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# The Crystal and Molecular Structure of Carminomycin I Hydrochloride Monohydrate

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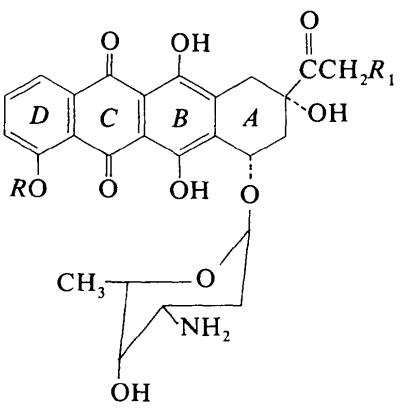
A crystal structure analysis of the anthracycline antibiotic carminomycin I hydrochloride monohydrate reveals a molecular conformation and bonding pattern that is strongly influenced by hydrogen bonding. The structure was solved by direct-methods analysis of data from a crystal with space group $P2_1$ and $a = 20{\cdot}027 \pm 0{\cdot}004$, $b = 5{\cdot}488 \pm 0{\cdot}001$, $c = 11{\cdot}901 \pm 0{\cdot}002$ Å, $\beta = 93{\cdot}710 \pm 0{\cdot}003°$, $Z = 2$, and density, $\rho_c = 1{\cdot}445$ g cm$^{-3}$ for $C_{26}H_{30}O_{11}NCl$. An anisotropic least-squares refinement converged to a conventional residual of $R = 0{\cdot}0695$ for 2631 independent reflections recorded with Ni-filtered Cu $K\alpha$ radiation on an automated four-circle diffractometer.

## Introduction

The antibiotic carminomycin I (1) (Gauze, Sveshikova, Ukholina, Gavrilina, Filicheva & Gladkikh, 1973) has been shown to be an effective antineoplastic agent and is structurally similar (Brazhnikova, Zbarsky, Ponomarenko & Potapova, 1974; Pettit, Einck, Herald, Ode, Von Dreele, Brown, Brazhnikova & Gauze, 1975) to the anthracyclines daunomycin (2) and adriamycin (3). A crystal-structure determination of *N*-bromoacetyldaunomycin (Angiuli, Foresti, Riva di Sanseverino, Isaacs, Kennard, Motherwell, Wampler & Arcamone, 1971) revealed the essential features of these molecules; however, difficulties with the structure analysis precluded a precise set of bonding parameters. Because of the availability of diffraction data of reasonable quality for carminomycin I $HCl.H_2O$, we can now report the bonding parameters and molecular conformation of this example of an important class of antineoplastic antibiotics.




(1) $R = R_1 = H$

(2) $R = CH_3$; $R_1 = H$

(3) $R = CH_3$; $R_1 = OH$

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## Experimental

A crystal of carminomycin I $HCl.H_2O$ of sufficient size for data collection was obtained from ethanol–toluene. Weissenberg and precession photographs displayed the Laue symmetry $2/m$ and the extinction $k = 2n + 1$ for $0k0$ which corresponds to the non-centrosymmetric monoclinic space group $P2_1$ for chiral molecules. There were 112 reflections in the angular range $7{\cdot}4 \leq 2\theta \leq 76{\cdot}7°$ for Cu $K\alpha$ radiation which were automatically centered on a Syntex $P\bar{1}$ auto-diffractometer; a least-squares refinement of the angular settings yielded the lattice parameters $a = 20{\cdot}027 \pm 0{\cdot}004$, $b = 5{\cdot}488 \pm 0{\cdot}001$, $c = 11{\cdot}901 \pm 0{\cdot}002$ Å, $\beta = 93{\cdot}710 \pm 0{\cdot}003°$ which for $Z = 2$ and $C_{26}H_{30}O_{11}NCl$ gives $\rho_c = 1{\cdot}445$ g cm$^{-3}$ ($\rho_o = 1{\cdot}42$ g cm$^{-3}$).

