TRABAJO DE FIN DE GRADO

Cristalización y caracterización estructural de un material molecular: el ácido butilmalónico.

Crystallization and structural characterization of a molecular material: the butylmalonic acid.

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ABSTRACT

Este Trabajo de Fin de Grado tiene como objetivo fundamental la preparación y caracterización estructural y espectroscópica de tres compuestos moleculares orgánicos de estructura cristalina desconocida, todos ellos derivados del ácido malónico ($C_3H_4O_4$). La importancia de utilizar derivados de este ácido reside en el hecho de que mediante la realización de modificaciones al propio ligando malonato es posible obtener cierto control sobre el empaquetamiento cristalino y, como consecuencia, sobre las propiedades físicas y químicas del material resultante.

Para alcanzar dicho objetivo, se lleva a cabo la cristalización de los compuestos y, posteriormente, el análisis de la difracción que presentan al ser bombardeados con un haz de rayos-X. En concreto, los compuestos estudiados son el ácido butilmalónico ($C_7H_{12}O_4$), el ácido 3-thiophenemalónico ($C_7H_6O_4S$) y el ácido 1,1-cyclopropanedicarboxílico ($C_5H_6O_4$).

Un cristal es un sistema en el que los átomos se encuentran ordenados manteniendo una cierta periodicidad que se prolonga en todo el espacio tridimensional. Existen distintas técnicas que permiten obtener cristales de composiciones químicas perfectamente definidas y de gran calidad. En particular, en este proyecto se ha llevado a cabo la síntesis cristalina por evaporación lenta, dado que en diversas publicaciones en que se trabaja con este tipo de compuestos orgánicos se establece como el método más adecuado para la adquisición de cristales válidos para difracción de rayos X. Los cristales resultantes han sido incoloros para los 3 compuestos, sin forma definida en el caso del ácido butilmalónico (I) y con forma de aguja los correspondientes a los ácidos 3-thiophenemalónico (II) y 1,1-cyclopropanedicarboxílico (III).

El proceso de caracterización comienza una vez se han conseguido cristales del tamaño y la calidad adecuados, imprescindibles para la determinación de cualquier estructura cristalina. Por un lado, se mide la difracción que presentan las muestras cristalinas, obteniéndose así información detallada acerca de la ordenación de las moléculas en el cristal. Por otro lado, se analiza la absorción que presentan en el rango infrarrojo del espectro electromagnético (IR), que proporciona información complementaria acerca de la presencia o ausencia de ciertos grupos funcionales.

Los enlaces intermoleculares que presentan las tres estructuras en su empaquetamiento cristalino son puentes de hidrógeno. En el ácido butilmalónico, de grupo espacial P-1 y sistema cristalino triclínico, cada molécula se une a otras dos formando cadenas paralelas unidimensionales en zigzag en la dirección del eje cristalográfico b. En el ácido 3-thiophenemalónico, de grupo espacial $P2_1$ y sistema cristalino monoclínico, una molécula se une a otras cuatro diferentes por enlaces de hidrógeno, por lo que empaquetamiento tiene lugar a lo largo de capas bidimensionales. Por último, el ácido 1,1-ciclopropanedicarboxílico, también triclínico P-1, muestra un empaquetamiento en forma de cadenas unidimensionales paralelas en la dirección del eje b. En particular, este último material presenta, además, enlaces de hidrógeno intramoleculares.

El conocimiento detallado de la estructura cristalina de compuestos orgánicos moleculares como los estudiados hace posible su utilización en estudios de ingeniería cristalina, en los que se crean nuevos materiales usando estos compuestos como ligandos o conectores con el fin de comprender cómo las propiedades intrínsecas de las moléculas afectan a las propiedades, tanto físicas como químicas, del material.

1. INTRODUCTION

En esta primera sección del trabajo se detallan la motivación del proyecto y los objetivos a alcanzar, esto es, por qué son importantes el correcto desarrollo del mismo y los resultados que se derivan de él. En el estado del arte se incluye el marco teórico que rodea el tema principal del trabajo: la ingeniería cristalina. Asimismo, se aclara la relevancia que poseen el ácido malónico y sus derivados en relación a dicha disciplina.

1.1. Motivation and objectives

A crystal is a very precise and specific type of molecular assembly, and *crystal engineering* shows us how to bring molecules together exactly as we need. In this subject, which can also be called crystal synthesis, one attempts to design crystal structures by using the molecule as a building block [1]. It is a matter of great scope and application that has developed by a coming together of thought streams from many other subjects [2], notably crystallography and chemistry.

In chemistry, a molecule is a set of at least two atoms held together through strong chemical bonds (covalent, coordination or ionic bonds). Therefore, a molecular material is build up from an arrangement of molecules. These materials can be classified into two groups, the organic and the inorganic [3]. In particular, organic molecular materials are those which contain at least one C-H or C-C bond, and one of the great advantages of working with them is the fact that their properties can change totally due to subtle changes in molecular structure.

Molecular crystals, defined as the crystalline form of any chemical substance that exists as molecules, have interesting physical and chemical properties that are not associated with other categories of crystalline substances. These properties are connected to, and closely related to, their internal periodic structures. These internal structures are known as *crystal structures* and are of outstanding importance in crystal engineering [2]. So, there is a need to be able to design particular crystal structures, wherein molecules are assembled in particular ways.

The main purpose of this project consists on the resolution of the crystal structure of several substituted malonic acids after their previous crystallization. These molecular compounds are, specifically: butylmalonic acid (I), 3-thiophenemalonic acid (II) and 1,1-cyclopropanedicarboxylic acid (III). The conformation and molecular structure of these acids in the crystalline state are studied by three-dimensional X-ray analysis of single crystals. Thus, crystal synthesis and X-ray diffraction analysis are also significant objectives to achieve.

The relevance of the detailed study of their crystal structures dwells in the subsequent use of these compounds as ligands or *building blocks* in crystal engineering, which leads to the understanding of how intrinsic properties of the molecules affect directly the bulk physical and chemical properties.

1.2. State of the art

1.2.1. Crystal engineering

The term *crystal engineering* was first used in 1955 by Ray Pepinsky, at a meeting of the American Physical Society, where he stated that "crystallization of organic ions with metal-containing complex ions of suitable sizes, charges and solubilities results in structures with cells and symmetries determined chiefly by packing of complex ions. These cells and symmetries are to a good extent controllable: hence crystals with advantageous properties can be *engineered*". However, it was Gerhard Schmidt who introduced this term into the chemical literature in 1971, when he and his colleagues in the Weizmann Institute of Science realized the power and significance of X-ray crystallography in organic chemistry [2].

Crystal engineering, as defined by Gautam R. Desiraju in 1989, consists on the "understanding of intermolecular interactions in the context of crystal packing and the utilization of such understanding in the design of new solids with desired physical and chemical properties" [1]. Therefore, it is all about the systematics of crystal construction.

In the same way that molecules are built from atoms with covalent bonds, crystals can be said to be built up with molecules using intermolecular interactions [2]. Hydrogen bonding, due to its strong and directional nature, is the master key in crystal engineering, supramolecular chemistry, and biological recognition. On this point, carboxylate

molecular crystals have been of interest because of the presence of this kind of intermolecular interaction [4]. At its most basic level, crystal engineering applied to the realm of molecular crystals seeks an understanding of the nature and structural implications of intermolecular forces in crystals [5].

Crystallography is an important experimental technique in this subject because it deals with diffraction, and crystals diffract beams of X-rays, neutrons and electrons. The internal structure of a crystal can be imaged with X-ray diffraction. Analysis cannot be performed on non-crystalline materials, since these amorphous substances contain only short-range order or random ordered atoms [6]. When the domains of the ordered, periodic regions of a crystal are sufficiently large, we have a single crystal. Single crystals may be examined with monochromatic X-rays and the diffraction patterns that are obtained are analyzed to get a direct image of the atomic positions in the crystal [2].

Supramolecular chemistry is the chemistry of the intermolecular bond and it is based on the theme of mutual recognition of molecules. Rather than working forwards from the reactant to the product, one works backwards from the product to the reactant. This strategy is called *retrosynthesis* and it involves the analysis of the product in terms of the bond connections that it contains. It is a remarkably powerful technique in organic synthesis [2].

Supramolecular synthons are structural units within supermolecules which can be formed and/or assembled by known or conceivable synthetic operations involving intermolecular interactions [7]. They are patterns of interacting groups and functionalities and may repeat in other crystal structures composed of molecules that contain similar functional groups. So, synthons that are made up of strong and/or directional interactions are more useful in crystal engineering strategies (Figure 1) [2].

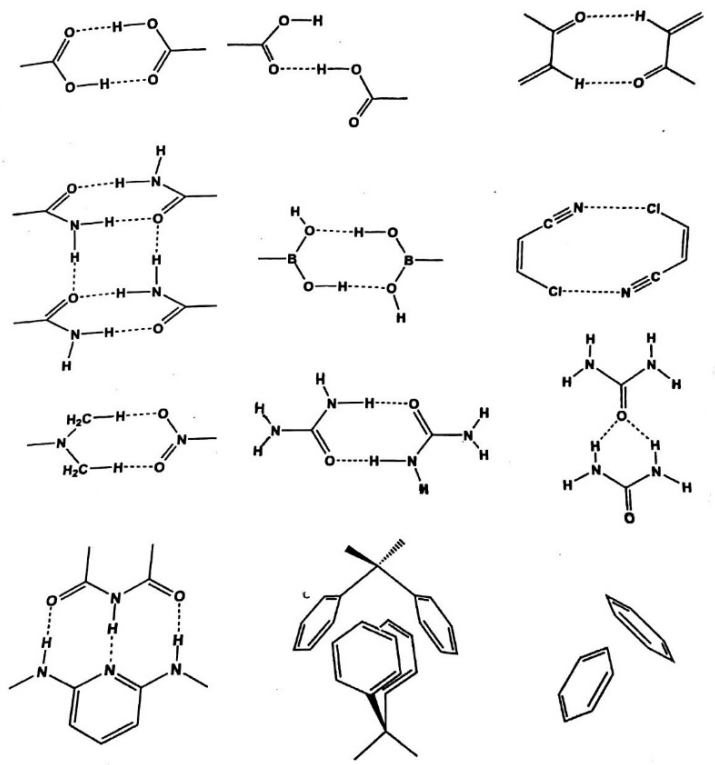


Figure 1: Some commonly used synthons: a few functional groups held together by strong and fairly directional interactions.

