J Therm Anal Calorim (2012) 109:585–593
DOI 10.1007/s10973-012-2550-9

Pattern recognition methods in the study of thermal decomposition of α-amino acids

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Bretsznajder Special Chapter

Abstract There are many examples in the literature of a strict relation between the pathways of decomposition of a drug substance and chemical structure of its molecule. For this reason, a study has now been performed on the relation between thermal decomposition of α-amino acids and their chemical structure. To achieve this goal, a group of a dozen or so compounds was chosen at random, and the results obtained using the DTA, TG and DTG analyses of their thermal decomposition were interpreted by highly advanced multivariate methods, principal component analysis and cluster analysis. By this statistical analysis, the influence of specific functional groups on thermal decomposition of α-amino acids was determined. It has been found that first two principal components explain together more than 75 % of variance, and in an exceptional case, about 90 %. The third stage of decomposition was that at which the thermoanalytical data were best correlated with chemical constitution of a compound. It has also been recognized that a better discrimination among the analysed compounds was obtained for the DTA data set. The results can be useful for identification of a relation between the pathway of degradation of a drug substance and chemical structure of its molecule, and for predicting chemical stability of the compounds studied.

Keywords α-Amino acids · DTA · TG · DTG · Thermal decomposition · Principal component analysis · Cluster analysis

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Introduction

The problem, which is of particular interest and also plays an important role in the process of evaluation of the quality and safety of application of drug substances and medicinal products, is their chemical stability, describing all possible changes in the chemical structure of a molecule being an active substance [1–3]. In studies on this issue it is important to recognize that chemical compounds have a much differentiated chemical structure of molecules, so due to this a variety of chemical transitions leading to their disintegration are possible. Most typical degradation processes are: hydrolysis, dehydration, isomerisation, racemization, elimination, oxidation, photodegradation and the reactions of interaction. Knowledge of the structure of a molecule and its possible pathways of degradation is useful for predicting molecule stability and for planning assessment of its stability, especially at the preliminary stage of medicinal products projecting. It also enables to find the way leading to preventing chemical degradation of a drug.

In the study of chemical stability especially useful are methods of thermal analysis, such as differential scanning calorimetry, differential thermal analysis (DTA), thermogravimetry (TG), and derivative thermogravimetry (DTG), which deliver in a relatively short time the valuable data on the behaviour of the investigated substances during heating [4–6]. In the literature many examples can be found of application of these methods in studies on chemical stability and thermal degradation of drug substances and medicinal products [7–11]. Among others, the studies were carried out to identify kinetic parameters of decomposition processes of some antibiotics for humans, e.g. oxacillin, cloxacillin and dicloxacillin [12]. As expected, based on complex structures of oxacillin salts, several stages with

different activation energies occurred during the decomposition processes.

A closer inspection of the results of studies on thermal degradation shows, among others, a strict relation between the pathways of decomposition of a drug substance and chemical structure of its molecule. It was confirmed by numerous investigations of thermal degradation of organic compounds differing by the type of substituents at the basic chemical structure of a compound [13–17]. For example, thermal degradation of cyclodextrins and substituted β-cyclodextrins in an inert atmosphere has shown that the temperature of decomposition, char yield and thermal stability depends on the type of substituent [18]. In particular, insertion of a substituent could increase the mass of the residue up to 300 %, as compared to that of the parent cyclodextrins. A relationship has also been found among the stability and a series of structural effects of the pharmaceutical compounds [19]. The compounds which contain an amide group in the centre of the molecule are more stable because they have comparatively higher melting and degradation temperatures. In addition, the stability of this type of compounds depends on the *ortho*, *meta* or *para* positions of electrophilic substitution. Likewise, the groups at the aromatic ring with high electronic density ensure stability, and therefore are able to delocalize the charge over a larger spatial interval.

Taking the above presented literature data into consideration, it was decided to investigate whether there exists any relation between thermal decomposition of α-amino acids and chemical structure of their molecules. To achieve this goal, a group of a dozen or so compounds was chosen at random, and the results obtained using the DTA, TG and DTG techniques for studies of their thermal decomposition were interpreted by highly advanced, multivariate statistical methods, principal component analysis (PCA) and cluster analysis (CA) [20, 21]. By assessing of the influence of different substituents on the course of thermal decomposition of α-amino acids, the results can be useful for identification of relations between the pathway of degradation of a drug substance and chemical structure of its molecule, and for predicting chemical stability of the substances.