The diffraction intensities were measured on a $0{\cdot}4 \times 0{\cdot}1 \times 0{\cdot}05$ mm crystal with Ni-filtered Cu $K\alpha$ radiation with the diffractometer operating in the variable speed $\theta$–$2\theta$ scan mode. For each reflection the scan speed, between 1 and 8° min$^{-1}$, was determined from the intensity found in a rapid sampling scan. The scans were taken over the range $(2\theta K\alpha_1 - 0{\cdot}8)°$ to $(2\theta K\alpha_2 + 0{\cdot}8)°$ with background counts for 0·25 of the scan time taken at each end of the scan. There were 2779 independent reflections investigated within the limits of the diffractometer ($2\theta \leq 120°$). Of these, 2631 reflections were retained as objectively observed with $|F_o| \geq 0{\cdot}675\sigma_F$; $\sigma_F = 0{\cdot}02|F_o| + [c + (B_1 + B_2)k^2]^{1/2}R/(2|F_o|\mathrm{Lp})$ where $C$ is the total count in a scan taken at the rate $R$ and $k$ (=4) is the ratio of scanning time to the time for each background count $B_1$

and $B_2$. Periodic monitoring of three reflections showed a maximum 4% random variation in intensity during the time of data collection. Corrections were applied for Lorentz and polarization effects but absorption ($\mu$ = 18·5 cm$^{-1}$) and extinction effects were considered to be negligible.

### Structure determination and refinement

The structure of carminomycin I HCl.$H_2O$ was readily solved with the *MULTAN* 74 system of computer programs (Germain, Main & Woolfson, 1971; Declercq, Germain, Main & Woolfson, 1973; Koch, 1974). A set of normalized structure factors, $E_{hkl}$, was obtained by means of a Debye curve calculated from the molecular scattering factors of the anthracycline ring system found in *N*-bromoacetyldaunomycin (Angiuli *et al.*, 1971). The 350 reflections with $E_{hkl} \geq 1{\cdot}40$ were expanded over 2000 $\Sigma_2$ interactions and were subjected to a convergence analysis to give the starting set $10,0,\bar{10}$ (0), 13,0,5 (0), $1,2,\bar{10}$ ($\pi/4$), $21,3,\bar{3}$ (0), $52\bar{5}$ ($\pm\pi/4$ or $\pm 3\pi/4$), 808 (0 or $\pi$), $62\bar{5}$ ($\pm\pi/4$ or $\pm 3\pi/4$). The first phase was determined by $\Sigma_1$ relationships, the next three fix the origin (Hauptman & Karle, 1956) with the $1,2,\bar{10}$ reflection determining the enantiomorph and the last three are variable. A multiple-solution tangent refinement of the 32 possible starting sets gave an absolute figure of merit of 1·004, a $\psi(0)$ = 296 (Cochran & Douglas, 1955), and a residual of 36·12 for the best overall solution. A Fourier synthesis of these phases revealed the positions of 33 atoms, all of which ultimately proved to be correct. These positions were used to phase ($R$ = 35%) successive difference Fourier syntheses* which revealed the positions of the rest of the 39 atoms in the structure.

The model was refined with isotropic thermal parameters by full-matrix least-squares analysis with each reflection assigned a weight, $w = 1/\sigma_F^2$, and with real atomic scattering factors for Cl°, N°, O°, C° and H° (*International Tables for X-ray Crystallography*, 1974). At convergence the standard residual was $R$ = 0·131 and the weighted residual, $R_w = [\Sigma w(|F_o| - |F_c|)^2/\Sigma w|F_o|^2]^{1/2}$, was 0·143. The model with anisotropic thermal parameters was refined by large-block least squares (351 independent variables in three blocks) to give the residuals $R$ = 0·087 and $R_w$ = 0·098. A difference Fourier synthesis based on these results gave the positions of all the H atoms. The C—H and N—H atoms were placed at ideal positions and all O—H atoms were placed as found in the map. The parameters for the nonhydrogen atoms were again refined by large-block least squares to yield $R$ = 0·0695 and $R_w$ = 0·0732 at convergence. All H atoms were included with fixed parameters and a fixed value of $U_{iso}$ = 0·06 Å$^2$.*

### Results

Final atomic coordinates for carminomycin I HCl.$H_2O$ are presented in Tables 1 and 2 along with the estimated standard deviations derived from the least-squares analysis. The stereoscopic view shown in Fig. 1 displays the essential configurational and

* From this point on all calculations were performed with the *CRYSTALS* system of computer programs adapted for the Univac 1110 (Rollett & Carruthers, 1974).