A synthon is more useful if it occurs more frequently in a given group of compounds (this has to do with the directionality and strength of the intermolecular interactions involved) and if its formation is more specific [2]. In this regard, the probability of a particular synthon in the crystal structure of a molecule that contains the requisite functional groups is of great significance.

1.2.2. Malonic acid

1,3-Propanedioic acid (commonly known as malonic acid) is a dicarboxylic acid with structure $CH_2(COOH)_2$. This acid, as well as its derivatives, is used as a chemical building block in order to produce many valuable compounds [8]. It is well known in coordination chemistry because of the versatility of its fully deprotonated form as a ligand towards metal ions [9]. The appropriate selection of the organic linker together with a rational synthetic route can be used to modulate structural diversity. Among the different organic ligands, those containing carboxylate groups are often selected due to their

abundant coordination modes, which allow the occurrence of different structural topologies, together with the ability of the carboxylate group to act as a hydrogen-bond acceptor and/or donor, which can help to stabilize the crystal structure [10].

The carboxylate group is a highly versatile ligand because, in addition to its monodentate and chelating coordination modes, it can adopt *syn–syn*, *anty–syn* and *anti–anti* conformations when acting as a bridge between metal ions (Figure 2) [2]. Carboxylate bridges are able to mediate ferro- or antiferromagnetic interactions and it is well known that carboxylate ligands provide robustness to the structure [11].

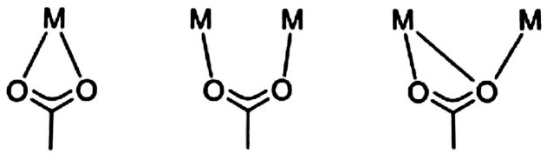


Figure 2: Coordination modes for carboxylate bridged ions showing *bisdentate, bis-monodentate* and *bisdentate monodentate* conformations (left to right).

A survey of the Cambridge Structural Database (CSD) shows that around a third of all carboxylic acids form carboxyl dimers. It appears that carboxyl groups make hydrogen bonds with each other not only to give dimers but also catemers (infinite O-H···O linear arrays). Catemers are not as common as dimers but they are observed in some rather common and well-known acids like acetic acid [2].

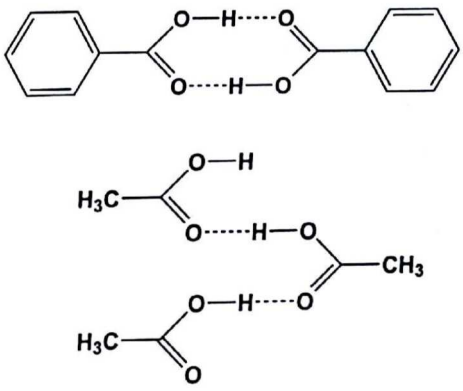
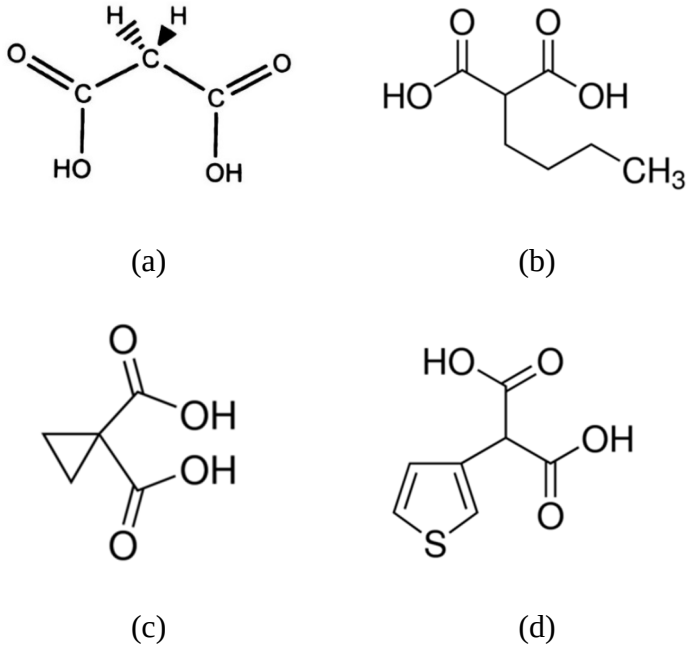


Figure 3: Dimer (top) and catemer (bottom) patterns in carboxylic acids.

Carboxylic acids are one of the most commonly used functional groups in crystal engineering because they generally form robust architectures via O-H···O hydrogen-bonded dimers [12]. The way in which the hydrogen bond motif changes in a particular system could subtly depend on the molecular structure. The final topology of molecules depends on the location of the carboxyl groups in the molecule, which assemble during crystallization to form the synthon.

When designing molecular networks, not only is important to take into account local interactions, or supramolecular synthons, but also to appreciate the whole three-dimensional structure of a crystal. At this respect, modifications of the malonic acid can provide some degree of control over the intermolecular interactions, which guide the arrangement of the constituent building blocks of a material and, consequently, are responsible for the physical properties of the designed crystal [9]. The substitution of one of the hydrogen atoms of the methylene group of the malonic acid for different functional groups has influence over the synthesis process and modifies the structural behaviour of the malonic acid (Figure 4).



(a) (b)

(c) (d)

Figure 4: Substituted malonate ligands: (a) malonic acid, (b) butylmalonic acid, (c) 1,1-cyclopropanedicarboxylic acid and (d) 3-thiophenemalonic acid.

2. METHODOLOGY AND EXPERIMENTAL PROCEDURE

En esta segunda sección se establecen los métodos experimentales empleados en el desarrollo del trabajo, se describe la teoría que hay detrás de ellos y se explica la razón de su elección, así como de su trascendencia. Las muestras a someter a difracción de rayos X son previamente preparadas por una de las técnicas de cristalización más conocidas: evaporación lenta del solvente. Tras la difracción, los datos cristalográficos obtenidos son resueltos y refinados mediante la utilización de software específico.

This project focuses on the synthesis and characterization of the three molecular materials yet mentioned in order to understand as much as possible their crystal structure or molecular composition. In this section, a brief theoretical background and the description of the crystallization and characterization methods used in this work are included.

The first step when studying any new molecular material, the crystal structure determination, is achieved through diffraction techniques using high-quality crystals. The appropriate choice of the crystallization method enables the control of parameters such as the homogeneity of the molecular distribution, the size of the crystal or the presence of impurities confined in the crystal, which allows getting better quality crystals.

Once the crystalline material has been prepared and crystals of enough quality have been grown, so as to obtain detailed information about the atomic arrangement within the solid, X-ray diffraction is carried out. Additional information about the vibrational modes of the bonds that form the solid is provided by infrared spectroscopy.

2.1. Synthesis and crystal growth method

Producing good quality crystals of a suitable size is the first and most important step in determining any crystal structure. Crystals are solids in which atoms are arranged regularly in a space lattice with specific geometrical symmetry elements. Thus, crystallization is the process of arranging atoms or molecules that are immersed in a fluid or solution into an ordered solid state.

Crystalline solids are built through nucleation and crystal growth. In nucleation, spontaneously or induced by vibrations, nanometric clusters are formed by aggregation of the molecules dispersed in a solvent [13]. When reaching a critical size, governed by growing conditions such as temperature or supersaturation, the clusters become stable. Slow changes on the concentration in the nucleation area enable the acquirement of good quality crystals. The greater the rate at which molecules arrive at the surface, the less time they have to orient themselves in relation to molecules already there: random accretion is more likely, leading to crystals which are twinned or disordered [14].

Even though several techniques can be carried out in order to obtain good quality crystals (liquid diffusion, gel technique, hydrothermal synthesis), single crystals of the reagents under consideration were obtained by slow evaporation at room temperature due to their soluble character and the results achieved in crystal synthesis of similar organic materials [15, 16]. This technique consists on the slow evaporation of the solvent or solvent mixture in which the organic compound is dissolved. It is vital to remember that the quality of the crystal from which diffraction data are acquired is generally the main determinant of the final quality of the structure [14].

The compounds employed for all the syntheses were obtained from commercial sources and used without further purification. To begin with, a solubility test is performed: a small amount of each compound is dissolved in several solvents easily found in the laboratory, such as water (H_2O), acetone, ethanol (EtOH), methanol (MeOH), dimethylformamide (DMF), acetonitrile and tetrahydrofuran (THF).

Supersaturation is the driving force of the crystallization: a saturated solution is prepared by dissolving the desired reagents into the selected solvent, which is then placed in a beaker. By partially covering the beaker with a film layer and making small holes in it, evaporation is allowed. This vessel is finally stored at the desired temperature, taking care to disturb the experiment as little as possible. A very quick precipitation of the material should be avoided in order to get a small number of relatively large single crystals instead of microcrystalline or virtually amorphous products that are useless for conventional single crystal work. To this end crystals have been grown slowly, taking from a few days to weeks depending on the solvent employed. The crystals get bigger as the solution becomes more concentrated and it is important to harvest them before all of

the solvent has evaporated. It is therefore essential not to let the solution dry out, as crystals could become encrusted and may not remain single or be degraded by loss of solvent of crystallization.

