

X-Ray Studies on Crystalline Complexes Involving Amino Acids and Peptides. XVII. Chirality and Molecular Aggregation: The Crystal Structures of DL-Arginine DL-Glutamate Monohydrate and DL-Arginine DL-Aspartate

JAYASHREE SOMAN, M. VIJAYAN,* ** B. RAMAKRISHNAN,† and T. N. GURU ROW††

**Molecular Biophysics Unit; †Department of Physics, Indian Institute of Science, Bangalore-560012; India

††Physical Chemistry Division, National Chemical Laboratory, Pune-411008, India

SYNOPSIS

DL-Arginine DL-glutamate monohydrate and DL-arginine DL-aspartate, the first DL-DL amino acid–amino acid complexes to be prepared and x-ray analyzed, crystallize in the space group $P\bar{1}$ with $a = 5.139(2)$, $b = 10.620(1)$, $c = 14.473(2)$ Å, $\alpha = 101.34(1)^\circ$, $\beta = 94.08(2)^\circ$, $\gamma = 91.38(2)^\circ$ and $a = 5.402(3)$, $b = 9.933(3)$, $c = 13.881(2)$ Å, $\alpha = 99.24(2)^\circ$, $\beta = 99.73(3)^\circ$, $\gamma = 97.28(3)^\circ$, respectively. The structures were solved using counter data and refined to R values of 0.050 and 0.077 for 1827 and 1739 observed reflections, respectively. The basic element of aggregation in both structures is an infinite chain made up of pairs of molecules. Each pair, consisting of a L- and a D-isomer, is stabilized by two centrosymmetrically or nearly centrosymmetrically related hydrogen bonds involving the α -amino and the α -carboxylate groups. Adjacent pairs in the chain are then connected by specific guanidyl–carboxylate interactions. The infinite chains are interconnected through hydrogen bonds to form molecular sheets. The sheets are then stacked along the shortest cell translation. The interactions between sheets involve two head-to-tail sequences in the glutamate complex and one such sequence in the aspartate complex. However, unlike in the corresponding LL and DL complexes, head-to-tail sequences are not the central feature of molecular aggregation in the DL-DL complexes. Indeed, fundamental differences exist among the aggregation patterns in the LL, the LD, and the DL-DL complexes.

INTRODUCTION

The x-ray studies on crystalline complexes involving amino acids and peptides, among themselves as well as with other molecules, being carried out in this laboratory have resulted in the elucidation of several biologically significant specific interactions and interaction patterns.^{1–6} These studies also led to the identification of head-to-tail sequences, in which the α - or the terminal amino and carboxylate groups are brought into periodic hydrogen-bonded proximity in a polypeptide-like arrangement, as the central feature of amino acid and

peptide aggregation.^{7–11} Such sequences have been suggested to be of probable relevance to prebiotic condensation during chemical evolution.^{12,13} Most of the complexes studied earlier involved two types of L-amino acids each (LL complexes). Recently the studies have been expanded to include complexes between an L-amino acid of one type and a D-amino acid of another (LD complexes).^{14–16} The comparison of these complexes with the corresponding LL complexes indicates that the reversal of chirality of one of the components in a complex could lead to profound changes in molecular aggregation, although these changes could be of more than one type. The LD complexes also provide insights into the role of chirality during chemical evolution. Encouraged by these results, we have now extended the studies to DL-DL complexes. The crystal structures of two such complexes, namely, DL-

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*To whom correspondence should be addressed.

arginine DL-glutamate monohydrate and DL-arginine DL-aspartate, are reported here.

EXPERIMENTAL

Crystals of the complexes were grown using the vapor diffusion technique from aqueous solutions of the respective amino acids (obtained commercially) in molar proportions. Acetone was used as precipitant for growing DL-arginine DL-glutamate monohydrate whereas propanol was used in the case of DL-arginine DL-aspartate. The crystals of DL-arginine DL-glutamate always grew as thin, long, double crystals. After repeated attempts, a few single crystals were obtained by cutting the double crystals carefully along the boundary between the two component crystals. The space group and the unit cell dimensions of the crystals were determined from x-ray diffraction photographs and the densities using flotation in a mixture of benzene and carbon tetrachloride. The intensity data from

a crystal of the glutamate complex were collected using CuK α radiation on a CAD4 diffractometer at the Department of Physics, Indian Institute of Science, Bangalore. A similar instrument at the National Chemical Laboratory, Pune, was used to collect data from the aspartate complex employing MoK α radiation. Unit cell dimensions were refined using 25 reflections in each case (range 20°–30° for DL-arginine DL-glutamate monohydrate and 10°–16° for DL-arginine DL-aspartate). Intensity data were collected to a maximum Bragg angle of 65° and 24° for DL-arginine DL-glutamate monohydrate and DL-arginine DL-aspartate, respectively. The data were corrected for Lorentz and polarization factors. Other experimental details are presented with additional pertinent crystallographic data in Table I.