* Lists of structure factors and anisotropic thermal parameters have been deposited with the British Library Lending Division as Supplementary Publication No. SUP 32658 (12 pp.). Copies may be obtained through The Executive Secretary, International Union of Crystallography, 13 White Friars, Chester CH1 1NZ, England.

Table 1. *Fractional coordinates* ($\times 10^4$) *for carminomycin* I HCl.$H_2O$

The estimated standard deviations are listed in parentheses.

| | $x$ | $y$ | $z$ |
|---|---|---|---|
| C(1) | 11420 (3) | 872 (18) | 8085 (6) |
| C(2) | 11854 (3) | −127 (21) | 8933 (6) |
| C(3) | 11677 (3) | −2041 (20) | 9554 (6) |
| C(4) | 11056 (3) | −3155 (17) | 9359 (5) |
| O(4) | 10906 (2) | −5014 (13) | 10024 (4) |
| C(4a) | 10603 (3) | −2206 (14) | 8495 (5) |
| C(5) | 9942 (3) | −3340 (15) | 8279 (5) |
| O(5) | 9770 (2) | −5135 (12) | 8846 (4) |
| C(5a) | 9490 (2) | −2301 (13) | 7397 (4) |
| C(6) | 8855 (3) | −3332 (13) | 7180 (4) |
| O(6) | 8637 (2) | −5242 (10) | 7759 (4) |
| C(6a) | 8412 (2) | −2406 (11) | 6296 (4) |
| C(7) | 7726 (2) | −3562 (10) | 6094 (4) |
| O(7) | 7309 (2) | −2637 (8) | 6948 (3) |
| C(8) | 7417 (3) | −3061 (11) | 4919 (4) |
| C(9) | 7466 (2) | −344 (12) | 4627 (4) |
| O(9) | 7112 (2) | 1140 (8) | 5378 (3) |
| C(10) | 8192 (3) | 425 (13) | 4634 (4) |
| C(10a) | 8611 (2) | −525 (12) | 5646 (4) |
| C(11) | 9243 (2) | 595 (12) | 5882 (4) |
| O(11) | 9407 (2) | 2488 (10) | 5233 (4) |
| C(11a) | 9682 (2) | −324 (13) | 6754 (4) |
| C(12) | 10336 (3) | 878 (15) | 6974 (5) |
| O(12) | 10506 (2) | 2656 (11) | 6432 (4) |
| C(12a) | 10797 (3) | −197 (16) | 7883 (5) |
| C(13) | 7107 (3) | 61 (12) | 3445 (4) |
| O(13) | 7399 (2) | −48 (12) | 2618 (3) |
| C(14) | 6376 (3) | 523 (20) | 3396 (5) |
| C(1′) | 7054 (2) | −4394 (13) | 7660 (4) |
| C(2′) | 6775 (3) | −3111 (14) | 8648 (4) |
| C(3′) | 6110 (3) | −1832 (12) | 8337 (4) |
| N(3′) | 5804 (2) | −943 (11) | 9356 (4) |
| C(4′) | 5626 (2) | −3615 (12) | 7710 (4) |
| O(4′) | 5465 (2) | −5406 (9) | 8512 (3) |
| C(5′) | 5963 (3) | −4650 (13) | 6719 (5) |
| O(5′) | 6566 (2) | −5875 (8) | 7092 (3) |
| C(6′) | 5524 (3) | −6476 (16) | 6051 (6) |
| Cl | 5672 (1) | 5820* | 1577 (1) |
| O(hyd) | 6683 (2) | 2026 (9) | 656 (3) |

* $y$ coordinate fixed in polar space group $P2_1$.