Once crystals have appeared there are some steps to follow in order to figure out whether they are suitable for data collection. Visual examination under a microscope can identify unsuitable crystals in a few minutes. First of all, looking at the crystals in normal light allows to determine if they are well-shaped, curved or deformed. Secondly, since most crystals in a typical sample will transmit polarized light, with the analyzer component of the polarizing attachment in, turning the microscope stage until the crystal turns dark will indicate its quality. Any crystal that does not extinguish completely is not single but an aggregate of smaller crystals and can be immediately rejected [14]. Cracks, dislocations and even twinned crystals can be clearly seen under the polarized light.

2.2. X-ray crystallographic data collection and refinement

X-ray radiation is a form of electromagnetic radiation with energies ranging from 100 eV to 100 KeV. For diffraction applications, due to their penetrating ability, only short wavelength X-rays are used. Since their wavelength is comparable to the size of atoms, energetic X-rays are ideally suited for exploring the structural arrangement of atoms and molecules in a wide range of materials: they can penetrate deep into them to provide information about their inner structure.

The phenomenon of diffraction is exhibited when a wave is scattered by an obstacle or a slit in constructive interference. X-ray diffraction is described as the interference of waves according to the Huygens Fresnel principle and it allows the determination of the atomic and molecular structure of a crystal [17]. When a wavefront of X-rays strikes an atom, the electrons in that atom interact with the incident radiation and immediately re-emit it, normally without change of wavelength, as a spherical wavefront (ideal situation). In a crystal, due to the interaction between the X-ray incident beam and the electron density, the beam is diffracted into many specific directions. The diffracted radiation can be collected as well-defined reflections if the sample consists in a single crystal, or as a succession of concentric circles if the sample is polycrystalline.

A crystal is built up of an infinite number of tiny unit cells which are stacked together in a three-dimensional lattice by simple translation. Each of the unit cells is identical to all others and the symmetry and shape of the whole crystal depends on the symmetry of that cell [18]. Every diffracted beam, or reflection, is associated with a set of regularly spaced sheets running through the crystal, passing through the center of the atoms of the crystal lattice. The orientation of a particular set of sheets is identified by its Miller indices (h k l) and their spacing by the distance d (Figure 5). X-ray crystallography is used to measure the intensities and angles of these reflections in order to reproduce a three-dimensional model of the atomic distribution. As a consequence, the structural features of the material under consideration can be established from the electron density located between the atoms.

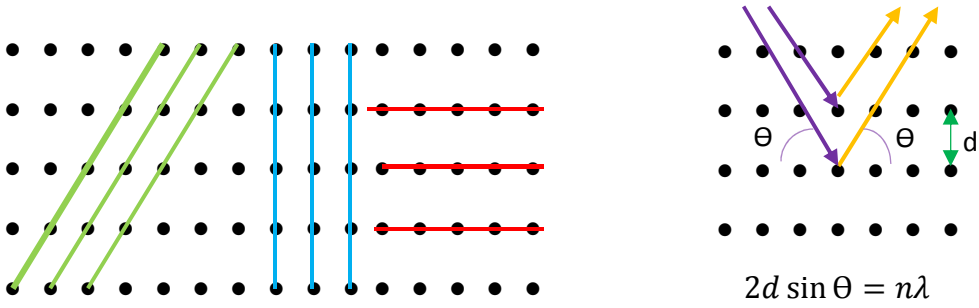


Figure 5: Lattice planes (left) and Bragg's Law (right), the condition for diffraction to occur, where d is the inter-plane distance, n the order of the diffraction peak and Θ the scattering angle.

The Bragg law describes a model on which the incoming X-rays are mirror-like scattered from each plane, thus every X-rays scattered from adjacent planes interfere constructively when the angle Θ between the plane and the X-ray results in a path-length difference that is an integer multiple n of the X-ray wavelength λ:

$$2d \sin \Theta = n\lambda \tag{1}$$

The mesurement of the unit cell parameters and the space group for a given crystal requires the index of the diffracted reflections. A reflection is indexed when its reciprocal lattice vector components (Miller indices) have been identified from the known λ and the

scattering angle 2Θ. The Bragg's law (1) does not interpret the relative intensities of the reflections and it is then not possible to solve the arrangement of atoms within the unit cell. For this reason, data need to be integrated and scaled. For each reflection, the integration of multiple intensity data is accomplished to determine a unique intensity value (I) for each reflection (hkl) and its corresponding standard deviation (σI). From the integrated intensities, structure factors and their deviation can be calculated. The structure factor F_{hkl} is a mathematical function which describes the amplitude and phase of a wave diffracted from crystal lattice planes characterized by Miller indices h, k, l, and it may be expressed as:

$$F_{hkl} = F_{hkl} \exp(i\alpha_{hkl}) =$$

$$= \sum_j f_j \exp\left[2\pi\left(hx_j + ky_j + lz_j\right)\right] =$$

$$= \sum_j f_j \cos\left[2\pi\left(hx_j + ky_j + lz_j\right)\right] + i \sum_j f_j \sin\left[2\pi\left(hx_j + ky_j + lz_j\right)\right] =$$

$$= A_{hkl} + iB_{hkl} \qquad (2)$$

The sum in (2) is over all atoms in the unit cell, x_j, y_j, z_j are the positional coordinates of the jth atom, f_j is the scattering factor of the jth atom, and α_{hkl} is the phase of the diffracted beam. The atomic factor, f_j, is a measure of the scattering amplitude of a wave by an isolated atom and it depends on the nature of the incident radiation. For X-ray radiation the atomic form factor shows a dependency with the 2Θ [9].

Single crystals of the three molecular compounds were mounted on an Agilent SuperNova X-ray diffractometer with Cu Kα radiation (λ=1.54184), located in the SEGAI (Servicio General de Apoyo a la Investigación) at University of La Laguna (Figure 6).

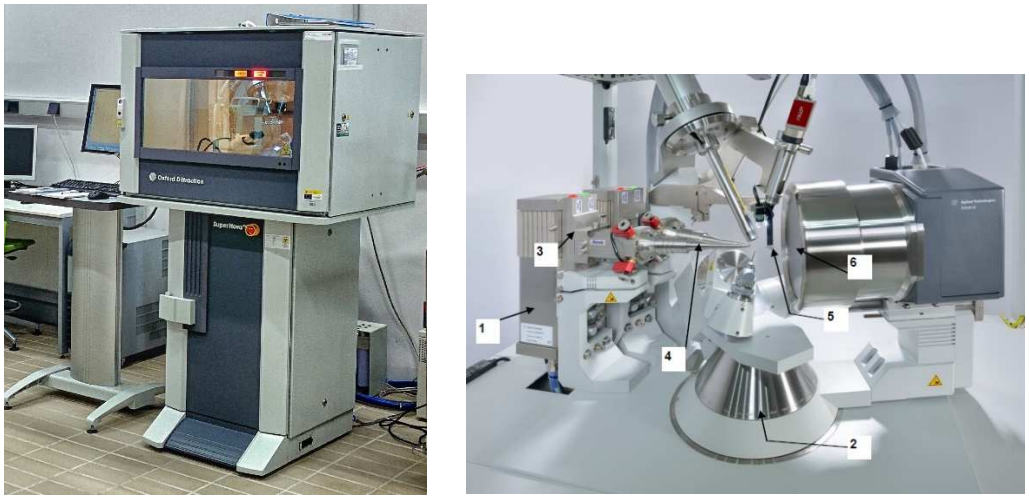


Figure 6: SuperNova diffractometer at SEGAI (left) and general view of the X-ray set up (right) with X-ray tube (1), Kappa goniometer (2), X-ray shutter (3), collimator (4), beamstop (5) and Beryllium window (6) [19].

The X-rays are generated by a dual micro-focus sealed tube, powered by the high voltage X-ray generator that works with Cu and Mo metal targets. The X-ray optics consist of a high speed shutter placed next to the tube shield, X-ray focusing optics and a collimator for refining the incident beam. The X-rays enter the CCD area detector through a Be window to the vacuum-sealed detector unit and X-ray photons are transformed to light, which is conducted towards the CCD chip and digitalized [19].

The structures were solved by direct methods and refined with a full-matrix least-squares technique on F^2 using the SHELXS [20] program included in the OLEX2 [21] software package. In general, all non-hydrogen atoms were placed geometrically and refined anisotropically. The hydrogen atoms were usually located from Fourier differences but when it has not been possible, they were positioned geometrically. The final geometrical calculations and graphical manipulations were carried out with DIAMOND [22] program.

2.3. Spectroscopic characterization

Infrared (IR) spectroscopy deals with the infrared region of the electromagnetic spectrum. The absorption showed by a material at this range of the electromagnetic radiation (700 nm - 1 mm) provides information relative to the presence or absence of certain functional groups.

The IR spectra of the crystals were recorded using the spectrometer located in the X-ray and Molecular Materials Laboratory at University of La Laguna. They are used as supplementary characterization for the crystallized compounds, which must be grinded into a powder before taking any spectroscopy measurement. This technique does not damage the sample, takes just a few minutes and provides useful information about the different bonding modes involved in the conformation of the crystal.

3. RESULTS AND DISCUSSION

A continuación se presentan los resultados a los que se ha llegado tras la resolución y el refinamiento de las estructuras cristalinas obtenidas por difracción de rayos X. Esta sección recoge una descripción detallada de la estructura de cada compuesto y una discusión de los aspectos más interesantes que presentan desde un punto de vista global.

In this section, the different crystal structures solved and refined are exposed and described, as well as the results concerning to the crystal packing and the spectroscopic characterization. A discussion about these results and an estimation of similarities and differences between them are also included.

3.1. Description of the crystal structures

As noted in the preceding section, X-ray quality crystals of the three reagents were synthesized by slow evaporation at room temperature. After the data collection and cell refinement, butylmalonic acid (I) and 1,1-cyclopropanedicarboxylic acid (III) are found to crystallize in triclinic P-1. On the other hand, 3-thiophenemalonic acid (II) crystallizes in monoclinic $P2_1$. Data collection parameters are summarized in Table 1.