Both structures were solved uneventfully by direct methods using the MULTAN¹⁷ system of programs. They were refined, nonhydrogen atoms anisotropically and hydrogen atoms (located from a difference Fourier map using geometrical consid-

Table I Crystal Data and Experimental Information

	DL-Arginine DL-Glutamate Monohydrate	DL-Arginine DL-Aspartate
Chemical formula	C ₆ H ₁₅ N ₄ O ₂ ⁺ C ₅ H ₈ NO ₄ · H ₂ O	C ₆ H ₁₅ N ₄ O ₂ ⁻ C ₄ H ₆ NO ₄ ⁻
Formula weight	339	307
Crystal system	Triclinic	Triclinic
Space group	P $\bar{1}$	P $\bar{1}$
<i>a</i>	5.139(2) Å	5.402(3) Å
<i>b</i>	10.620(1)	9.933(3)
<i>c</i>	14.473(2)	13.881(2)
α	101.34(1)°	99.24(2)°
β	94.08(2)	99.73(3)
γ	91.38(2)	97.28(3)
<i>v</i>	771.96(4) Å ³	715.45(5) Å ³
<i>Z</i>	2	2
Density (calc.)	1.46 gcm ⁻³	1.43 gcm ⁻³
Density (meas.)	1.49(1)	1.41(2)
μ (cm ⁻¹)	10.53 (CuK α)	1.31 (MoK α)
Crystal size	0.08 × 0.15 × 0.70 mm	0.13 × 0.60 × 0.60 mm
Maximum Bragg angle	65°	24°
Unique reflections measured	2618	2109
Observed reflections [<i>I</i> > 2 σ (<i>I</i>)]	1827	1739
<i>R</i>	0.050	0.077
<i>wR</i>	0.052	0.107
Weighting scheme	1/(<i>a</i> + <i>bF</i> + <i>cF</i> ²)	1/(<i>a</i> + <i>bF</i> + <i>cF</i> ²)
	<i>a</i> = 1.1319	<i>a</i> = 0.3916
	<i>b</i> = 0.0259	<i>b</i> = 0.2643
	<i>c</i> = 0.0003	<i>c</i> = -0.0029

Table II Positional Parameters ($\times 10,000$) and Equivalent Isotropic Temperature Factors of Nonhydrogen Atoms in DL-Arginine DL-Glutamate Monohydrate (The Estimated Standard Deviations Are Given in Parentheses)

Atom	X	Y	Z	Equivalent B
N1	6859(11)	3647(6)	10303(4)	1.8(1)
O1	5102(10)	2558(6)	11653(4)	3.2(2)
O2	1044(9)	2300(5)	11007(4)	2.7(1)
C1	3457(13)	2553(7)	10991(5)	1.8(2)
C2	4328(13)	2888(7)	10078(5)	1.7(2)
C3	4668(14)	1745(7)	9303(5)	2.2(2)
C4	2122(15)	996(8)	8886(6)	2.8(2)
C5	2437(15)	177(7)	7930(5)	2.5(2)
N6	212(12)	-742(6)	7659(4)	2.4(2)
C7	-697(14)	-1225(7)	6776(5)	2.1(2)
N8	222(13)	-880(6)	6031(4)	2.7(2)
N9	-2674(13)	-2112(6)	6637(4)	2.7(2)
N11	10475(11)	5499(6)	7354(4)	2.1(2)
O11	8861(9)	4498(5)	8817(3)	2.7(1)
O12	4766(9)	4372(5)	8206(4)	2.6(1)
C11	7187(13)	4488(7)	8147(5)	1.8(2)
C12	8154(12)	4575(7)	7194(5)	1.8(2)
C13	9016(14)	3280(7)	6686(5)	2.1(2)
C14	6952(16)	2190(7)	6531(5)	2.5(2)
C15	4779(14)	2171(7)	5771(5)	2.2(2)
O16	4800(11)	3017(6)	5269(4)	3.4(2)
O17	3041(11)	1304(5)	5680(4)	3.2(2)
W1	7607(15)	4495(7)	4363(5)	5.6(2)