Experimental

Materials

α-Amino acids used in this study were as follows (manufacturers given in parentheses): L-aspartic acid (1), DL-glutamic acid hydrate (3), DL-arginine hydrochloride (9), DL-cysteine hydrate and hydrochloride (10), L-tyrosine (11), D-tyrosine (12), DL-tryptophan (13) (Roanal, Budapest, Hungary); DL-aspartic acid (2) (POCh, Gliwice, Poland); L-asparagine (4) (Ubichen Limited, Hampshire, Great Britain); DL-asparagine hydrate (5), D-glutamine (6) (Loba Feinchemie, Fischamend, Austria); L-lysine hydrate (7) (Serva Feinbiochemica, Heidelberg, Germany); DL-lysine hydrate (8) (Tavistock International, Pershore, Great Britain). All compounds were analysed without further purification.

Methods

The DTA, TG and DTG analyses of thermal decomposition of the α-amino acids were carried out using an OD-103 derivatograph (MOM, Budapest, Hungary). 100-mg samples placed in platinum crucibles were heated in air at a heating rate of 3, 5, 10 and 15 K min^{-1}. In addition, 50 and 200 mg samples were heated at a rate of 5 K min^{-1}. As the reference material, α-Al_2O_3 was used. Each analysis was replicated at least three times.

From the DTA curves, the temperatures of the onset (T_i), end (T_f) and peak (T_p), and the temperature ranges of the endo- and exothermic peaks (ΔT), in three consecutive stages of decomposition of the compounds, were determined. In the case of the TG and DTG curves, the temperatures of the onset (T_i) and end (T_f) of mass losses, the temperature ranges of reaction intervals (ΔT) and the mass losses (Δm), for three stages of decomposition, were established. Moreover, the temperatures of the DTG peaks (T_p) were also recorded.

Calculations

Two multivariate statistical techniques, PCA and CA were applied for interpretation of the results [20, 21]. Starting point for calculations were matrix of the data **X** with $n \times p$ dimensions, where n is the number of objects (rows) and p is the number of variables (columns). In the matrix, α-amino acids were used as the rows, whereas columns were the thermal parameters read from the DTA (T_i, T_f, T_p and ΔT) and TG–DTG (T_i, T_f, ΔT, Δm and T_p) curves of the analysed compounds. Statistical calculations were accomplished by using of the Statistica 7.1 (Statsoft®, Krakow, Poland) software.

For PCA and CA calculations, six matrices were constructed—two for DTA curves, two for TG–DTG curves, and two for the pooled results from the DTA, TG and DTG curves. The matrices for the first stage of decomposition have not been constructed, because this stage was missing for the majority of the α-amino acids. For the remaining stages, the matrices consisted of 13 rows (all the α-amino acids under study). In contrast to the results obtained from the TG–DTG curves, matrices of which included 30 columns (6 samples at four heating rates and for each sample 5

Table 1 General characterization of α-amino acids

No.	α-Amino acid	Molecular formula	Molar mass	Melting point/K
1	L-Aspartic acid	$C_4H_7NO_4$	133.11	543–544 [22]; 573^D [23]
2	DL-Aspartic acid	$C_4H_7NO_4$	133.11	573^D [23]
3	DL-Glutamic acid hydrate	$C_5H_9NO_4{\cdot}H_2O$	165.15	458^D [23]; 456^D [24]
4	L-Asparagine	$C_4H_8N_2O_3$	132.12	499–500 [22], 507–508 [22]; 508^D [23]
5	DL-Asparagine hydrate	$C_4H_8N_2O_3{\cdot}H_2O$	150.14	493^D [23]
6	D-Glutamine	$C_5H_{10}N_2O_3$	146.15	458^D [23]
7	L-Lysine hydrate	$C_6H_{14}N_2O_2{\cdot}H_2O$	164.21	498^D [22]; in 97 % at 488^D [24]
8	DL-Lysine hydrate	$C_6H_{14}N_2O_2{\cdot}H_2O$	164.21	498^D [22]
9	DL-Arginine hydrochloride	$C_6H_{14}N_4O_2{\cdot}HCl$	210.67	480 [22]
10	DL-Cysteine hydrate and hydrochloride	$C_3H_7NO_2S{\cdot}HCl{\cdot}H_2O$	175.64	382–395 [23]
11	L-Tyrosine	$C_9H_{11}NO_3$	181.19	568^D [22]; >573^D [23]
12	D-Tyrosine	$C_9H_{11}NO_3$	181.19	>573^D [23]
13	DL-Tryptophan	$C_{11}H_{12}N_2O_2$	204.23	562–563^D [23]

^{D} Melting with decomposition

parameters determined from the TG–DTG curves), the matrices obtained from the DTA curves consisted of 24 columns (6 samples at four heating rates and for each sample 4 parameters from the DTA curves). The matrices for the pooled data sets obtained from the DTA, TG and DTG curves consisted of 54 columns.