Table 2. *Fractional coordinates* ($\times 10^3$) *for the hydrogen atoms*

| H atom on | $x$ | $y$ | $z$ |
|---|---|---|---|
| C(1) | 1156 | 235 | 763 |
| C(2) | 1231 | 63 | 906 |
| C(3) | 1202 | −264 | 1016 |
| O(4) | 1057 | −589 | 977 |
| O(6) | 910 | −530 | 840 |
| C(7) | 776 | −538 | 619 |
| C(8) | 765 | −405 | 436 |
| C(8) | 693 | −355 | 488 |
| O(9) | 703 | 46 | 596 |
| C(10) | 839 | −17 | 391 |
| C(10) | 822 | 229 | 462 |
| O(11) | 979 | 325 | 562 |
| C(14) | 619 | 75 | 261 |
| C(14) | 627 | 203 | 385 |
| C(14) | 614 | −90 | 374 |
| C(1′) | 743 | −554 | 789 |
| C(2′) | 711 | −188 | 898 |
| C(2′) | 669 | −434 | 927 |
| C(3′) | 620 | −40 | 782 |
| N(3′) | 538 | −10 | 918 |
| N(3′) | 612 | 22 | 980 |
| N(3′) | 572 | −237 | 988 |
| C(4′) | 517 | −292 | 749 |
| O(4′) | 513 | −642 | 837 |
| C(5′) | 607 | −324 | 619 |
| C(6′) | 576 | −711 | 540 |
| C(6′) | 543 | −789 | 656 |
| C(6′) | 509 | −572 | 578 |
| O(hyd) | 690 | 120 | 120 |
| O(hyd) | 635 | 325 | 100 |

conformational features of the carminomycin I cation. Each nonhydrogen atom is represented by an ellipsoid consistent with the anisotropic thermal parameters obtained.* The six chiral centers are C(7)-*S*, C(9)-*S*,

* See deposition footnote on p. 3284.

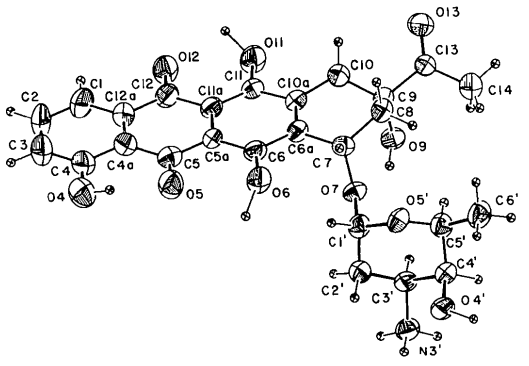


Fig. 1. A perspective representation of the structure of the carminomycin I cation. A hydrogen atom on C(10) is hidden from view.

Table 3. *Bond distances and angles for carminomycin* I HCl.$H_2O$

Values in parentheses are estimated standard deviations in the last figure.