Table III Positional Parameters ($\times 10,000$) and Equivalent Isotropic Temperature Factors of Nonhydrogen Atoms in DL-Arginine DL-Aspartate (The Estimated Standard Deviations Are Given in Parentheses)

Atom	X	Y	Z	Equivalent B
N1	8219(14)	1290(9)	10872(6)	2.6(2)
O1	3137(12)	1177(7)	10616(6)	3.2(2)
O2	3529(14)	3332(8)	11387(7)	4.7(2)
C1	4416(16)	2364(10)	10979(7)	2.4(2)
C2	7212(17)	2602(9)	10869(7)	2.4(2)
C3	7529(18)	3210(10)	9937(8)	2.9(3)
C4	6386(23)	2214(12)	8942(8)	3.7(3)
C5	6753(20)	2912(11)	8069(8)	3.1(3)
N6	4987(17)	3840(9)	7839(7)	3.3(2)
C7	2800(19)	3474(10)	7156(7)	2.7(3)
N8	1860(16)	2175(8)	6787(6)	2.9(2)
N9	1526(17)	4457(9)	6891(7)	3.5(3)
N11	2890(16)	3233(9)	3841(7)	3.2(2)
O11	6652(15)	3906(8)	5467(6)	4.3(2)
O12	7464(16)	1756(8)	5386(6)	4.4(2)
C11	6205(20)	2653(11)	5123(8)	3.0(3)
C12	3815(18)	2085(10)	4323(8)	2.7(3)
C13	4281(18)	944(10)	3533(7)	2.6(2)
C14	6580(18)	1316(9)	3089(6)	2.2(2)
O15	7509(13)	2589(6)	3205(5)	3.1(2)
O16	7461(14)	383(7)	2612(5)	3.1(2)

erations) isotropically, by the block-diagonal structure factors least-squares method. The form factors for nonhydrogen atoms were taken from Cromer and Waber,¹⁸ and those for hydrogen atoms from Stewart, Davidson, and Simpson.¹⁹ The final positional and equivalent isotropic thermal parameters²⁰ of the nonhydrogen atoms in the two complexes are given in Tables II and III.

RESULTS AND DISCUSSION

The crystal structures of the two complexes are given in Figs. 1 and 2. The structures consist of

zwitterionic positively charged arginine molecules and zwitterionic negatively charged glutamate or aspartate ions. They are stabilized by electrostatic interactions and hydrogen bonds. The parameters of the hydrogen bonds are given in Tables IV and V.

Molecular Dimensions

The bond lengths and angles in the structures are normal. The torsion angles that define the conformation of the molecules²¹ are given in Table VI. Fifteen independent conformations of arginine have so far been observed in crystal structures containing this amino acid^{14,22} (also G. Shridhar Prasad