	I	**II**	**III**
Crystal data			
Formula	$C_7H_{12}O_4$	$C_7H_6O_4S$	$C_5H_6O_4$
Formula weight	160.170		
Crystal system	Triclinic	Monoclinic	Triclinic
Space group	P-1	$P2_1/b$	P-1
a (Å)	5.1972(3)	6.9439(3)	5.2801(2)
b (Å)	8.3161(5)	5.8979(2)	9.3325(3)
c (Å)	10.0272(6)	9.1859(3)	12.0347(6)
α (°)	79.831(5)		87.6522(37)
β (°)	83.900(5)	98.581(3)	87.8220(37)
γ (°)	73.813(5)		87.6909(30)
V ($Å^3$)	408.92(4)	371.99(2)	591.66(4)
Z	2	2	2

D (Mg m^{-3})	1.3007	1.662	1.461
F(000)	172.7	192.00	272.00
μ (mm^{-1})	0.906	3.671	1.126
Crystal size (mm)		0.239 x 0.179 x 0.109	0.527 x 0.402 x 0.099
Data collection			
Θ_{min} (°)	4.49°	4.825°	3.605°
Measured reflections	8708	11337	12622
Independent reflections	1624	1239	2363
Observed reflections	1474		2185
R_{int}	0.0317	0.0418	0.0330
Refinement			
$\boldsymbol{R[F^2 > 2\sigma(F^2)]}$	0.0375	0.0409	0.0915
wR	0.1308	0.1209	0.2821
S	1.110	1.103	1.186
No.reflections/parameters	1624/108	1239/111	2363/199
Weighting scheme, w, $\boldsymbol{P = (F_o^2 + 2F_c^2)/3}$		$w = 1/[\sigma^2(\boldsymbol{F_o^2}) + (0.0767P)^2 + 0.19P]$	$w = 1/[\sigma^2(\boldsymbol{F_o^2}) + (0.0880P)^2 + 1.70P]$
$\Delta\boldsymbol{\rho_{min}}, \Delta\boldsymbol{\rho_{max}} = (\boldsymbol{e}$ Å$^{-3})$	-0.19 , 0.21	-0.30 , 0.28	-0.33 , 0.48

Table 1: Crystal data.

Crystal structures of (I), (II) and (III) prepared with Diamond software, showing the atomic labeling scheme as found in corresponding molecules, are shown in Figure 7. Displacement ellipsoid for non-hydrogen atoms are plotted at 50% probability and hydrogen atoms are shown as small spheres of arbitrary radii. Selected bond distances of the three structures are exposed in Table 2.

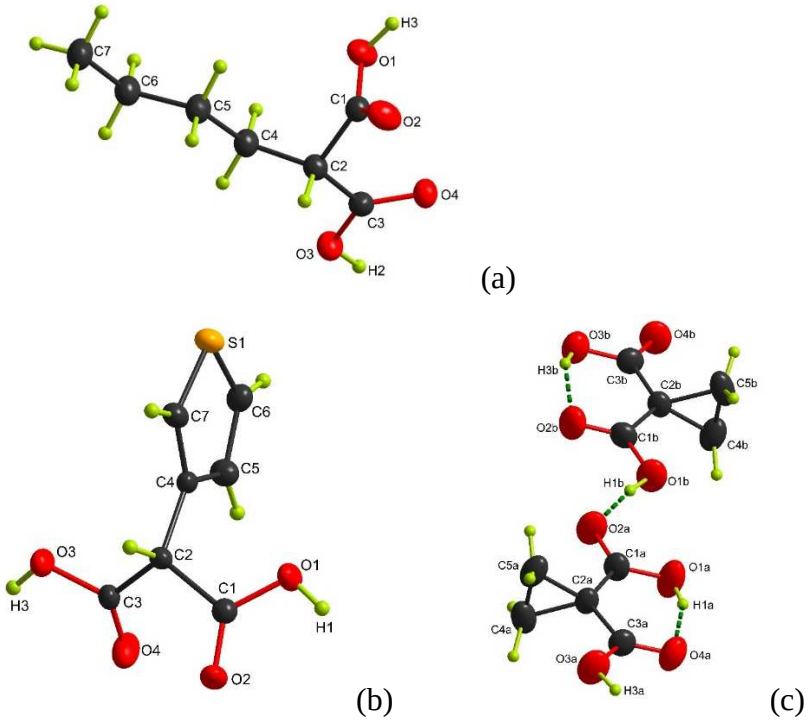


Figure 7: Crystal structures of butylmalonic acid (a), 3-thiophenemalonic acid (b) and 1,1-cyclopropanedicarboxylic acid (c).

	I	**II**	**IIIa**	**IIIb**
C1 — O1	1.3044(1) Å	1.3048(1) Å	1.3027(1) Å	1.3004(1) Å
C1 — O2	1.2182(1) Å	1.2123(0) Å	1.2160(1) Å	1.2183(1) Å
C3 — O3	1.2773(1) Å	1.3267(1) Å	1.3092(1) Å	1.3073(1) Å
C3 — O4	1.2474 (1) Å	1.2109 (0) Å	1.2143(1) Å	1.2192(1) Å

Table 2: Selected bond distances.

As explained before, the three compounds under study have in common that they are derivatives of the malonic acid (Figure 4). In this regard, as expected, the values of the distances between the C and O atoms present in these acids are very similar (Table 2).

3.1.1. Butylmalonic acid

Single crystals of (I) were obtained by slow evaporation of acetonitrile and an ethanol-water (70/30) solution (Figure 8). Only the ones obtained using acetonitrile as solvent were suitable for X-ray diffraction. Butylmalonic acid forms colorless crystals without a well-defined shape and crystallizes in triclinic P-1 with cell parameters of $a = 5{,}1972(3)$ Å, $b = 8{,}3161(5)$ Å, $c = 10{,}0272(6)$ Å, $\alpha = 79{,}831(5)°$, $\beta = 83{,}900(5)°$ and $\gamma = 73{,}813(5)°$. The molecular centrosymmetric structure of this compound is shown in Figure 9.

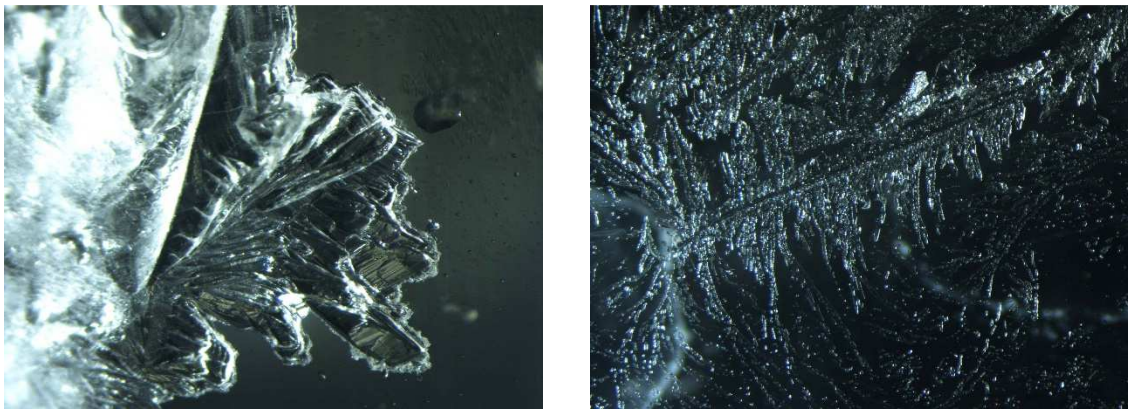


Figure 8: Crystals of butylmalonic acid grown from acetonitrile (left) and ethanol-water (70/30) solution (right). Images obtained at laboratory using a microscope.

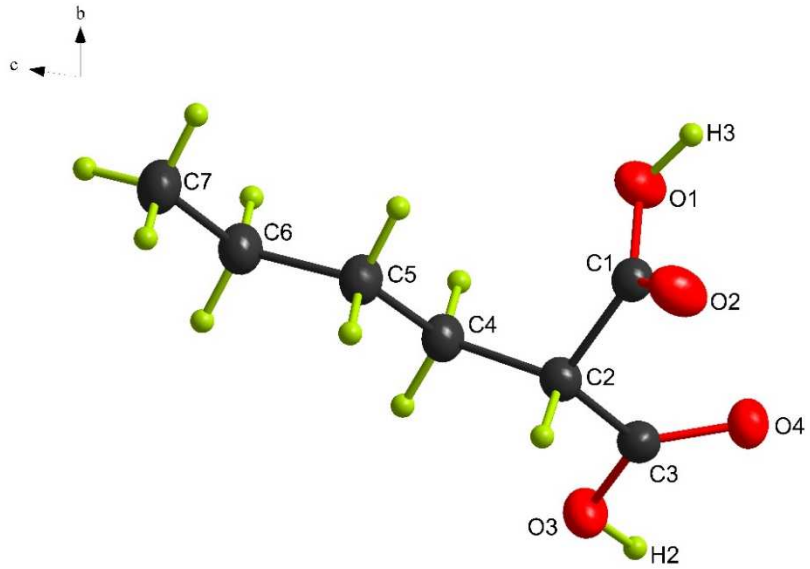


Figure 9: Diagram of butylmalonic acid, showing the atomic labeling scheme, viewed down the crystallographic *a* axis. Symmetry: (1+x, 1+y, -1+z).

In the crystal structure of (I), molecules join together through carboxyl dimer synthons (Figure 10). Pairs of O—H···O hydrogen bonds between the carboxy groups related by a center of symmetry connect molecules into a one-dimensional zigzag chain running along the *b* direction (Figure 11).