| | | | |
|---|---|---|---|
| C(1)–C(2) | 1·400 (10) | C(2)–C(1)–C(12a) | 118·0 (14) |
| C(1)–C(12a) | 1·385 (8) | | |
| C(2)–C(3) | 1·345 (12) | C(1)–C(2)–C(3) | 121·9 (15) |
| C(3)–C(4) | 1·391 (10) | C(2)–C(3)–C(4) | 121·1 (11) |
| C(4)–C(4a) | 1·426 (8) | C(3)–C(4)–C(4a) | 118·7 (13) |
| C(4)–O(4) | 1·337 (9) | C(3)–C(4)–O(4) | 118·0 (11) |
| | | O(4)–C(4)–C(4a) | 123·2 (10) |
| C(4a)–C(5) | 1·470 (8) | C(4)–C(4a)–C(5) | 119·8 (12) |
| C(4a)–C(12a) | 1·391 (10) | C(4)–C(4a)–C(12a) | 118·7 (12) |
| | | C(5)–C(4a)–C(12a) | 121·6 (12) |
| C(5)–C(5a) | 1·457 (8) | C(4a)–C(5)–C(5a) | 118·1 (11) |
| C(5)–O(5) | 1·254 (8) | C(4a)–C(5)–O(5) | 120·8 (10) |
| | | C(5a)–C(5)–O(5) | 121·1 (10) |
| C(5a)–C(6) | 1·401 (7) | C(5)–C(5a)–C(6) | 119·2 (10) |
| C(5a)–C(11a) | 1·396 (8) | C(5)–C(5a)–C(11a) | 121·3 (10) |
| | | C(6)–C(5a)–C(11a) | 119·5 (10) |
| C(6)–C(6a) | 1·426 (7) | C(5a)–C(6)–C(6a) | 120·4 (10) |
| C(6)–O(6) | 1·342 (7) | C(5a)–C(6)–O(6) | 122·8 (9) |
| | | C(6a)–C(6)–O(6) | 116·8 (10) |
| C(6a)–C(7) | 1·518 (7) | C(6)–C(6a)–C(7) | 118·8 (9) |
| C(6a)–C(10a) | 1·365 (8) | C(6)–C(6a)–C(10a) | 119·8 (10) |
| | | C(7)–C(6a)–C(10a) | 121·5 (10) |
| C(7)–C(8) | 1·517 (7) | C(6a)–C(7)–C(8) | 112·4 (9) |
| C(7)–O(7) | 1·448 (6) | C(6a)–C(7)–O(7) | 107·4 (10) |
| | | O(7)–C(7)–C(8) | 111·4 (10) |
| C(8)–C(9) | 1·536 (8) | C(7)–C(8)–C(9) | 110·9 (11) |
| C(9)–O(9) | 1·430 (6) | C(8)–C(9)–O(9) | 111·7 (11) |
| C(9)–C(10) | 1·515 (7) | C(8)–C(9)–C(10) | 110·1 (10) |
| C(9)–C(13) | 1·553 (7) | C(8)–C(9)–C(13) | 108·1 (10) |
| | | O(9)–C(9)–C(10) | 110·6 (10) |
| | | O(9)–C(9)–C(13) | 105·4 (10) |
| | | C(10)–C(9)–C(13) | 110·7 (9) |
| C(10)–C(10a) | 1·515 (7) | C(9)–C(10)–C(10a) | 113·0 (10) |
| C(10a)–C(11) | 1·417 (7) | C(10)–C(10a)–C(11) | 116·7 (9) |
| | | C(10)–C(10a)–C(6a) | 122·9 (8) |
| | | C(11)–C(10a)–C(6a) | 120·4 (9) |
| C(11)–C(11a) | 1·409 (7) | C(10a)–C(11)–C(11a) | 119·8 (10) |
| C(11)–O(11) | 1·347 (7) | C(10a)–C(11)–O(11) | 118·0 (9) |
| | | C(11a)–C(11)–O(11) | 122·2 (9) |
| C(11a)–C(12) | 1·475 (8) | C(11)–C(11a)–C(12) | 118·4 (10) |
| | | C(11)–C(11a)–C(5a) | 120·1 (9) |
| | | C(12)–C(11a)–C(5a) | 121·5 (9) |
| C(12)–C(12a) | 1·497 (8) | C(11a)–C(12)–C(12a) | 116·9 (12) |
| C(12)–O(12) | 1·230 (8) | C(11a)–C(12)–O(12) | 122·3 (9) |
| | | C(12a)–C(12)–O(12) | 120·8 (9) |
| | | C(12)–C(12a)–C(1) | 117·7 (12) |
| | | C(12)–C(12a)–C(4a) | 120·6 (9) |
| | | C(1)–C(12a)–C(4a) | 121·6 (12) |
| C(13)–O(13) | 1·179 (6) | C(9)–C(13)–O(13) | 121·6 (8) |
| C(13)–C(14) | 1·483 (8) | C(9)–C(13)–C(14) | 117·2 (9) |
| | | O(13)–C(13)–C(14) | 121·2 (9) |
| | | C(7)–O(7)–C(1′) | 115·6 (9) |
| C(1′)–O(7) | 1·401 (6) | O(7)–C(1′)–C(2′) | 108·5 (12) |
| C(1′)–C(2′) | 1·509 (8) | O(7)–C(1′)–O(5′) | 112·0 (9) |
| C(1′)–O(5′) | 1·410 (6) | C(2′)–C(1′)–O(5′) | 111·2 (10) |
| C(2′)–C(3′) | 1·531 (8) | C(1′)–C(2′)–C(3′) | 112·7 (10) |
| C(3′)–C(4′) | 1·535 (8) | C(2′)–C(3′)–C(4′) | 109·7 (11) |
| C(3′)–N(3′) | 1·477 (7) | C(2′)–C(3′)–N(3′) | 110·7 (10) |
| | | N(3′)–C(3′)–C(4′) | 109·1 (10) |
| C(4′)–C(5′) | 1·507 (7) | C(3′)–C(4′)–C(5′) | 108·7 (10) |
| C(4′)–O(4′) | 1·421 (7) | C(3′)–C(4′)–O(4′) | 106·2 (10) |
| | | O(4′)–C(4′)–C(5′) | 113·4 (11) |
| C(5′)–O(5′) | 1·428 (6) | C(4′)–C(5′)–O(5′) | 110·3 (10) |
| C(5′)–C(6′) | 1·522 (8) | C(4′)–C(5′)–C(6′) | 112·6 (10) |
| | | O(5′)–C(5′)–C(6′) | 107·5 (13) |
| | | C(5′)–O(5′)–C(1′) | 115·1 (9) |