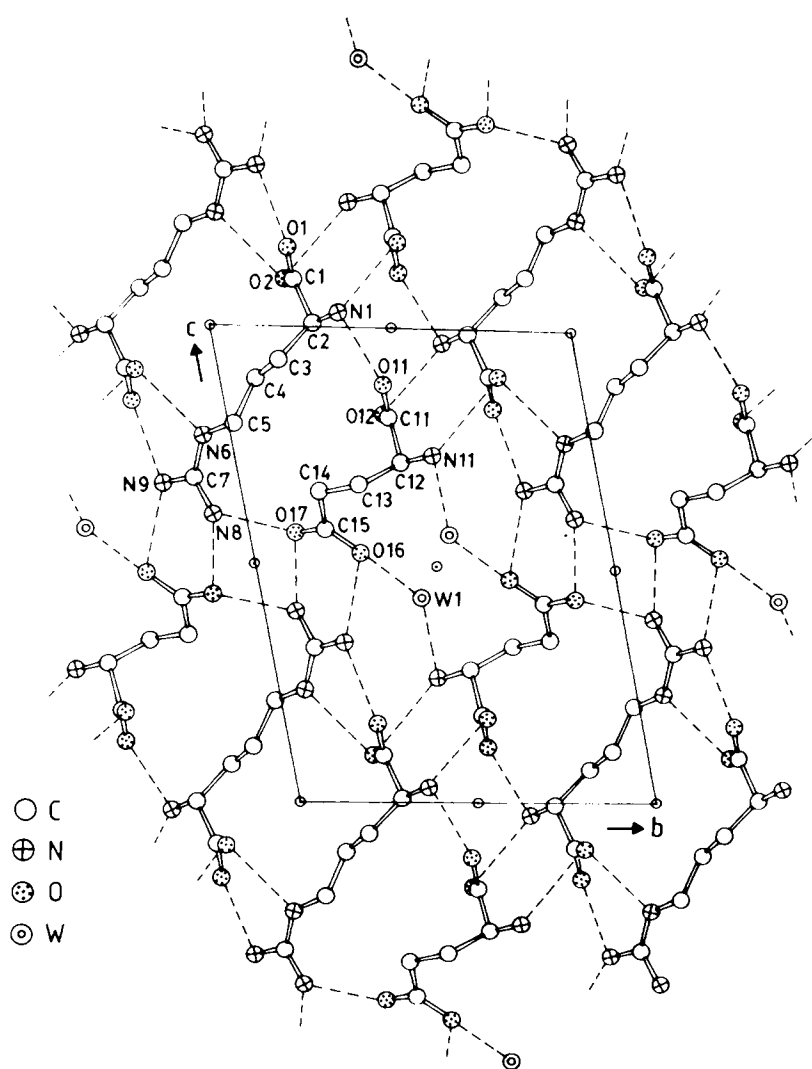


Figure 1. Crystal structure of DL-arginine DL-glutamate monohydrate viewed along the a^* axis. Broken lines in this and the subsequent figures represent hydrogen bonds. Pseudoinversion centers exist at $x \sim 0.69$, $y \sim 0.59$, $z \sim 0.86$, and the symmetry related position at $x \sim 0.31$, $y \sim 0.41$, $z \sim 0.14$. See text for details.

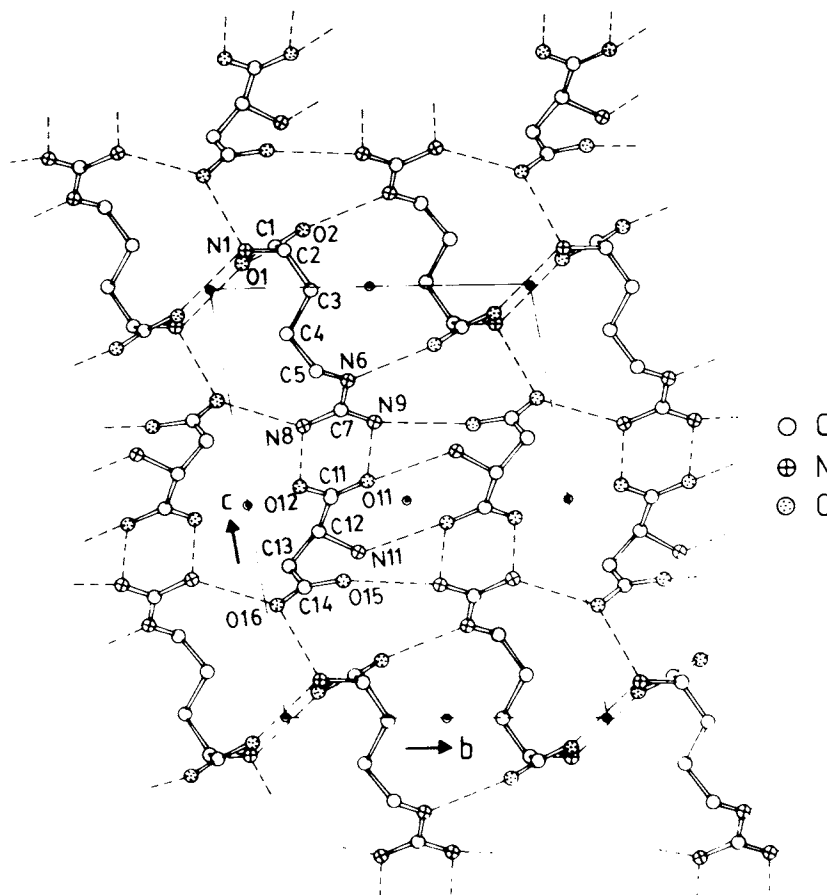


Figure 2. Crystal structure of DL-arginine DL-aspartate viewed along the a^* axis.

and M. Vijayan, unpublished results, 1989). The arginine molecule in the glutamate complex has an all *trans* side chain *trans* to the α -amino group as in the crystal structure of L-arginine HCl.²² The conformation of the molecule in the aspartate complex is similar to that in L-arginine L-aspartate²³ with a rather folded side chain staggered between the α -amino and the α -carboxylate groups. The side chain of the glutamate ion is also somewhat folded and is *trans* to the α -amino group as in the α -form of L-glutamic acid.²⁴ The orientation of the side-chain carboxyl (carboxylate) group is, however, somewhat different in the two structures. The aspartate ion adopts the energetically least favorable conformation²⁵ with the side-chain carboxylate group staggered between the α -amino and the α -carboxylate groups. Such a conformation of the aspartate ion has earlier been observed in the crystals of L-histidine L-aspartate monohydrate²⁶ and L-arginine D-aspartate.¹⁴ This conformation could, for certain values of χ^{21} and χ^{22} , permit the formation of an internal hydrogen bond between the

α -amino and the side-chain carboxylate groups.¹⁶ Such a hydrogen bond exists in the aspartate complex although the H-N—O angle associated with it is somewhat large.