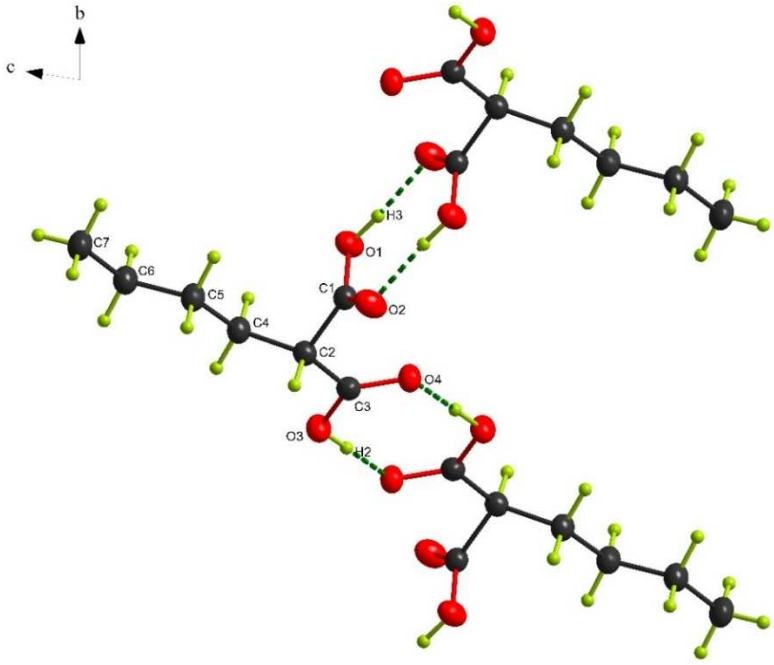


Figure 10: Diagram showing how a molecule of (I) connects with the others. Viewing direction: *a* axis. Hydrogen bonds are shown by broken lines.

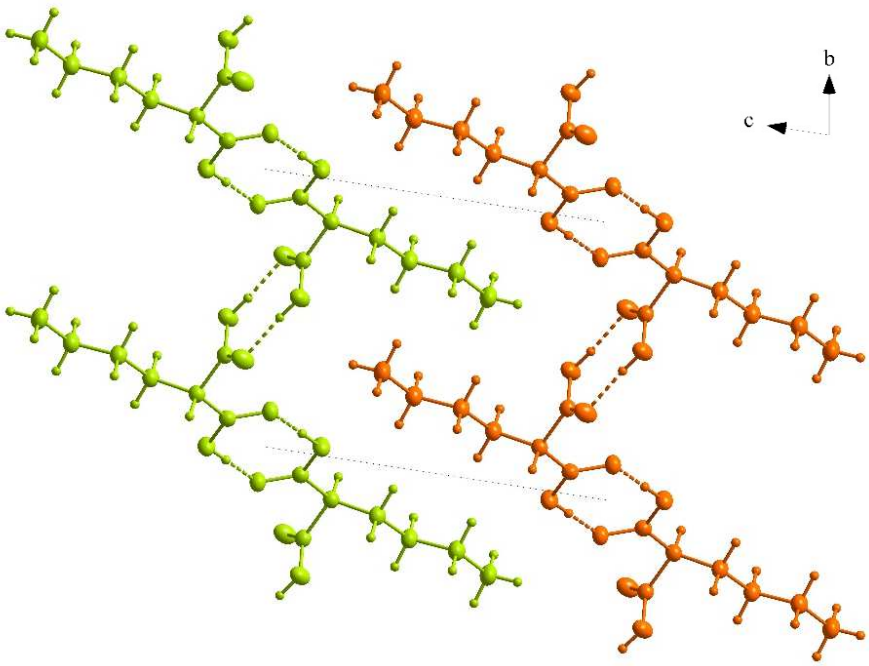


Figure 11: Part of the crystal packing of (I) viewed down the *a* axis, showing parallel zigzag chains. Hydrogen bonds are shown by broken lines.

The intermolecular hydrogen-bond geometry (D—H···A,where D is the donor atom and A is the atom that acts as acceptor) is presented in Table 3.

D— H ··· A	**D— H**	**H ··· A**	**D ··· A**	**D—$\widehat{H}$··· A**
O1—H3···O2^{i}	0.9014 (1) Å	1.7729 (1) Å	2.6727 (2) Å	175.857 (5) °
O3—H2···O4^{ii}	1.0158 (1) Å	1.6007 (1) Å	2.6162 (1) Å	178.344 (4) °

Symmetry codes: (i) 2 - x, 2 - y, 1 – z; (ii) 1 - x, 1 - y, 1 - z.

Table 3: Intermolecular hydrogen-bond geometry.

Typical values of the hydrogen bonds (H···A) rangebetween 1.5 Å and 2.1 Å, donor-acceptor distances range between 2.6 Å and 3.0 Å forming an angle from 140° to 180°, and donor-hydrogen bonds usually measure from 0.85 Å to 1.0 Å. Therefore, experimental results agree with the expected.

3.1.2. 3-Thiophenemalonic acid

Colorless needle-like crystals of (II) were grown by slow evaporation of acetonitrile (Figure 12). 3-Thiophenemalonic acid crystallizes in monoclinic $P2_1$ (Laue group 2/m and monoclinic axis b) with cell parameters $a = 6{,}9439(3)$ Å, $b = 5{,}8979(2)$ Å, $c = 9{,}1859(3)$ Å and $\beta = 98{,}581(3)°$. The molecular structure of (II) is shown in Figure 13.

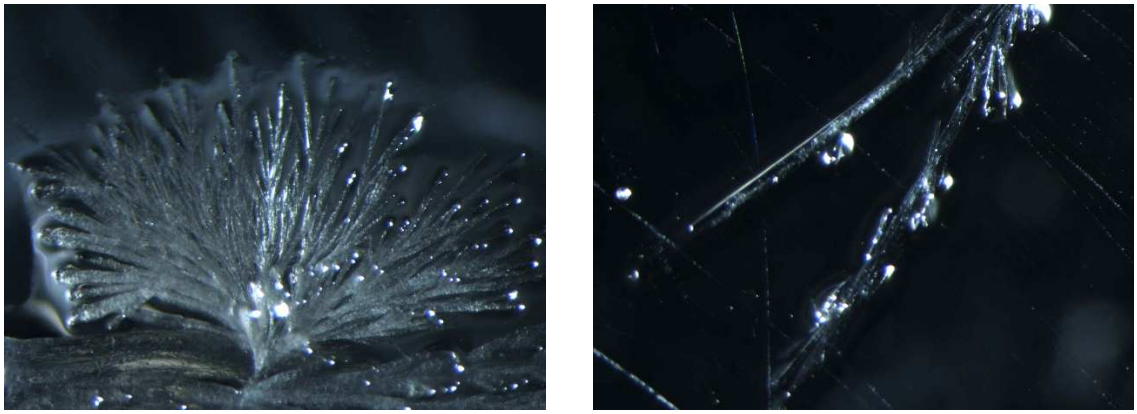


Figure 12: Crystals of 3-thiophenemalonic acid grown from acetonitrile. Images obtained at laboratory using a microscope.

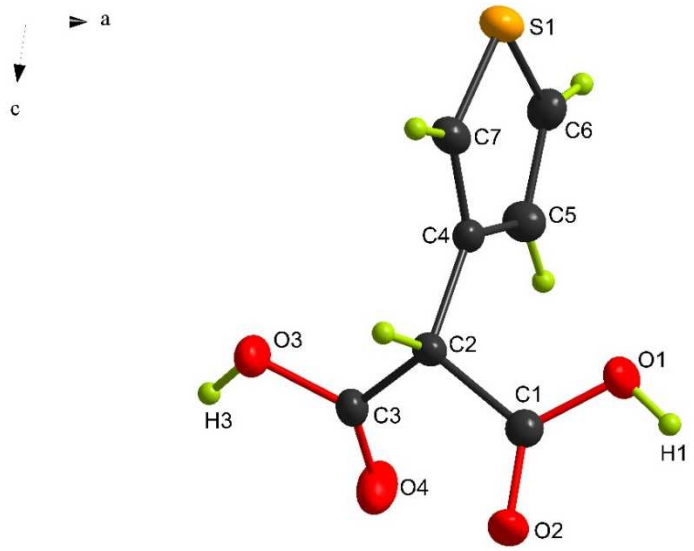


Figure 13: Diagram of 3-thiophenemalonic acid, showing the atomic labeling scheme, viewed down the crystallographic *b* axis. Symmetry: (1+x, -1+y, z).

In the crystal structure of (II), each individual molecule connects to four molecules through O—H···O hydrogen bonds (Figures 14, 15 and 16). The intermolecular hydrogen-bond geometry (D—H···A) is shown in Table4. As can be seen in the figures specified, atoms O1 and O3 act as donors while atoms O2 and O4 act as acceptors (O1—H1···O4^{i}; O3—H3···O2^{ii}, Table 4).

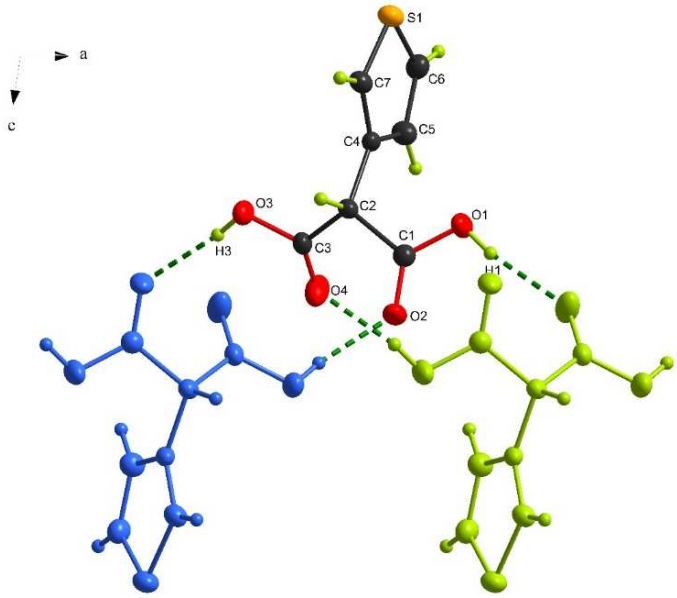


Figure 14: Diagram showing how a molecule of (II) connects with the others. Viewing direction: *b* axis. Hydrogen bonds are shown by broken lines.