Table 4. *Selected torsion angles* (°) *for carminomycin* I HCl.$H_2O$

| Ring *A* | | Ring *B* | |
|---|---|---|---|
| C(6a)C(7)C(8)C(9) | −48·2 | C(5a)C(6)C(6a)C(10a) | 0·9 |
| C(7)C(8)C(9)C(10) | 62·0 | C(6)C(6a)C(10a)C(11) | −3·3 |
| C(8)C(9)C(10)C(10a) | −45·2 | C(6a)C(10a)C(11)C(11a) | 3·5 |
| C(9)C(10)C(10a)C(6a) | 17·7 | C(10a)C(11)C(11a)C(5a) | −1·3 |
| C(10)C(10a)C(6a)C(7) | −4·6 | C(11)C(11a)C(5a)C(6) | −1·1 |
| C(10a)C(6a)C(7)C(8) | 20·1 | C(11a)C(5a)C(6)C(6a) | 1·3 |
| Ring *C* | | Ring *D* | |
| C(4a)C(5)C(5a)C(11a) | 1·5 | C(1)C(2)C(3)C(4) | 1·6 |
| C(5)C(5a)C(11a)C(12) | −3·1 | C(2)C(3)C(4)C(4a) | −1·0 |
| C(5a)C(11a)C(12)C(12a) | 2·9 | C(3)C(4)C(4a)C(12a) | −0·1 |
| C(11a)C(12)C(12a)C(4a) | −1·3 | C(4)C(4a)C(12a)C(1) | 0·7 |
| C(12)C(12a)C(4a)C(5) | −0·1 | C(4a)C(12a)C(1)C(2) | −0·1 |
| C(12a)C(4a)C(5)C(5a) | 0·0 | C(12a)C(1)C(2)C(3) | −1·1 |
| Daunosamine | | | |
| C(1′)C(2′)C(3′)C(4′) | 50·1 | | |
| C(2′)C(3′)C(4′)C(5′) | −54·5 | | |
| C(3′)C(4′)C(5′)O(5′) | 59·1 | | |
| C(4′)C(5′)O(5′)C(1′) | −61·2 | | |
| C(5′)O(5′)C(1′)C(2′) | 55·3 | | |
| O(5′)C(1′)C(2′)C(3′) | −49·6 | | |