Pseudosymmetry in the Glutamate Complex

Binary complexes containing amino acids of mixed chirality often exhibit pseudosymmetry^{14,15} even in cases where there is only one set of molecules in the asymmetric unit on account of the near centrosymmetric relation between the main chain and β -carbon atoms of the L-amino acid of one type and the corresponding atoms of the D-amino acid of the other type. The same is true of the glutamate complex reported here (Fig. 1). When the two sets of six atoms each in the complex are superposed through the application of the pseudoinversion center, the maximum and the mean deviations between the corresponding atoms are 0.055 and 0.013 Å respectively. The pseudosymmetry is thus

Table IV Hydrogen-Bond Parameters in DL-Arginine DL-Glutamate Monohydrate (Estimated Standard Deviations Are Given in Parentheses)

A-H...B	A...B (Å)	H-A...B (°)	Symmetry of Atom B
N1-H1(N1)...O12	2.887(7)	11(4)	$-x + 1, -y + 1, -z + 2$
N1-H2(N1)...O11	2.745(8)	7(5)	x, y, z
N1-H3(N1)...O2	2.849(8)	6(5)	$x + 1, y, z$
N6-H1(N6)...O2	2.875(9)	6(5)	$-x, -y, -z + 2$
N8-H1(N8)...O17	2.853(9)	21(5)	x, y, z
N8-H2(N8)...O17	2.843(8)	13(6)	$-x, -y, -z + 1$
N9-H1(N9)...O1	2.961(9)	3(5)	$-x, -y, -z + 2$
N9-H2(N9)...O16	2.865(8)	5(5)	$-x, -y, -z + 1$
N11-H1(N11)...O12	2.865(8)	4(6)	$x + 1, y, z$
N11-H2(N11)...W1	2.739(9)	8(5)	$-x + 2, -y + 1, -z + 1$
N11-H3(N11)...O2	3.142(8)	13(5)	$-x + 1, -y + 1, -z + 2$
W1-H1(W1)...O16	2.690(9)	15(8)	x, y, z

Table V Hydrogen-Bond Parameters in DL-Arginine DL-Aspartate (Estimated Standard Deviations Are Given in Parentheses)

A-H...B	A...B (Å)	H-A...B (°)	Symmetry of Atom B
N1-H1(N1)...O1	2.84(1)	30(9)	$-x + 1, -y, -z + 2$
N1-H2(N1)...O1	2.76(1)	16(9)	$x + 1, y, z$
N1-H3(N1)...O16	2.78(1)	10(6)	$x, y, z + 1$
N6-H1(N6)...O2	2.77(1)	9(9)	$-x + 1, -y + 1, -z + 2$
N8-H1(N8)...O16	2.86(1)	12(6)	$-x + 1, -y, -z + 1$
N8-H2(N8)...O12	2.73(1)	11(7)	$x - 1, y, z$
N9-H1(N9)...O15	2.92(1)	24(7)	$-x + 1, -y + 1, -z + 1$
N9-H2(N9)...O11	2.93(1)	6(6)	$x - 1, y, z$
N11-H1(N11)...O15	2.91(1)	44(7)	x, y, z
N11-H2(N11)...O15	2.83(1)	11(7)	$x - 1, y, z$
N11-H3(N11)...O11	2.81(1)	35(8)	$-x + 1, -y + 1, -z + 1$

Table VI The Torsion Angles (°) that Define the Conformation of the Molecules in DL-Arginine DL-Glutamate Monohydrate and DL-Arginine DL-Aspartate (The Signs of the Torsion Angles Correspond to the L Enantiomer; Estimated Standard Deviations Are Given in Parentheses)

Molecule	ψ'	ψ^2	χ^1	χ^2/χ^{21}	χ^3/χ^{31}	χ^4	χ^5
DL-arginine DL-glutamate monohydrate							
L-arg	-21.9(9)	157.4(6)	-170.0(6)	160.7(6)	166.5(6)	151.6(7)	-3.7(11)
L-glu	-38.7(8)	143.4(6)	175.5(6)	75.0(8)	2.9(9)		
DL-arginine DL-aspartate							
L-arg	-31.2(11)	150.7(9)	54.3(11)	179.1(9)	-77.9(11)	-95.3(12)	13.8(15)
L-asp	19.6(13)	-163.1(9)	71.9(10)	-17.5(12)			

good. No pseudosymmetry, however, exists in the aspartate complex.

