Structure of Oligomers of Glycine and ϵ-Aminocaproic Acid as a Model of Nylon 2/6

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ABSTRACT: We have determined the structure of acetyl−(glycyl−ϵ-aminocaproyl)$_2$−NH−propyl by X-ray diffraction methods as a model of nylon 2/6. The structure obtained confirms the tendency of glycine copolyamides to adopt a structure similar to polyglycine II with hydrogen bonds in three different directions. Our results also show that the ϵ-aminocaproyl residue adopts a conformation in which its two terminal peptide groups form hydrogen bonds with an angle of about 120°. This observation might be of interest in order to understand the polymorphism of nylon 6.

Introduction

In our laboratory we have studied several alternating copolymers of glycine and longer ω-amino acids.[1−6] These polyamides are quite different from the conventional nylons,[7,8] since they usually do not crystallize in the α or γ forms, but have a structure related to polyglycine II,[9] with three hydrogen bonding directions. Thus all of them crystallize in a hexagonal cell, as determined by electron diffraction, but depending on the length of the ω-amino acid used, the copolymers tend to crystallize with either a trigonal or hexagonal habit. This difference in behavior has been explained[10] as due to the different orientation of the peptide groups depending on the even or odd number of methylene groups in the ω-amino acid.

Some time ago we crystallized and determined the structure of a model oligomer for nylon 2/3.[11] In view of the interesting results obtained from that model, we decided to study two models for poly(glycyl−ϵ-aminocaproic acid) or in short, nylon 2/6, namely, acetyl−(glycyl−ϵ-aminocaproyl)$_2$−NH−propyl (GAGA), represented in Figure 1, and acetyl−glycyl−ϵ-aminocaproyl−glycyl−NH−propyl (GAG). The structure found for these compounds, while confirming the main features of the 2/*n* polyamides, raises some interesting questions on their detailed organization and on the chirality of the helices formed by these polymers. Furthermore, the structure of the ϵ-aminocaproyl residue is different from that found in the usual conformations[8,12] of nylon 6 and may be of interest to understand the polymorphism[13,14] of this polyamide.

Experimental Section

The oligomers were obtained by the conventional methods of peptide synthesis. A scheme of the synthesis of GAGA is shown in Figure 2. A similar outline was used to obtain GAG. Further details can be found elsewhere.[15]

Crystals suitable for X-ray diffraction were obtained by vapor diffusion in trifluoroethanol/water mixtures. The crystals grew as thin plates with irregular borders. The precession diagram showed a quasi-hexagonal pattern with cell parameters $a = b = 4.9$ Å. The cell parameter c along a normal to the plate was found to be about 29.2 Å for GAGA and 43.6 Å for GAG. All the investigated crystals exhibited a strong mosaic structure, reflected in the arcing of spots in the *h*0*l* and 0*kl* precession diagrams, as shown in Figure 3. In the case of GAG the mosaic structure was so large that no further attempt was made to determine its molecular structure. Attempts to grow more perfect crystals failed in either case.

X-ray data were collected for GAGA at room temperature in the triclinic crystal system using an Enraf-Nonius CAD-4 diffractometer with Cu Kα radiation and a graphite monochromator ($2\theta < 136°$, ω- scanning mode). Three reflections were measured every hour as an intensity control. Intensity data were corrected for Lorentz, polarization, and decay effects, and absorption was disregarded. Cell dimensions are given in Table 1 together with other experimental parameters.

The structure was solved by direct methods using the SHELXS-86 computer program package[16] and refined by a full-matrix least-squares procedure.[17] The E-map revealed all the non-hydrogen atoms except for the terminal C atom of the propyl group. Difference Fourier syntheses calculated after some cycles of isotropic refinement showed one weak peak whose position could be considered as the position of this carbon atom. Only six different sets of anisotropic temperature factors were refined. Thermal parameters for oxygen atoms were 1.3 times the value for the corresponding carbon atoms. Two terminal carbon atoms of the propyl group were refined isotropically. All hydrogen atoms were included at calculated positions and refined with geometrical constraints ("ride model"). Bond length constraints were applied to all bonds. Full-matrix refinement converged to a standard agreement factor $R = 0.163$ for 1030 reflections with $I > 2.5\sigma(I)$. The maximum and minimum heights in the final difference Fourier map were +0.37 and −0.41 e Å^{-3}, respectively. A micro-Vax 2000 computer was used for all the calculations.