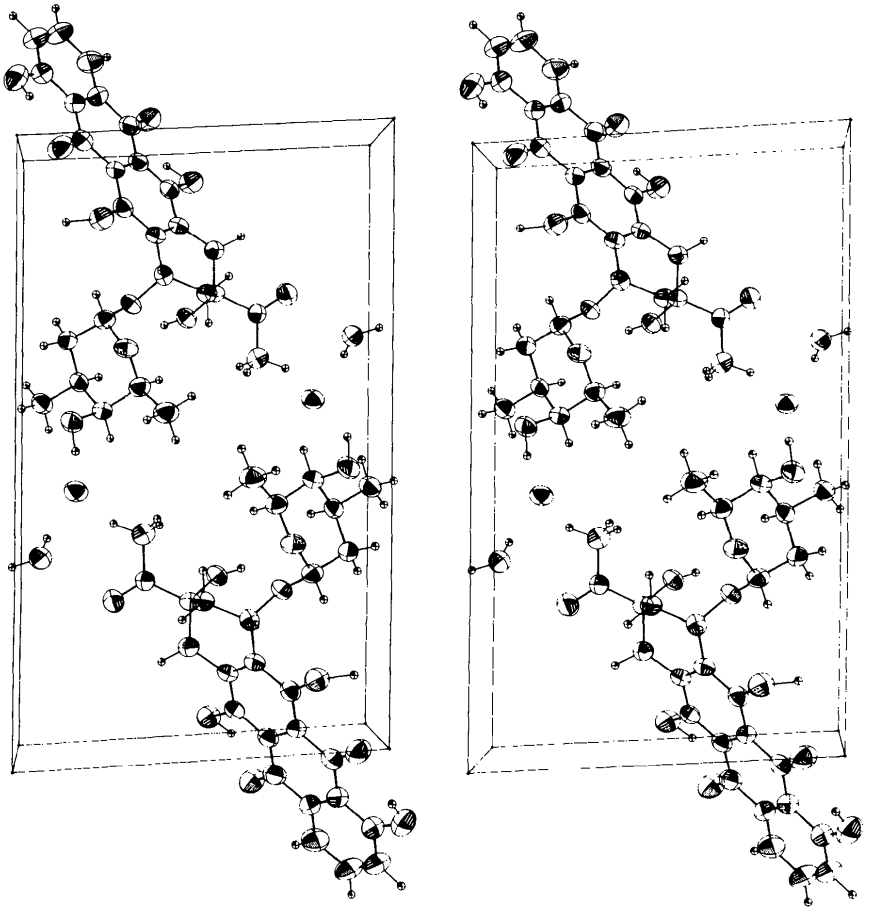

Fig. 2. A stereodiagram of the unit cell and two molecules of carminomycin I. Also shown is the water of hydration and the chloride ion.

Table 5. *Hydrogen-bonding parameters for carminomycin* I HCl.$H_2O$ (Å)

The arrow indicates the probable direction of proton donation.

| | |
|---|---|
| O(4) → O(5) | 2·595 (6) |
| O(6) → O(5) | 2·539 (6) |
| O(11) → O(12) | 2·546 (6) |
| O(9) → O(7) | 2·801 (5) |
| O(9) → O(5′) | 2·885 (5) |
| N(3′) → O(hyd) | 2·791 (6) |
| O(4′) → Cl | 3·075 (4) |
| N(3′) → Cl | 3·210 (5) |
| N(3′) → Cl | 3·238 (5) |
| O(hyd) → Cl | 3·150 (4) |
| O(hyd) → O(13) | 2·893 (6) |

C(1′)-*R*, C(3′)-*S*, C(4′)-*S* and C(5′)-*S*. Since the absolute configuration of the daunosamine unit of carminomycin I has been shown to be the same as that obtained from daunomycin (Brazhnikova *et al.*, 1974) whose absolute configuration is known (Angiuli *et al.*, 1971; Arcamone, Cassinelli, Franceschi, Orezzi & Mondelli, 1968), carminomycin I is herein shown in the correct enantiomorphic form which is in accord with the results of Wani, Taylor, Wall, McPhail & Onan (1975).

Bond lengths and angles within the molecular ion are recorded in Table 3. The set of torsion angles listed in Table 4 fully characterizes all the conformational features of the molecule. The hydrogen-bonding parameters in Table 5 and the stereoscopic drawing of the unit-cell contents shown in Fig. 2 display the molecular packing interactions in the structure.