Hydrogen Bonding and Molecular Aggregation

The hydrogen-bonding potential of the α -amino and the guanidyl nitrogen atoms in the structures is fully realized, with each proton taking part in a

hydrogen bond. On the other hand, the number of hydrogen bonds accepted by the carboxylate oxygen atoms varies between 3 and 1, with an average value close to 1.8. The water molecule in the glutamate complex accepts one hydrogen bond and is a donor in another. This structure presents a rare case in which a water hydrogen is not involved in a hydrogen bond.

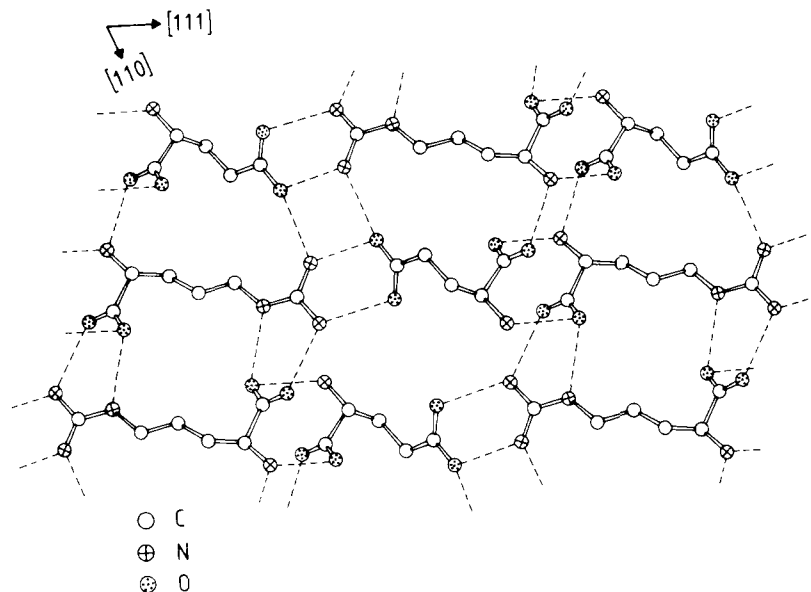


Figure 3. Arrangement of molecules in the $(-1\ 1\ 0)$ plane in DL-arginine DL-glutamate monohydrate.

The molecules in each crystal structure are interconnected by a three-dimensional network of hydrogen bonds. Unlike in the case of the LL and the LD complexes, these networks do not appear at first glance to lend themselves to descriptions in terms of pronounced patterns. However, closer examination reveals that both structures could be described in terms of two-dimensional hydrogen-bonded patterns with comparable features. These two-dimensional patterns, illustrated in Figs. 3 and 4, run parallel to the $(-1, 1, 0)$ and $(-1, 0, 2)$ planes in the glutamate and the aspartate complexes, respectively.

The basic element in the pattern in the glutamate complex is an infinite chain of alternating arginine molecules and glutamate ions arranged along the $[1, 1, 1]$ direction. Two sets of hydrogen bonds, which alternate along the chain, stabilize this arrangement. One set consists of two $N-H \cdots O$ hydrogen bonds, related to each other by the pseudoinversion center referred to earlier, which connect the α -amino and the α -carboxylate groups of an arginine molecule of one chirality and a glutamate ion of opposite chirality. The other set also connects two unlike molecules of opposite chirality through side-chain-side-chain (guanidyl-carboxy-