The rather poor R factor is probably due to the strong arcing of the reflections which did not allow an accurate determination of the diffracted intensities. Attempts to introduce either solvent molecules or some disorder in the structure failed to improve the R factor. On the other hand, there is no doubt that the general features of the structure determined by us are correct. As shown in Table 1, the number of data used in the calculations (1030 unique reflections) is much larger than what is common in polymer studies with fibers. Furthermore, as will be shown below (Table 2), the conformational angles of the two equivalent subunits of the molecule are all approximately identical in absolute value, without imposing any constraints in the structure determination. The conformational angles also coincide with those found in some related molecules (Table 3).

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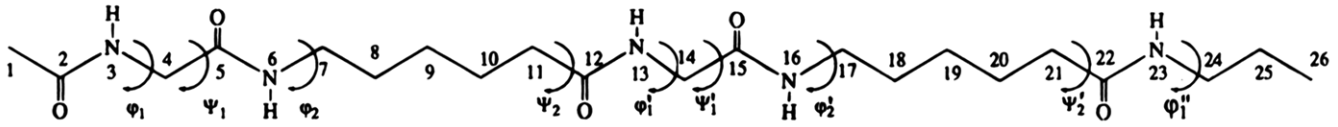

Figure 1. Scheme of the GAGA molecule with atom numbering and main torsion angles.

Table 1. Crystallographic Data

molecular formula	$C_{21}H_{39}O_5N_5$	V (Å^3)	607 (2)
cryst size (mm)	0.2 × 02 × 0.05	Z	1
cryst syst	triclinic	calcd density (g/cm^3)	1.208
space group	$P1$	Cu Kα radiatn	λ = 1.541 78 Å
cell		collected reflcns (2θ < 136°)	2070
a (Å)	4.84 (1)	unique reflcns	2055
b (Å)	4.85 (1)	R(int) = $\Sigma\|F^2 - (F^2)_{mean}\|/\Sigma F^2$	0.089
c (Å)	29.26 (3)	$R(\sigma) = \Sigma\sigma(F^2)/\Sigma F^2$	0.048
α (deg)	86.4 (4)	unique reflcns with $I > 2.5\sigma(I)$	1030
β (deg)	86.1 (6)	no. of refined param	127
γ (deg)	62.4 (3)	R factor	0.163

Table 2. Torsion Angles of GAGA (deg)

C1–C2–N3–C4 (ω_1)	−178	C12–N13–C14–C15 (φ'_1)	−75
O2–C2–N3–C4	7	N13–C14–C15–O15	−24
C2–N3–C4–C5 (φ_1)	69	N13–C14–C15–N16 (ψ'_1)	148
N3–C4–C5–O5	38	C14–C15–N16–C17 (ω'_2)	176
N3–C4–C5–N6 (ψ_1)	−151	O15–C15–N16–C17	−13
C4–C5–N6–C7 (ω_2)	−174	C15–N16–C17–C18 (φ'_2)	−155
O5–C5–N6–C7	−2	N16–C17–C18–C19	179
C5–N6–C7–C8 (φ_2)	163	C17–C18–C19–C20	180
N6–C7–C8–C9	180	C18–C19–C20–C21	−173
C7–C8–C9–C10	176	C19–C20–C21–C22	−179
C8–C9–C10–C11	176	C20–C21–C22–O22	31
C9–C10–C11–C12	178	C20–C21–C22–N23 (ψ'_2)	−158
C10–C11–C12–O12	−26	C21–C22–N23–C24 (ω''_1)	−171
C10–C11–C12–N13 (ψ_2)	153	O22–C22–N23–C24	0
C11–C12–N13–C14 (ω'_1)	177	C22–N23–C24–C25 (φ''_1)	82
O12–C12–N13–C14	−4	N23–C24–C25–C26	−98