## Discussion

The molecular structure of carminomycin I consists of a tetracycline moiety containing a trihydroxy anthraquinone group as the first three rings with the unusual sugar residue, daunosamine, attached to the saturated fourth ring. In the anthraquinone system the two outer rings, *B* and *D*, are most nearly aromatic with average C—C distances, 1·390 (26) and 1·402 (21) Å respectively, which are very close to that of benzene, 1·397 Å (Langseth & Stoicheff, 1956). The inner ring, *C*, has two more localized double bonds in the carbonyls, C(5)—O(5) (1·254 Å) and C(12)—O(12) (1·230 Å), and hence the average C—C distance, 1·448 (43) Å, within the ring is much larger than the aromatic value. There is, however, a wide variation in the individual distances from the average values for each ring. In particular, the bonds in the ring junctions, C(4a)—C(12a) and C(5a)—C(11a), and especially the two end bonds, C(2)—C(3) and C(6a)—C(10a), are less than the average values. All the remaining bonds along the edges of the anthraquinone system are the same as or longer than the average values with one, C(12)—C(12a), nearly 1·50 Å long. Similar variations in C—C bond lengths have been observed in 1,8-, 1,5- and 1,4-dihydroxyanthraquinones (Prakash, 1965; Hall & Nobbs, 1966; Guilhem, 1967; Swaminathan & Nigam, 1967) and are due in the present case to the changes in the conjugation induced by the formation of the hydrogen bonds between the hydroxyl groups O(4)—H, O(6)—H and O(11)—H and the two carbonyl groups C(5)—O(5) and C(12)—O(12). As in the cases of the dihydroanthraquinones, the hydrogen bonding and conjugation result in short C—O distances in the hydroxyl groups and long C—O distances in the carbonyl groups. The O···O distances in these hydrogen bonds, 2·54 to 2·59 Å, are typical and compare well with those found for similar conjugated enolic systems (Donohue, 1968; Brown, 1976).

The *A* ring is saturated, except of course C(6a)—C(10a), and is constrained to a twist-chair conformation by its attachment to the anthraquinone system. This in turn produces a slight right-handed twist in the anthraquinone which is most severe in the *B* ring (average deviation 0·012 Å) and progressively less in the *C* (average deviation 0·009 Å) and *D* (average deviation 0·005 Å) rings. The twist-chair conformation of the *A* ring is further stabilized by the formation of a hydrogen bond from the axial hydroxyl group, O(9)—H, at C(9) to O(7) which links the daunosamine residue axially to the *A* ring. The O···O distance, 2·801 Å, for this hydrogen bond is normal and the H atom was found to be properly positioned between the two O atoms. This hydrogen bond was also found in the recently determined structure of daunomycin (Neidle & Taylor, 1977) and results in a molecular conformation virtually identical with that of carminomycin I.

The six-membered ring of the daunosamine residue is in a normal chair conformation and is attached axially *via* O(7) to the *A* ring. All of the bonds in this group are normal single bonds with normal tetrahedral angles at each atom. Both the ammonium group, N(3′), and the hydroxyl group, O(4′), on the daunosamine participate in hydrogen bonding to the chloride ion. The O(4′)···Cl distance, 3·075(4) Å, is indicative of a strong hydrogen bond and the H(4′) atom was found directly between the O atom and $Cl^-$ ion. The ammonium group is at normal hydrogen-bonding distances, 3·210 (5) and 3·238 (5) Å, from two different $Cl^-$ ions. In addition, O(hyd) of the water molecule is also within hydrogen-bonding distance, 2·791 (6) Å, as an acceptor of the donor ammonium N; thus, all three protons on the ammonium appear to participate in hydrogen bonding. Finally, the water molecule is at distances appropriate for hydrogen bonding to the $Cl^-$ ion, 3·150 (4) Å, and to O(13), 2·893 Å. In this instance the water molecule is the proton donor and the other two atoms are acceptors.

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