

OLIGONUCLEOTIDE STUDIES. PART II.
OPTICAL ROTATORY DISPERSION OF TWO PAIRS OF SEQUENCE
ISOMERS OF TRINUCLEOTIDES¹⁾

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Optical rotatory dispersion (ORD) is understood as the most powerful physical method in the characterization of the conformational structures of oligo- and polynucleotides of different composition and sequence. For this reason, in recent years, ORD data have been reported for several oligonucleotides²⁻⁷⁾. However, these studies have been restricted to the observation of the oligonucleotides obtained either from bovine pancreatic ribonuclease I (EC 2. 7. 7. 16) digestion of ribonucleic acids (RNA) or from a partial degradation of synthetic polynucleotides. Recently, we have succeeded in the isolation in pure form of seven trinucleotides (ApApGp, ApCpGp, ApUpGp, CpApGp, CpCpGp, UpApGp, and UpUpGp)⁸⁾ out of nine possible trinucleotides⁹⁾ produced on Taka-Diastase ribonuclease T₁ (EC 2. 7. 7. 26) digestion of high molecular weight RNA¹⁾.

The purpose of this communication is to report the results of an ORD¹⁰⁾ study of the two pairs of sequence isomers, ApCpGp and CpApGp, and ApUpGp and UpApGp. The fact that no ORD work has been reported previously in the structural characterization of trinucleotides having the guanylic acid moiety as the terminal residue represents a missing link in study, to date, of oligonucleotides as models of nucleic acids. Although the absorption spectra are, in general, not sensitive to base-sequence, a detailed analysis of these spectra together with hyperchromicity measurements makes it possible to determine nucleotide sequence of di- and trinucleotides¹⁾. However, the ORD criteria for the identification of sequence isomers are more convenient as can be clearly seen in Fig. 1.

Since it is evident from the literature^{4, 7)} that a 3' terminal phosphate does not substan-

tially change the conformation of a trinucleoside diphosphate, the absolute value of maximum difference in molecular rotation between trinucleotides, say, ApCpGp, and its component monomers, A + pC + pG, for wavelengths longer than 230 m μ , viz., $|[M]_t - [M]_m|$, was employed as ORD criterion of stacking (see also ref. 4). The results at pH 7 are included with hyperchromicity data in Table I.

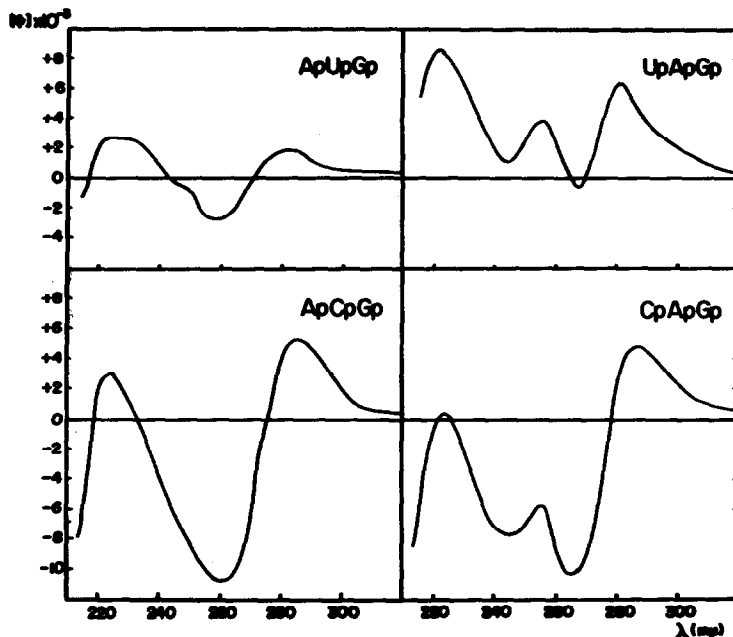


FIG. 1. Ultraviolet rotatory dispersion of ApCpGp, CpApGp, ApUpGp, and UpApGp at pH 7 and the ionic strength 0.1 at 20°.

TABLE I. Hyperchromicity and $|[M]_t - [M]_m|$ at pH 7

Substance	Hyperchromicity at 260 m μ , h(%) ^a	$ [M]_t - [M]_m \frac{b}{x} 10^{-4}$
ApCpGp	15.7	2.70 (261 m μ)
CpApGp	15.3	2.49 (268 m μ)
ApUpGp	10.3	0.83 (280 m μ)
UpApGp	13.2	2.24 (257 m μ)

$$\text{a } h = \frac{A_{Xp} + A_{Yp} + A_{Zp} - A_{XpYpZp}}{A_{XpYpZp}} \times 100 = 100 \left(\frac{\sum \epsilon_m}{\epsilon_t} - 1 \right)$$

$$\text{b } \text{Interaction Parameter} = |[M]_t - [M]_m| = |[M]_{XpYpZp} - ([M]_X + [M]_{pY} + [M]_{pZ})|_{\max}$$

Stacking of the nearest-bases in the pair of sequence isomers, ApCpGp and CpApGp, is more or less comparable, since both the hyperchromicity and $|[M]_t - [M]_m|$ value are much the same, whereas in another pair of the isomers, ApUpGp and UpApGp, the former is less stacked at pH 7 than the latter. This finding may be compared to the previous observation by Ts'o et al.¹¹⁾, i. e., an insertion of uridyl residue into the purines exerts destacking effect. Thus, for the two pairs of sequence isomers, the stacking decreases in the order of ApCpGp \approx CpApGp $>$ UpApGp $>$ ApUpGp.

A full account of the ORD study of di- and trinucleotides obtained from ribonuclease T₁ will soon be reported elsewhere.

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- 8) Abbreviations used: ApApGp, adenylyl-(3'-5')-adenylyl-(3'-5')-guanosine-3'-phosphate; ApCpGp, adenylyl-(3'-5')-cytidylyl-guanosine-3'-phosphate; ApUpGp, adenylyl-(3'-5')-uridylyl-(3'-5')-guanosine-3'-phosphate; etc.
- 9) A pair of sequence isomers, CpUpGp and UpCpGp, are not yet resolved.
- 10) ORD measurements were made on a JASCO recording spectropolarimeter model ORD/UV-5. Optical rotations used in this communication are defined as $[\phi] = \frac{[M]}{3} = \frac{1}{3} \cdot [\alpha] \cdot \frac{\text{Molecular weight}}{100}$, where $[\phi]$, $[M]$, and $[\alpha]$ are molecular rotation per residue, molecular rotation, and specific rotation, respectively.
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