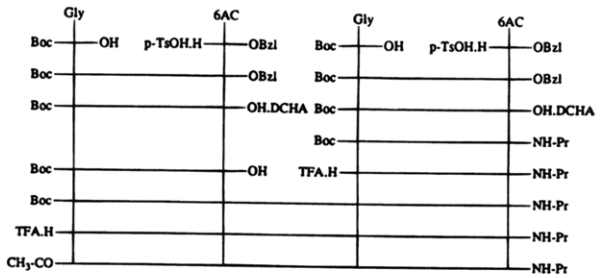

Figure 2. Scheme of the synthesis of GAGA. The abbreviations used are Boc = benzyloxycarbonyl, TFA = trifluoroacetic acid, p-TsOH = *p*-toluenesulfonic acid, Bzl = benzyl, DCHA = dicyclohexylamine, 6AC = 6-aminocaproic acid, and Pr = propyl.

Results and Discussion

A stereopair of the molecule is shown in Figure 4, and the main-chain torsion angles are given in Table 2. Molecules are organized in the unit cell as shown in Figure 5. All molecules are organized in parallel and consecutively within the crystal, so that the whole crystal is polar, with an N-terminal and a C-terminal end. The molecules are kinked approximately at the center. A similar kink is present at the N-terminal glycine residue.

The structure of GAG should be very similar. From precession photographs we determined a pseudohexagonal cell with $a \approx b \approx 4.9$ Å and $c = 43.6$ Å. The values of a and b are identical to those of GAGA. The value of c coincides also if the length of one ϵ-aminocaproic acid unit is substracted and the cell is doubled. Odd reflections $00l$ are present on the meridian, which indicates that the unit cell is probably made by two mirror image molecules of GAG, one on top of the other, but in opposite directions.

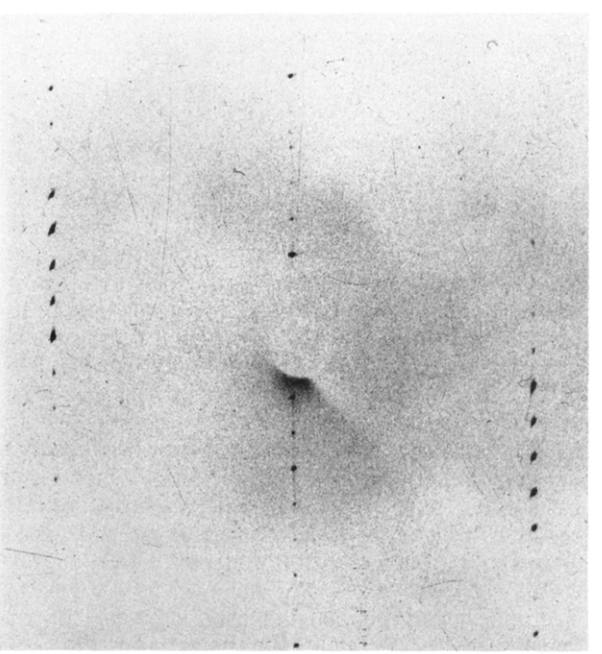

Figure 3. Precession photograph in the $h0l$ plane obtained from one of the GAGA crystals used in structure determination. The mosaic structure of the crystals is obvious from the arcing of the $10l$ row of spots. A variable degree of arcing was found in other precession photographs (hhl, $0kl$ planes).

Inspection of Table 2 shows that the first unit of the molecule (from C1 to N13) is practically an exact mirror image of the second unit of the molecule (from C11 to N23), with all torsion angles with similar values, but with their signs changed. The angle φ''_1 at the end of the molecule is again equal to the φ_1 angle at the start of the molecule. Such organization of the crystal shows

Table 3. Molecular Repeat of Nylon 2/6 According to Different Models

nylon structure	molecular repeat (Å)	crystallographic repeat (Å)
obsd[10]	11.5	69.0
fully extended (α form)[a]	12.1	12.1
γ form[a]	11.7	11.7
2/n model[10]	11.5	69.2
GAGA model	11.2	22.4

[a] Values for the theoretical α and γ forms have been extrapolated from average experimental values for nylon 6: 16.8 Å (γ form) and 17.2 Å (α form).[14] The length of four methylene units (5.1 Å) has been subtracted from these values.