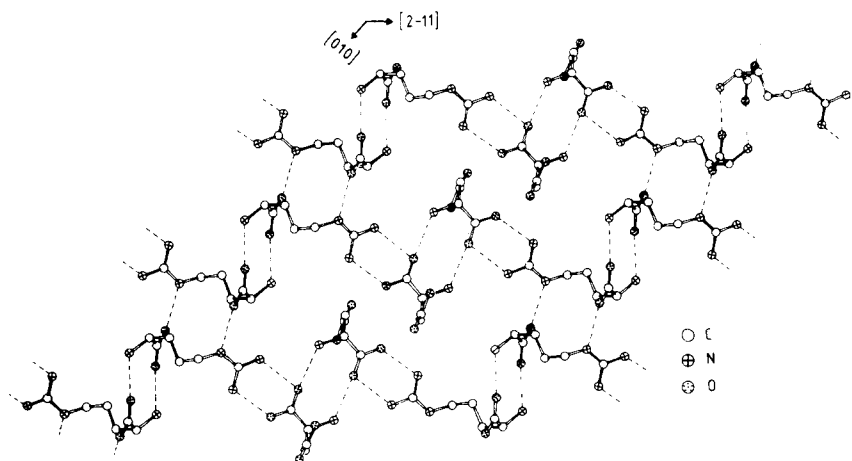


Figure 4. Arrangement of molecules in the $(-1\ 0\ 2)$ plane in DL-arginine DL-aspartate.

late) interactions. Thus L and D molecules alternate along the chain. The infinite chains thus formed are interconnected through hydrogen bonds to form the two-dimensional pattern. On one side of every chain, the interchain hydrogen bonds involve interactions between the guanidyl group of an arginine molecule in one chain and the α -carboxylate group of a centrosymmetrically related arginine molecule in the other chain. These hydrogen bonds can incidentally be considered to give rise to a hydrogen-bonded centrosymmetric arginine dimer. On the other side of the chain, there are side-chain-side-chain (guanidyl- γ -carboxylate) and main-chain-main-chain (α -amino- α -carboxylate) hydrogen bonds. The two-dimensional sheets thus formed are stacked along the crystallographic a axis to form the crystal. There are two N-H — O hydrogen bonds that directly connect adjacent sheets. One involves the α -amino and the α -carboxylate groups of arginine molecules, and the other those of glutamate ions. Both give rise to S2 type of head-to-tail sequences.⁷ It is interesting to note that each head-to-tail sequence involves only molecules of the same chirality. In addition to these hydrogen bonds, adjacent sheets are also linked together through a water bridge.

There are interesting similarities as well as differences between the aggregation patterns in the two complexes. In the aspartate complex also, the basic element of aggregation is a chain of hydrogen-bonded molecules, in this case running parallel to the $[2, -1, 1]$ direction (Fig. 4). Again, the sets of hydrogen bonds that stabilize the chains include those consisting of pairs of hydrogen bonds that connect in a centrosymmetric fashion the α -amino and the α -carboxylate groups of neighboring amino acid molecules. In the aspartate complex, however, the two molecules are of the same type and the center of inversion is crystallographic. Consequently, a pair of arginine molecules and a pair of aspartate ions alternate along the chain. Each pair consists of a L isomer and a D isomer. It may also be noted that the carboxylate oxygen atoms *cis* to the α -amino nitrogen atom is involved in the hydrogen bonds concerned whereas the one *trans* to the amino nitrogen atom is involved in the corresponding hydrogen bond in the glutamate complex. A set of hydrogen bonds involving the guanidyl group of arginine and the α -carboxylate group of the aspartate ion then interconnect the unlike pairs along the chains. Unlike in the case of the glutamate complex, the chain passes through a series of crystallographic centers of inversion. Consequently, the interactions on either side of the chain are

crystallographically related. These interactions again involve hydrogen bonds which give rise to what may be broadly described as dimerization of arginine molecules across centers of inversion, a situation similar to that found in the glutamate complex. However, this dimerization involves one hydrogen bond and its symmetry equivalent in the aspartate complex, whereas it involves two hydrogen bonds and their symmetry equivalents in the glutamate complex. Also, unlike in the case of the glutamate complex, no other hydrogen bonds are involved in interchain interactions in the two-dimensional sheets. The sheets again stack along the shortest cell dimension to form the crystal. The interconnections among the sheets include a hydrogen bond that gives rise to a head-to-tail sequence of type S1 containing arginine molecules of the same chirality. There are four other nonspecific interlayer hydrogen bonds, all of which involve side-chain carboxylate oxygens as acceptors. The donors in these hydrogen bonds are the two α -amino nitrogen atoms and the guanidyl nitrogen atoms N8 and N9.

Specific Interactions Involving Guanidyl Groups

We had earlier demonstrated that the guanidyl group of each arginine molecule has the intrinsic propensity to form two of the four possible types of specific interactions, each involving two hydrogen bonds.³ This potential is fully realized in the glutamate complex. A type A interaction connects the side-chain guanidyl and carboxylate groups in the chain of molecules parallel to the $[1, 1, 1]$ direction (Fig. 3). The second specific interaction, one of type B, is involved in the "dimerization" of the arginine molecule. The aspartate complex, however, contains only one specific interaction. This is of type A and occurs between the guanidyl and the α -carboxylate groups of the aspartate ion in the molecular chain parallel to the $[2, -1, 1]$ direction (Fig. 4).