Results and discussion

General data characterizing the α-amino acids are summarized in Table 1, whereas their structures are presented in Fig. 1. In all compounds, the amine group is attached to a carbon atom at the neighbouring carboxylic group, in the case of amino acids considered as the main group. This group decides on the numbering of a chain and the nomenclature of an α-amino acid. The analysed compounds can also contain the second amine group, which is at the end of the aliphatic chain. To this group belong such compounds as DL-arginine hydrochloride, L-lysine hydrate and DL-lysine hydrate, as well as compounds such as L-asparagine, DL-asparagine hydrate and D-glutamine, which are amides. Among the compounds studied there are also α-amino acids containing in their side chain an additional carboxylic group, such as L-aspartic, DL-aspartic and DL-glutamic acids. DL-cysteine hydrochloride is an example of a compound having a sulfhydryl (thiol) group, whereas L-tyrosine and D-tyrosine have additional hydroxyl group. To the group of α-amino acids with aromatic ring belong L-tyrosine, D-tyrosine and DL-tryptophan.

Inspection of the melting points of the α-amino acids (Tables 1 and 2) shows that the DL-cysteine hydrate and hydrochloride, and DL-arginine hydrochloride, melt at the lowest temperature [22–24]. They are characterized by melting points below 480 K. Other compounds melt with simultaneous decomposition above 480 K. In some amino acids, crystalline phase transitions can also occur, these being described in the literature [25, 26].

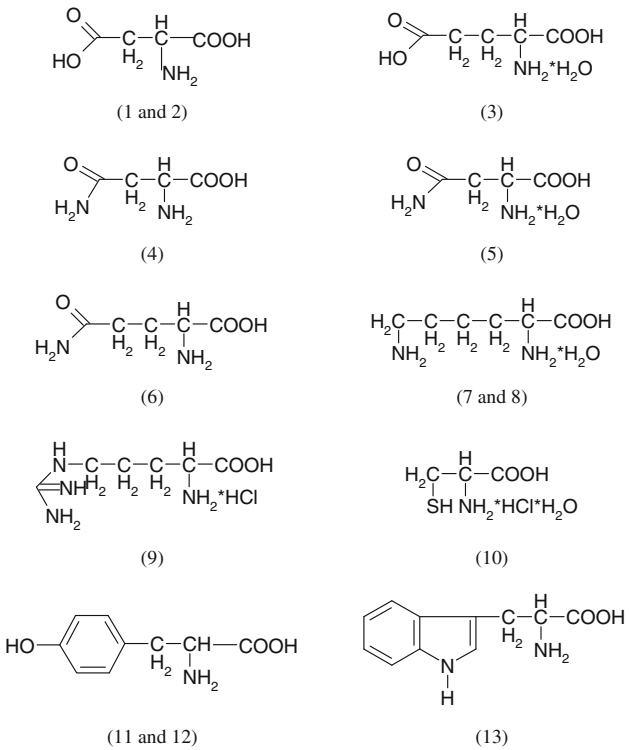

Fig. 1 Chemical structure of α-amino acids: L-aspartic acid (*1*), DL-aspartic acid (*2*), DL-glutamic acid hydrate (*3*), L-asparagine (*4*), DL-asparagine hydrate (*5*), D-glutamine (*6*), L-lysine hydrate (*7*), DL-lysine hydrate (*8*), DL-arginine hydrochloride (*9*), DL-cysteine hydrate and hydrochloride (*10*), L-tyrosine (*11*), D-tyrosine (*12*), DL-tryptophan (*13*)