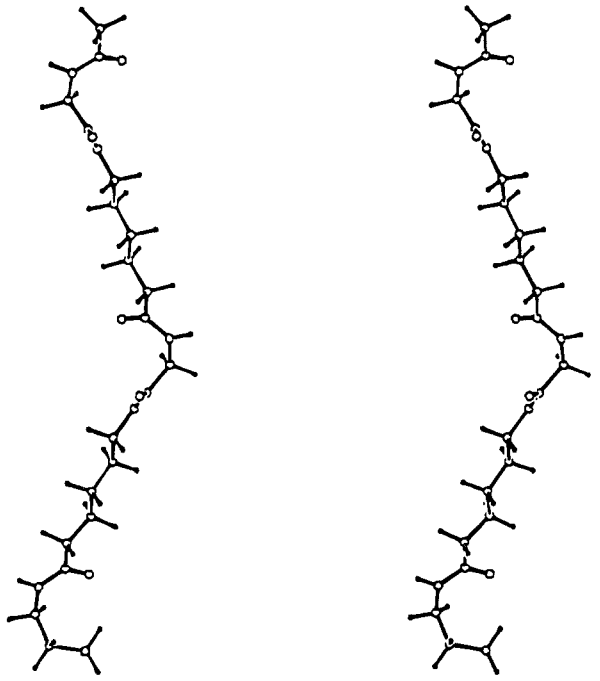

Figure 4. Stereopair of the GAGA molecule.

that it is chiral, since all molecules in an individual crystal have the same conformation.

The structure of GAGA may be transformed into a polymer structure by placing molecules like the one shown in Figure 4 one on top of the other. An oblique view of the crystal illustrates how such a conformation will appear on projection, as shown in Figure 6. However, such a conformation does not appear to coincide with that present in nylon 2/6. In the polymer it is necessary to pack chains running in opposite directions, since the polymer forms lamellar crystals which require chain folding. In our model studies we have not found it possible to pack polymer chains in an antiparallel fashion with a conformation similar to that found in GAGA.

A comparison of the model suggested by us[10] for nylon 2/6 with a model derived from the structure of GAGA is shown in Figure 7. The latter model is inadequate for several reasons:

(a) Antiparallel packing does not appear to be possible, as mentioned above.

(b) The unit cell would not be truly hexagonal, as is experimentally observed.[2]

(c) The molecular repeat would be shorter than the experimentally observed value, as shown in Table 3.

The structure of GAGA retains the main conformational features of polyamides derived from glycine, namely, its conformational angles and the tendency to form hydrogen bonds in three different directions. For

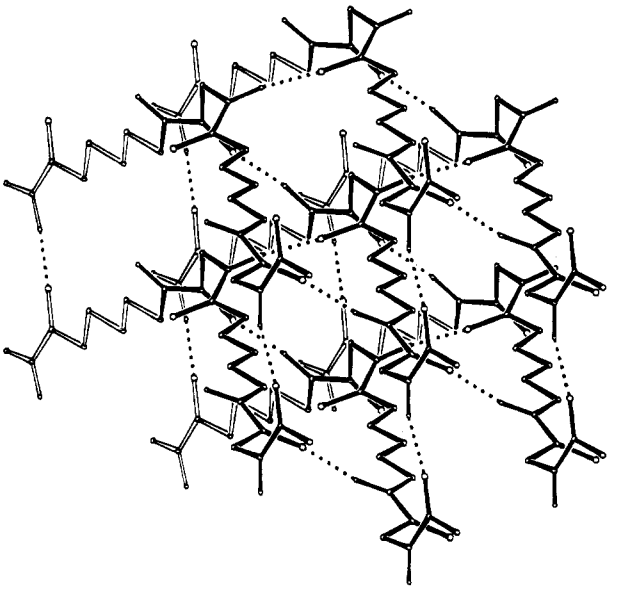

Figure 5. Projection of several unit cells of GAGA onto the *ab* plane. The white part of the molecules corresponds to atoms 23 to 17 and lies below the black part of the molecule (atoms 17 to 1). The propyl group (atoms 24 to 26) is not represented.

