shows the dependence of this quantity on the concentration of AuT4 for fixed $[t\text{-}H_2P_{agg}]_{tot}$ and [DNA]. A linear regression analysis of the data gives: $[t\text{-}H_2P_{agg}]_{app} = (3.53 \pm 0.05) + (0.277 \pm 0.015)$ [AuT4]. The slope of this straight line reflects the ability of the nonaggregating porphyrin to displace *t*-H_2P_{agg} from an intercalation/groove-bound site, making it available for aggregation. The value is expected to reflect solution conditions and to be related to the different nearest-neighbor exclusion factors of the two competing porphyrins[16] and to their overall charges, electron densities, and steric properties. Qualitatively, this value is a convenient way of comparing different competing species for their efficiency in promoting *t*-H_2P_{agg} aggregation, but a systematic study of this quantity could also provide insight into the various factors involved in porphyrin binding and aggregation.

In conclusion, the proposed competition approach shows great promise as a sensitive way to control the extent of porphyrin aggregation on a nucleic acid scaffold. The extent of aggregation can be readily changed by varying the concentration of an added nonaggregating porphyrin and depends on the charge of the added species and the concentration of available binding sites.

Acknowledgment. We thank the MIUR, PRIN-Cofin. 2002−2003 (MSL, A.R.) for financial support. We also acknowledge support from the National Institutes of Health for Grant No. 1 R15AG019302 (R.F.P.).

Supporting Information Available: RLS and CD intensity dependencies for the porphyrin/DNA supramolecular assemblies as function of porphyrin and DNA (PDF). This material is available free of charge via the Internet at http://pubs.acs.org.

References

(1) Borovkov, V. V.; Anikin, M.; Wasa, K.; Sakata, Y. *Photochem. Photobiol.* **1996**, *63*, 477−482.
(2) Lindsey, J. S. *New J. Chem.* **1991**, *15*, 153−180.
(3) Bjornholm, T.; Geisler, T.; Larsen, J.; Jorgensen, M. *J. Chem. Soc., Chem. Commun.* **1992**, 815−817.
(4) (a) *Photochemical Conversion and Storage of Solar Energy*; Pellizzetti, E., Schiavello, M., Eds.; Kluwer: Dordrecht, The Netherlands, 1991. (b) Bard, A. J. *Integrated Chemical Systems*; Wiley: New York, 1994.
(5) de Witte, P. A. J.; Castriciano, M.; Cornelissen, J.; Scolaro, L. M.; Nolte, R. J. M.; Rowan, A. E. *Chem.−Eur. J.* **2003**, *9*, 1775−1781.
(6) Pasternack, R. F.; Gurrieri, S.; Lauceri, R.; Purrello, R. *Inorg. Chim. Acta* **1996**, *246*, 7−12.
(7) Bellacchio, E.; Lauceri, R.; Gurrieri, S.; Scolaro, L. M.; Romeo, A.; Purrello, R. *J. Am. Chem. Soc.* **1998**, *120*, 12353−12354.
(8) Purrello, R.; Scolaro, L. M.; Bellacchio, E.; Gurrieri, S.; Romeo, A. *Inorg. Chem.* **1998**, *37*, 3647−3648.
(9) Bustamante, C.; Gurrieri, S.; Pasternack, R. F.; Purrello, R.; Rizzarelli, E. *Biopolymers* **1994**, *34*, 1099−1104.
(10) Pasternack, R. F.; Bustamante, C.; Collings, P. J.; Giannetto, A.; Gibbs, E. J. *J. Am. Chem. Soc.* **1993**, *115*, 5393−5399.
(11) Pasternack, R. F.; Giannetto, A.; Pagano, P.; Gibbs, E. J. *J. Am. Chem. Soc.* **1991**, *113*, 7799−7800.
(12) Pasternack, R. F.; Fleming, C.; Herring, S.; Collings, P. J.; dePaula, J.; DeCastro, G.; Gibbs, E. J. *Biophys. J.* **2000**, *79*, 550−560.
(13) Pasternack, R. F.; Gibbs, E. J.; Collings, P. J.; dePaula, J. C.; Turzo, L. C.; Terracina, A. *J. Am. Chem. Soc.* **1998**, *120*, 5873−5878.
(14) Pasternack, R. F.; Goldsmith, J. I.; Szep, S.; Gibbs, E. J. *Biophys. J.* **1998**, *75*, 1024−1031.
(15) Purrello, R.; Raudino, A.; Scolaro, L. M.; Loisi, A.; Bellacchio, E.; Lauceri, R. *J. Phys. Chem. B* **2000**, *104*, 10900−10908.
(16) Gibbs, E. J.; Maurer, M. C.; Zhang, J. H.; Reiff, W. M.; Hill, D. T.; Malicka-Blaszkiewicz, M.; McKinnie, R. E.; Liu, H. Q.; Pasternack, R. F. *J. Inorg. Biochem.* **1988**, *32*, 39−65.
(17) Pasternack, R. F.; Gibbs, E. J. *Met. Ions Biol. Syst.* **1996**, *33*, 367−397.
(18) Pasternack, R. F.; Collings, P. J. *Science* **1995**, *269*, 935−939.

JA049669M