Effect of Chirality on Molecular Aggregation

The work reported here completes the x-ray analysis of the LL^{23,27} the LD,¹⁴ and the DL-DL complexes of arginine with glutamic and aspartic acids, and it is of interest to compare the aggregation patterns in them. The glutamate and the aspartate complexes qualitatively exhibit the same type of changes when the chirality of the components is systematically altered. However, the planar fea-

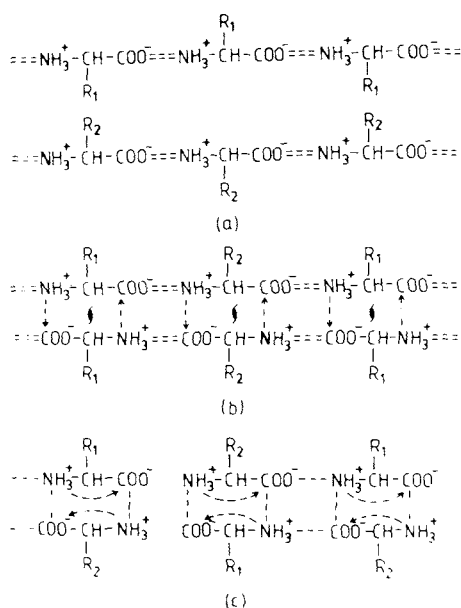


Figure 5. Schematic representation of main-chain interactions in (a) L-arginine-L-glutamate monohydrate (b) L-arginine-D-glutamate trihydrate, and (c) DL-arginine-DL-glutamate monohydrate. Curved broken lines in (c) represent hydrogen bonds perpendicular to the plane of the paper.

tures in the aggregation patterns are much less distorted in the glutamate complexes than in the aspartate complexes, presumably because the difference in length between the side chains of the two component molecules is less pronounced in the former than in the latter. Therefore, the glutamate complexes provide a better set of structures for examining the effect of chirality on molecular aggregation.

Head-to-tail sequences are the most important structural features in the LL and the LD complexes. They also can be considered to define the basic two-dimensional patterns from which the structures are built. The situation is somewhat different in the DL-DL complex. However, two head-to-tail sequences, one involving the arginine molecules and the other glutamate ions exist in the structure. The plane containing these head-to-tail sequences and other main-chain interactions may be considered as equivalent to the planes defined by the head-to-tail sequences in the LL and the LD complexes, for the sake of comparison. The essential features of the aggregation patterns in the glutamate complexes, with special reference to the main-chain atoms, can then be represented schematically, as in Fig. 5.

As can be seen from Fig. 5, the arginine molecules and the glutamate ions aggregate into separate

alternating layers in the LL complex. Each layer is stabilized primarily by head-to-tail sequences. The layers are then interconnected mainly through interactions involving the side-chain atoms. In the LD complex, however, the molecules form double layers. The central core of the double layer consisting of a complex network of head-to-tail sequences is flanked on either side by side chains. Adjacent double layers are then interconnected through water bridges involving side chains. In the DL-DL complex, the main-chain atoms of the two types of molecules are close together as in the LD complex. Two head-to-tail sequences exist, one involving arginine and the other glutamate ions. The unlike molecules of opposite chirality are then interconnected by pairs of hydrogen bonds related to each other by pseudoinversion centers. The side chains point away on either side from the central group of main-chain atoms. It should be emphasized that unlike in the case of the LL and the LD complexes, the interactions involving the main-chain atoms do not by themselves give rise to or promote infinite two-dimensional patterns. As discussed earlier, a natural description of the structure consists of two-dimensional patterns involving main-chain as well as side-chain interactions.

The LL, the LD, and the DL-DL complexes were crystallized under identical conditions using the same solvent as well as precipitant. Therefore the changes in the aggregation patterns should have been caused by requirements arising out of changes in the chirality of the component molecules. Although the changes are very striking, they cannot yet be rationalized in terms of simple steric or other considerations. However, it is interesting to note that the pattern is the simplest in the LL complex with well-separated sheets containing head-to-tail sequences. It becomes very complicated in the LD complex with a pair of interconnected sheets at the core of a double layer. The pattern in the DL-DL complex can no longer be explained primarily in terms of head-to-tail sequences, and its basic elements involve a combination of main-chain and side-chain interactions.

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