Table 4. Selected Torsion Angles (deg) of Different Compounds[a]

	Gly unit		ω-amino acid unit		
	φ	ψ	φ′	ψ′	ref
GAGA	72	−150	159	156	this work
nylon 2/6	88	−152	106	−106	10
(Gly-β-Ala)$_2$	71	−150	172	−167	11
nylon 2/3	77	−154	117	−123	10
nylon 6 (γ form)			115	−115	12

[a] The values given for the model compounds are the average of the values determined for the individual monomer units in the molecule.

comparison, we present in Table 4 the main conformational angles of nylons 2/3 and 2/6 calculated by Bella et al.[10] and the equivalent angles in the oligomers. The conformation of glycine is the same in all cases and coincides with its conformation in polyglycine II[9] ($\varphi = 77°$, $\psi = -145°$). Such glycine conformation determines the orientation of the peptide groups which form hydrogen bonds in three different directions in space. It is striking that in all polymers and oligomers studied by us glycine maintains the conformational angles typical for polyglycine II, as shown in Table 4.

On the other hand, the φ' and ψ' angles do not coincide. In the case of the polymers, φ' and ψ' have values close to +110° and −110° in both cases. These angles are similar to those found in the γ form of polyamides,[12,18] but the resulting structure is different due to the presence of the glycine residue. They are fully compatible with straight polymer chains packed in an antiparallel direction and with hydrogen bonds in three directions of space.

The model compounds have φ' and ψ' values very close to the trans conformation, a fact which originates the kinked appearance of the molecules, as shown in Figure 4. However, there is a fundamental difference between both cases. The Gly-β-Ala model has all units with equal torsion angles and thus a helical conformation is generated, whereas GAGA has one unit with the angles given in Table 3 and the next unit with all angles

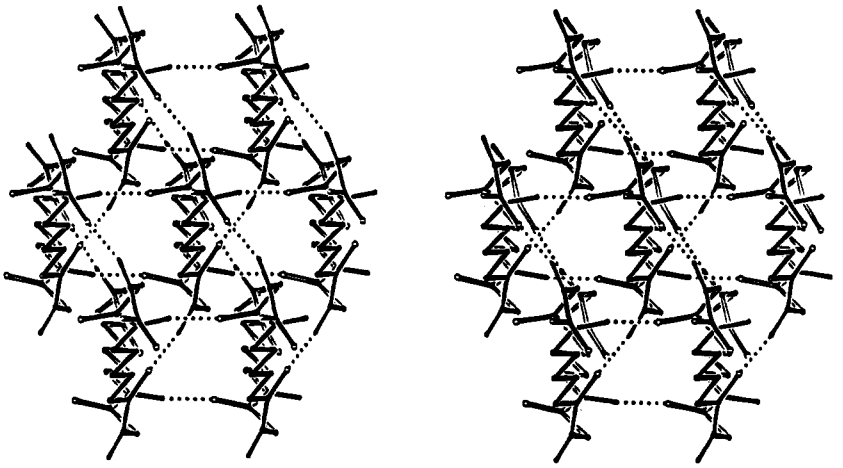

Figure 6. Oblique stereoview of one molecule of GAGA and its six hydrogen-bonded neighbors.