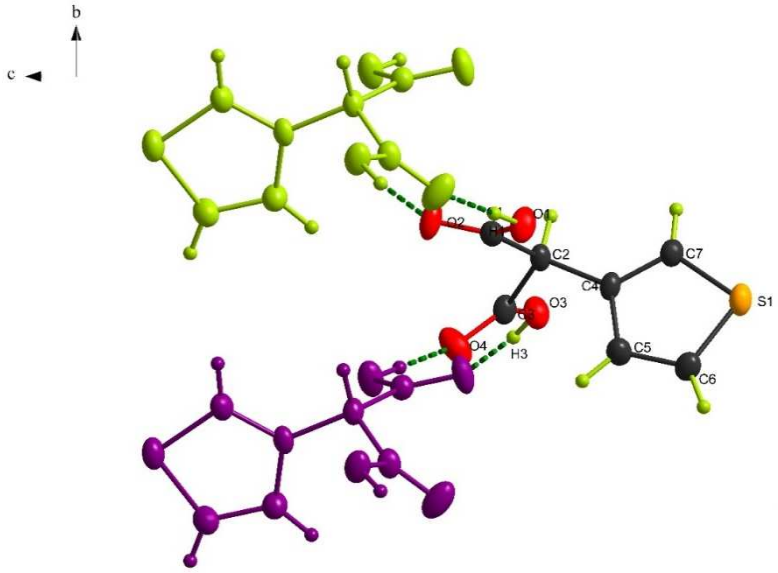


Figure 15: Diagram showing how a molecule of (II) connects with the others. Viewing direction: *a* axis. Hydrogen bonds are shown by broken lines.

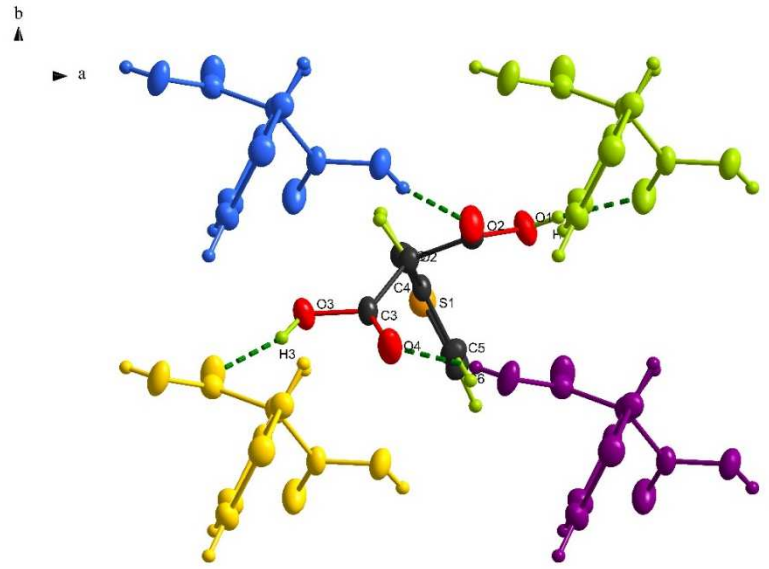


Figure 16: Diagram showing hydrogen-bonding between molecules. Viewing direction: *c* axis. Hydrogen bonds are shown by broken lines.

D— H ··· A	**D— H**	**H ··· A**	**D ··· A**	**D—$\widehat{\text{H}}$··· A**
O1—H1···O4^{i}	0.820 () Å	1.9226 (1) Å	2.7348 (1) Å	170.515 (2) °
O3—H3···O2^{ii}	0.820 () Å	1.9342 (1) Å	2.7344 (1) Å	164.986 (2) °

Symmetry codes: (i) 1 - x, -1/2 + y, 1 - z; (ii) –x, -3/2 + y, 1 - z.

Table 4: Intermolecular hydrogen-bond geometry.

According to the results expected, hydrogen bonds take values between 1.5 Å and 2.1 Å, donor-acceptor distances range between 2.6 Å and 3.0 Å forming an angle from 140° to 180°, and donor-hydrogen bonds measure from 0.85 Å to 1.0 Å.

Crystal packing, as viewed down *b* axis, consists of parallel zigzag chains running along the *a* direction, that can be observed in Figure 17. Looking down the *a* axis, separated chains can also be distinguished (Figure 18). However, the view down the crystallographic axis *c* does not show different layers but the continuous union of molecules by hydrogen bonds (Figure 19). Consequently, this compound exhibits a two-dimensional crystal packing.

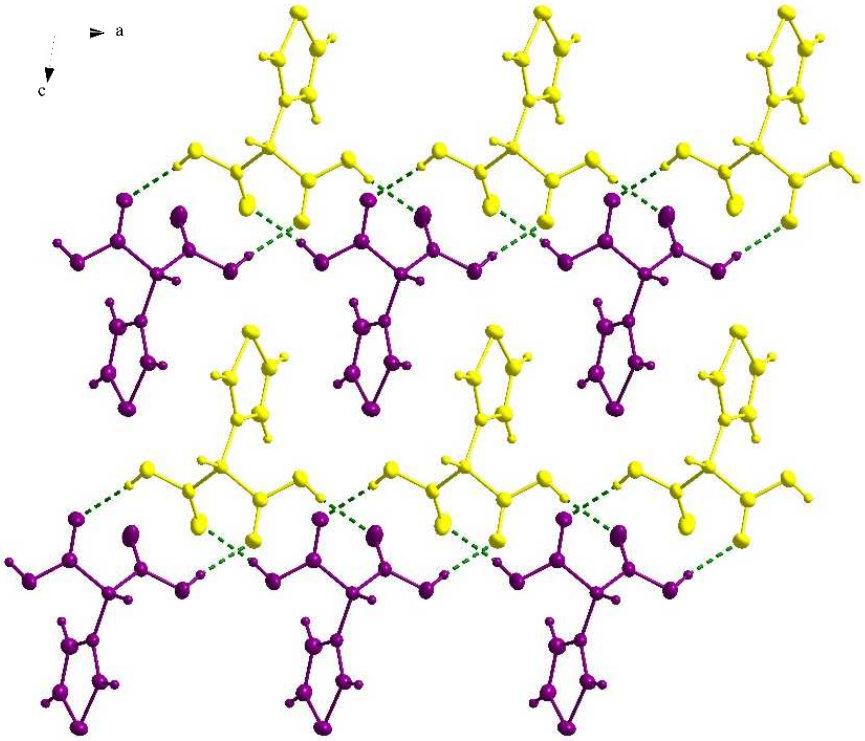


Figure 17: Part of the crystal packing of (II) viewed down the *b* axis, showing parallel zigzag chains. The adjacent layers fit each other like a zip. Hydrogen bonds are shown by broken lines.

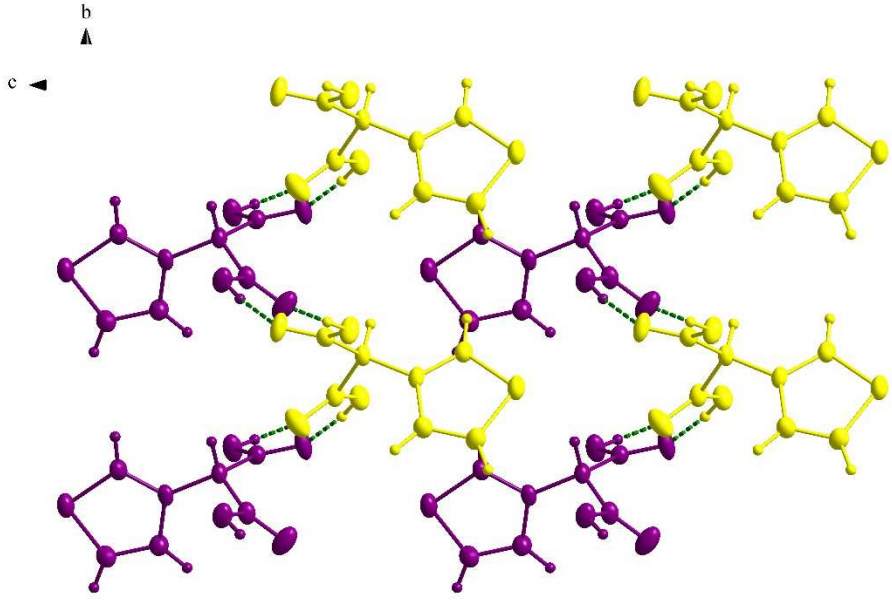


Figure 18: Part of the crystal packing of (II) viewed down the *a* axis, showing parallel zigzag chains. Hydrogen bonds are shown by broken lines.

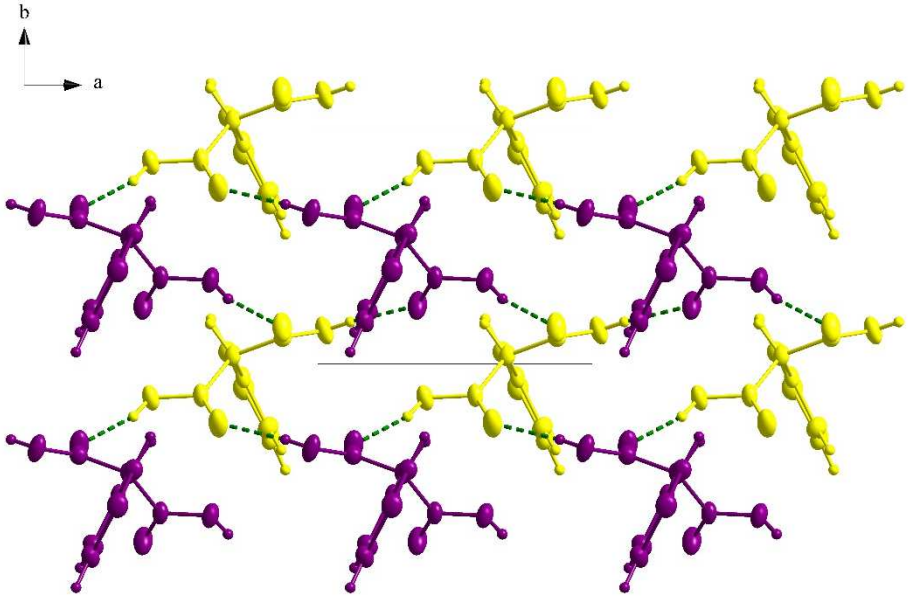


Figure 19: Part of the crystal packing of (II) viewed down the *c* axis. Hydrogen bonds are shown by broken lines.

3.1.3. 1,1-Cyclopropanedicarboxylic acid

Colorless needle-crystals of (III) appeared from acetonitrile slow evaporation (Figure 20). This compound crystallizes in triclinic P-1 with cell parameters of $a = 5{,}2801(2)$ Å, $b = 9{,}3325(3)$ Å, $c = 12{,}0347(6)$ Å, $\alpha = 87{,}6522(37)°$, $\beta = 87{,}8220(37)°$ and $\gamma = 87{,}6909(30)°$. The molecular centrosymmetric structure of (III) is shown in Figure 21.

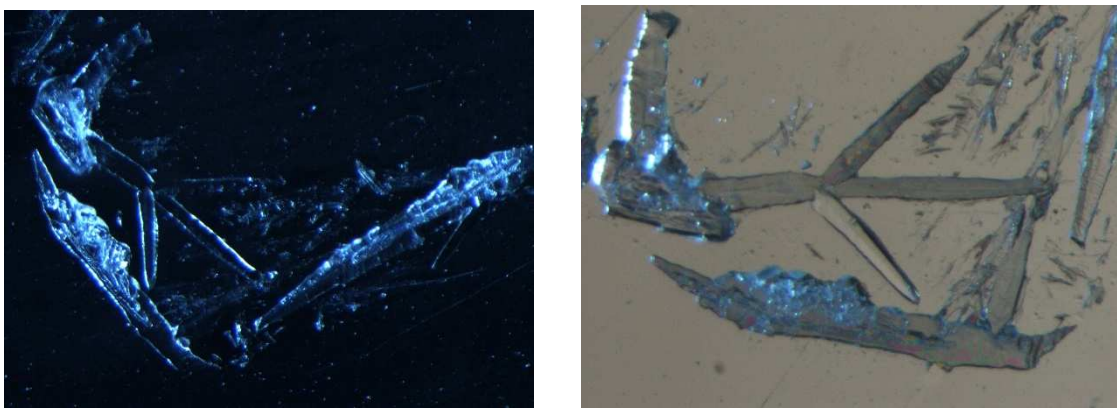


Figure 20: Crystals of 1,1-cyclopropanedicarboxylic acid grown from acetonitrile. Images obtained at laboratory using a microscope.

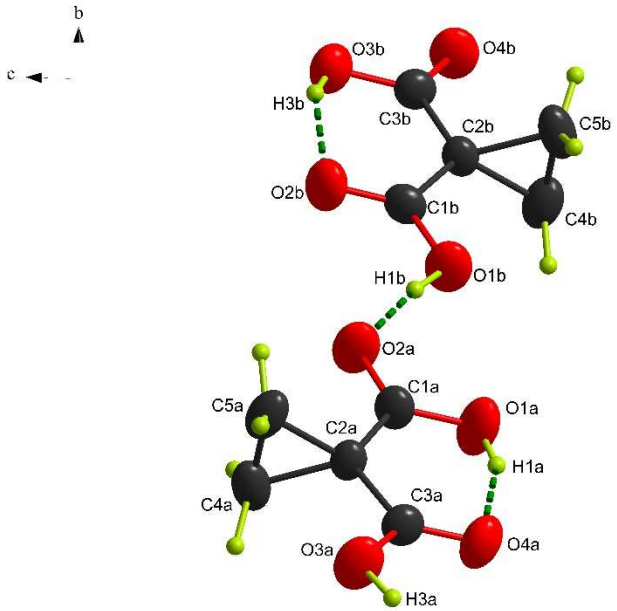


Figure 21: Diagram of 1,1-cyclopropanedicarboxylic acid, showing the atomic labeling scheme, viewed down the crystallographic *a* axis. Symmetry: a = (1 + x, y, z); b=(-x, 1 - y, 1 – z).

This crystal structure differs from the previous ones in the fact that two molecules repeat all over the crystal and that intramolecular hydrogen-bonds appear. In the crystal structure of (III), molecules are linked through O—H···O hydrogen bonds (Figure 22): atoms O1b and O3a act as donors while atoms O2a and O4b act as acceptors (O1b—H1b···O2a^{ii} ; O3a—H3a···O4b^{i}, Table 6). The intramolecular and intermolecular hydrogen-bond geometry are presented in Tables 5 and 6, respectively.

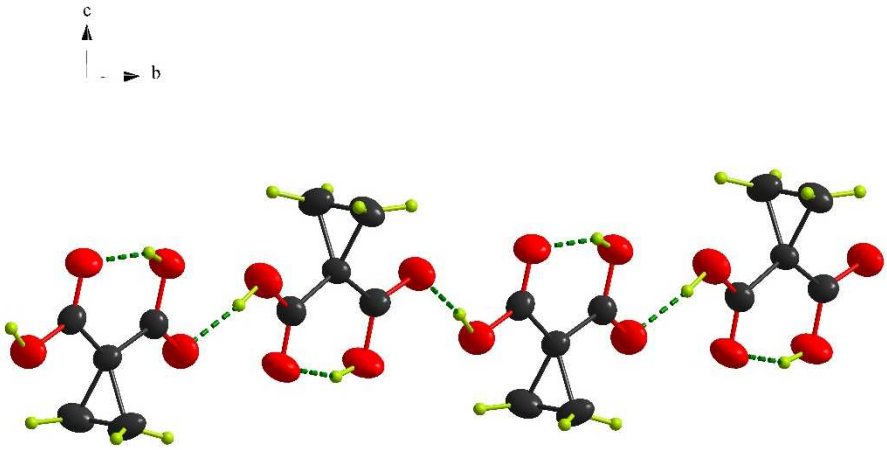


Figure 22: Diagram showing how a molecule of (III) connects with the others. Viewing direction: *a* axis. Hydrogen bonds are shown by broken lines.

D— H ··· A	**D— H**	**H ··· A**	**D ··· A**	**D—$\widehat{\text{H}}$··· A**
O1a—H1a···O4a	0.820 () Å	1.7823 (1) Å	2.5363 (1) Å	151.129 (4) °
O3b—H3b···O2b	0.820 () Å	1.7951 (1) Å	2.5337 (1) Å	149.057 (4) °

Table 5: Intramolecular hydrogen-bond geometry.

D— H ··· A	**D— H**	**H ··· A**	**D ··· A**	**D—$\widehat{\text{H}}$··· A**
O3a—H3a···O4b^{i}	0.820 () Å	1.8277 (1) Å	2.6436 (1) Å	173.071 (5) °
O1b—H1b···O2a^{ii}	0.820 () Å	1.8288 (1) Å	2.6418 (1) Å	171.064 (4) °

Symmetry codes: (i) 2 – x, -y, 1 - z; (ii) 1 + x, y, z (=a).

Table 6: Intermolecular hydrogen-bond geometry.

These results agree with the typical values: hydrogen bonds range between 1.5 Å and 2.1 Å, donor-acceptor distances range between 2.6 Å and 3.0 Å forming an angle from 140° to 180°, and donor-hydrogen bonds usually measure from 0.85 Å to 1.0 Å.

The hydrogen-bonding scheme of this crystal structure is similar to that in (I): one-dimensional zigzag chains running along the *b* direction (Figure 23). In contrast to the carboxy dimers that appear in (I), these chains are formed by simple hydrogen bonds.

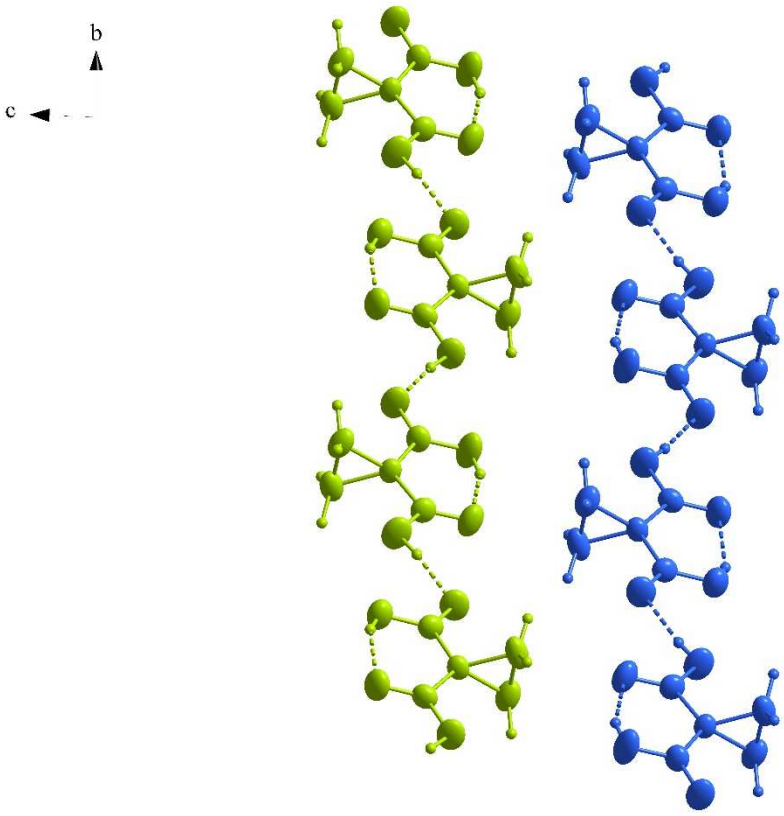


Figure 23: Part of the crystal packing of (III) viewed down the *a* axis, showing parallel zigzag chains. Hydrogen bonds are shown by broken lines.