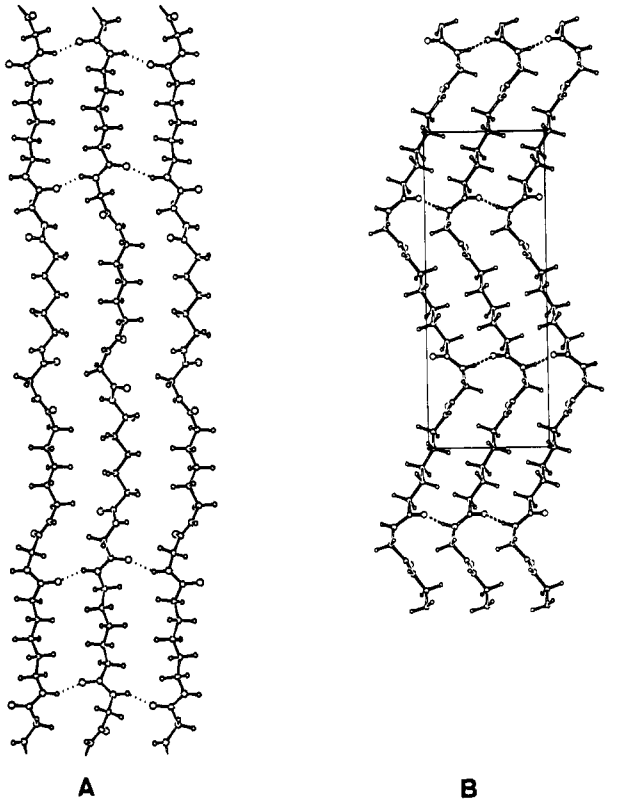

Figure 7. (A) Hexagonal model of nylon 2/6 (from Bella et al.[10]), with antiparallel chains and six monomer units per crystallographic repeat. (B) Polymer conformation derived from the structure of GAGA. The thin lines indicate an eventual unit cell with $a = 5.02$ Å, $b = 8.26$ Å, $c = 22.40$ Å, $\beta = 109.2°$, and space group *Cc*. It contains two molecular repeats along the polymer axis. The experimental data available[2] on nylon 2/6 favor the model shown in A, as discussed in the text.

identical, but with signs changed. This alternation of angles would generate a polymer with a zigzag conformation, as shown in Figure 7B. It will also generate a structure with three hydrogen bonding directions, as shown in Figure 6, although there would be twice as many hydrogen bonds in one direction (horizontal in Figure 6) than in the other two.

It is worth noting that the GAGA oligomer and the previously studied Gly-β-Ala model[11] both have their molecules in a parallel orientation in the crystal, whereas the corresponding polymers have an antiparallel orientation, a fact which requires changes in the molecular conformation, as shown in Figure 7 and in Table 4. It is not clear whether such a polymer conformation either is its intrinsic lowest energy form or is required by folding in lamellar crystals. In the latter case it is conceivable that structural differences might appear between lamellar crystals, which will be forced to have a conformation and hydrogen bond system compatible with chain folding, and extended polymer chains in oriented fibers, which could have a parallel organization. Such eventual structural changes which would depend on sample preparation deserve further study.

The conformation of the aminocaproic residue in GAGA also shows some interesting features. As shown in Table 4, the angles φ' and ψ' which connect the methylene chain with the peptide unit both have the same sign, whereas in all other cases both angles have similar values but an opposite sign. As a result, the aminocaproic unit induces a change in the orientation of hydrogen bonding in its two terminal peptide groups, whereas in all other cases shown in the table both groups have the same hydrogen bond orientation. This fact is also apparent in Figure 7.

It is striking that a small deviation (20–25°) from the trans conformation in the torsion angles φ' and ψ' results in two different orientations of the attached peptide groups, with hydrogen bonding directions at 120° from each other. It is interesting to speculate whether such a conformation of ϵ-aminocaproic acid could be present in its homopolymer, nylon 6. Parker and Lindenmeyer[14] showed that, in the latter nylon, metastable forms are often found with a structure intermediate between the α and γ forms. Murthy[19] in fact has suggested that hydrogen bonds in different directions may appear in nylon 6 metastable structures. In such cases a conformation similar to that found in GAGA could be present.

Conclusion

The model compound described here confirms the tendency of glycine residues to acquire a conformation similar to that found in polyglycine II. As a result the polyamide copolymers adopt conformations related to polyglycine II which deviate from the usual α and γ sheet structures of nylons. On the other hand, the parallel packing of GAGA does not appear to be compatible with a folded polymer structure, so that the conformational angles φ' and ψ' of the aminocaproic unit are expected to be different in the polymer, as suggested

by Bella et al.[10] The conformation of the aminocaproic unit found here, with two hydrogen bond directions, might also be present in some forms of nylon 6.

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Supplementary Material Available: Tables of fractional atomic coordinates and equivalent isotropic thermal parameters, thermal parameters U_{ij}, bond lengths and angles, and interatomic distances and bond angles associated with intramolecular hydrogen bonds N–H···O and a listing of mean plane calculation equations (5 pages). Ordering information is given on any current masthead page.

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