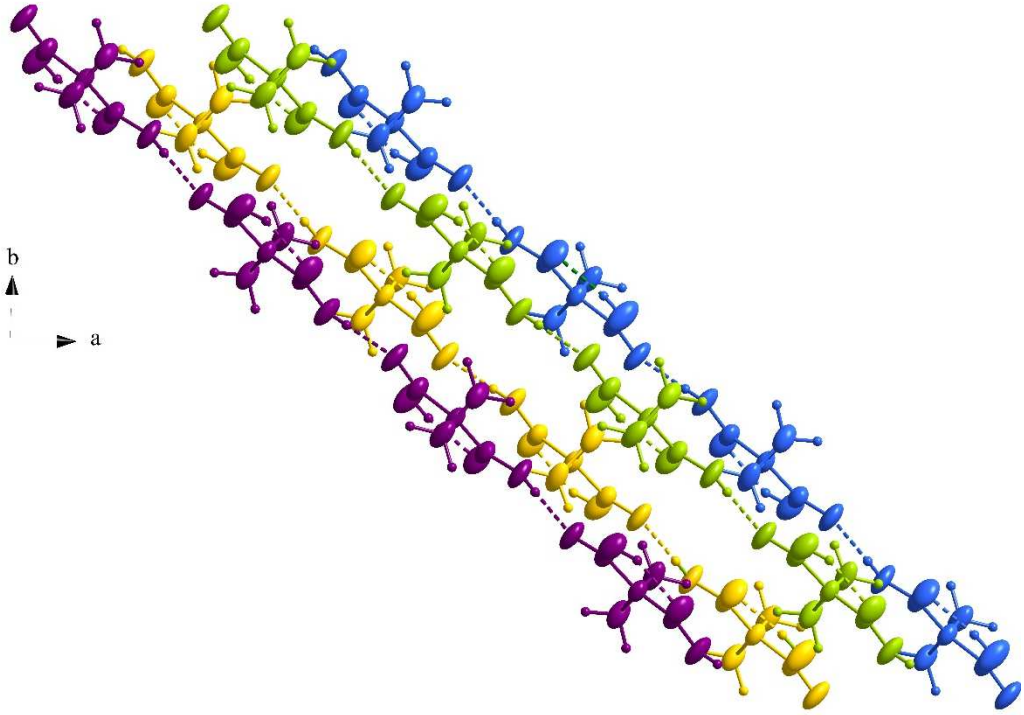


Figure 24: Part of the crystal packing of (III) viewed down the *c* axis, showing differentiated chains. Hydrogen bonds are shown by broken lines.

3.2. Structural remarks

Critical examination of the crystal structures of the three compounds shows similarities in stacking. The intermolecular hydrogen-bonding is of O—H···O type. None of the crystal structures pack in a three-dimensional network. Depending from the viewing direction, different layers can be identified along the crystal structures. No significant interaction is observed between the layers.

Data collected from the IR spectra show strong peaks in the region comprised between 1300 cm^{-1} and 1700 cm^{-1}, indicating that the compounds have the carboxylate group in their structure. Spectra show the presence of O—H bonds (around 3000 cm^{-1}) and C—C bonds of the carboxylic acids (between 1000 cm^{-1} and 1300 cm^{-1}).

The sharp peak common to the three materials that appears around 2300 cm^{-1} could be due to the utilization of isopropanol to clean the spectrometer before each measurement or to a failure of the instrument, considering that the same peaks appeared in all the measurements taken. As can be seen in Figure 25, the IR spectra corresponding to the three compounds are quite similar.

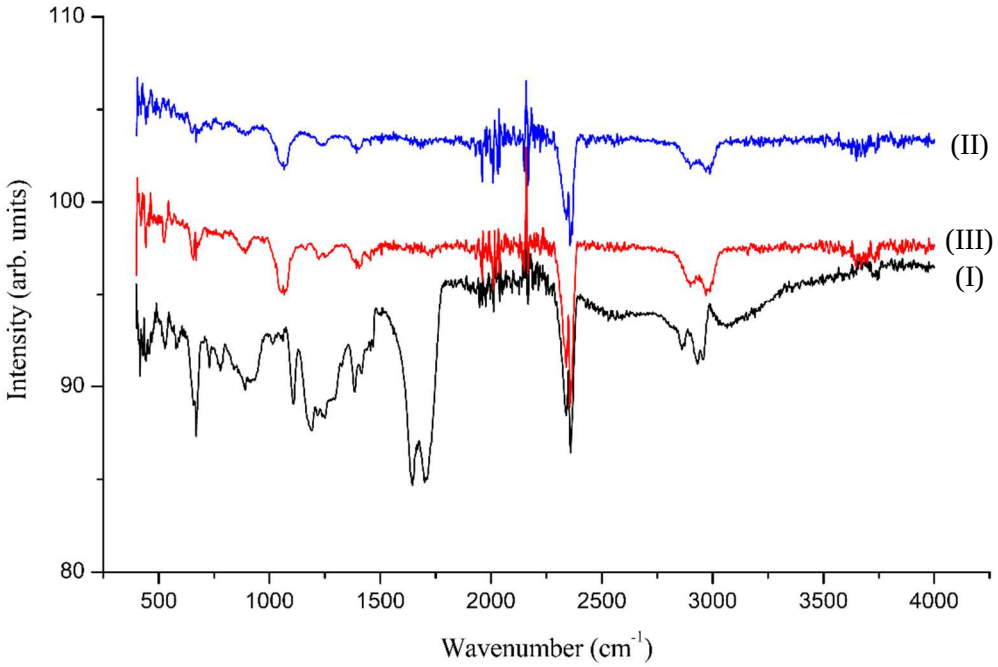


Figure 25: IR transmission spectra in the -400 to 4000 cm^{-1} energy range taken from butylmalonic acid (I), 3-thiophenemalonic acid (II) and 1,1-cyclopropanedicarboxylic acid (III).

4. CONCLUSIONS

En esta última sección se resumen los resultados obtenidos a lo largo de todo el trabajo y se establecen perspectivas de futuro a la hora de continuar trabajando con estos compuestos orgánicos.

The results obtained during the project development and some future prospects can be summarized in the following issues:

1. Butylmalonic acid crystallizes in triclinic P-1 with cell parameters of $a = 5{,}1972(3)$ Å, $b = 8{,}3161(5)$ Å, $c = 10{,}0272(6)$ Å, $\alpha = 79{,}831(5)°$, $\beta = 83{,}900(5)°$ and $\gamma = 73{,}813(5)°$.

2. 3-Thiophenemalonic acid crystallizes in monoclinic $P2_1$ (Laue group 2/m and monoclinic axis *b*) with cell parameters $a = 6{,}9439(3)$ Å, $b = 5{,}8979(2)$ Å, $c = 9{,}1859(3)$ Å and $\beta = 98{,}581(3)°$.

3. 1,1-Cyclopropanedicarboxylic acid crystallizes in triclinic P-1 with cell parameters of $a = 5{,}2801(2)$ Å, $b = 9{,}3325(3)$ Å, $c = 12{,}0347(6)$ Å, $\alpha = 87{,}6522(37)°$, $\beta = 87{,}8220(37)°$ and $\gamma = 87{,}6909(30)°$.

4. Crystal synthesis of 3-thiophenemalonic and 1,1-cyclopropanedicarboxylic acids provides crystals of better quality (needle-like) than the ones obtained through the crystallization of butylmalonic acid. It may be due to the "branch" of carbon atoms present in the butylmalonic acid, which leads to a less ordered structure. The form of the functional groups present in the other acids allows a better arrangement of the atoms and the consequent better-quality crystals.

5. As expected for carboxylate molecular crystals, in which hydrogen-bonding plays a significant role, all of the intermolecular connections present in the three crystal structures consist of O—H···O hydrogen bonds.

6. The results reveal that the crystal packing of butylmalonic acid and 1,1-cyclopropanedicarboxylic acid consists of one-dimensional zigzag chains, while 3-thiophenemalonic acid form two-dimensional supramolecular frameworks. No significant interaction is observed between the layers.

7. In the crystal structure of butylmalonic acid, molecules are connected through carboxyl dimer synthons (pairs of O—H···O bonds). In contrast, chains of molecules in 1,1-cyclopropanedicarboxylic acid are formed by simple O—H···O bonds.

8. While intramolecular H-bonds appear in the crystal structure of 1,1-cyclopropanedicarboxylic acid, this kind of hydrogen-bonds does not appear in the crystal structure of the other compounds.

9. The IR spectra of the three substituted malonic acids are quite similar, indicating the presence of the carboxylate group in their structures.

10. It would be of great interest to carry out the thermal analysis of the samples in order to complete the study of the crystal structures.

11. The publication of a scientific paper reporting the three crystal structures studied, unknown until the development of this project, is expected.

12. The detailed knowledge of these crystal structures and their crystal packing is essential to future studies of crystal engineering, based on the design of new molecular materials using these acids as organic ligands or linkers.

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