Table 2 Results of the DTA, TG and DTG analysis of α-amino acids

No.	α-Amino acid	Decomposition stages				
		Temperature range of DTA peak, ΔT/K; temperature of DTA peak, T_p/K				
		Temperature range of decomposition stage, ΔT/K; temperature of DTG peak, T_p/K; mass loss in TG, Δm/%				
		The first stage	The second stage			The third stage
1	L-Aspartic acid		433–488; 473[a]	488–568; 498[a]	568–658; 633[a]	658–883; 808[b]
			448–483; 468 (14.0)	483–558; 498 (16.5)	558–688; 608 (31.0)	688–868; 813 (38.5)
2	DL-Aspartic acid		448–598; 493[a]	598–683; 648[a]		683–893; 803[b]
			458–563; 488 (30.0)	563–698; 633 (34.5)		698–883; 808 (35.5)
3	DL-Glutamic acid hydrate	328–398; 353[a]	398–463; 413[a]	463–578; 513[a]		678–833; 763[b]
		328–393; 353 (8.5)	393–448; 413 (12.5)	448–678; 523 (46.0)		678–828; 773 (33.0)
4	L-Asparagine		433–528; 478[a]	528–568; 538[a]	568–653; 593[a]	653–893; 803[b]
			443–513; 473 (29.5)	513–608; 558 (17.5)	608–683; 643 (9.5)	683–883; 798 (43.5)
5	DL-Asparagine hydrate	343–403; 358[a]	403–543; 473[a]	543–653; 608[a]		653–868; 788[b]
		333–398; 353 (12.0)	398–528; 468 (26.0)	528–693; 583 (26.0)		693–863; 788 (36.0)
6	D-Glutamine		433–493; 443[a]	493–578; 528[a]		673–843; 778[b]
			433–473; 443 (14.0)	473–673; 538 (49.5)		673–833; 778 (36.5)
7	L-Lysine hydrate	313–378; 338[a]	378–573; 463[a]	573–718; 673[a]		718–863; 803[b]
		298–363; 343 (9.0)	363–543; 463 (41.0)	543–728; 668 (32.0)		728–863; 793 (18.0)
8	DL-Lysine hydrate	328–413; 348[a]	413-433; 423[a]	433-513; 458[a]	513-718; 668[a]	718-853; 783[b]
		328–423; 363 (13.5)	423–513; 463 (22.0)	513–603; 578 (16.5)	603–733; 668 (31.5)	733–838; 788 (16.5)
9	DL-Arginine hydrochloride	308–428; 323[a]	428–478; 448[a]	478–648; 493[a]		723–888; 783[b]
		303–448; 318 (6.5)	448–523; 503 (14.5)	523–683; 558 (43.5)		683–878; 793 (35.5)
10	DL-Cysteine hydrate and hydrochloride	308–428; 318[a]	428–533; 448[a]	533–593; 578[a]		593–828; 628[b]
		303–408; 338 (11.5)	408–518; 443 (52.0)	518–603; 578 (17.0)		603–818; 768 (19.5)
11	L-Tyrosine		503–713; 553[a]			713–923; 828[b]
			498–708; 548 (62.5)			708–918; 813 (37.5)
12	D-Tyrosine		473–573; 538[a]	573–713; 673[a]		713–963; 818[b]
			473–588; 528 (48.5)	588–738; 633 (16.0)		738–938; 828 (35.5)
13	DL-Tryptophan		463–583; 513[a]	583–733; 663[a]		733–958; 858[b]
			463–533; 503 (29.0)	533–688; 588 (22.5)		688–948; 863 (48.5)

100 mg samples of the α-amino acids were heated at 5 K/min heating rate, the peak: [a] endothermic, [b] exothermic

Thermal decomposition

Results of thermal decomposition of the α-amino acids are compiled in Table 2. It was found that decomposition of the majority of the compounds runs in three stages, as shown in Figs. 2 and 3. In the first stage, no endothermic peaks due to melting or other phase transitions of the compounds were detected. At this stage usually the release of water of crystallization and hydrogen chloride from α-amino acids took place, e.g. the water of crystallization

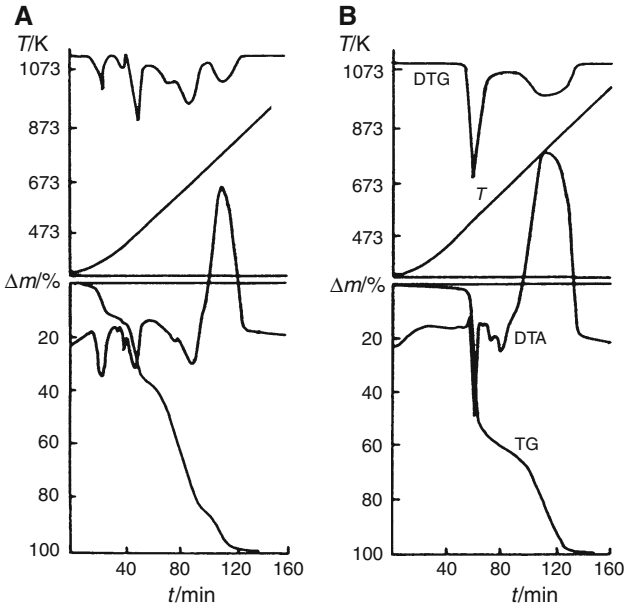

Fig. 2 DTA, TG and DTG curves of thermal decomposition of: **a** DL-lysine hydrate (8), **b** L-tyrosine (11). 100 mg samples were heated at 5 K min^{-1} heating rate

from DL-glutamic acid, DL-asparagine, L-lysine, DL-lysine and DL-cysteine, and hydrogen chloride from DL-arginine and DL-cysteine. The release of the water of crystallization or hydrogen chloride is indicated by an endothermic peak on the DTA curve and clearly reflects a several or dozen or so per cent loss of mass on the TG curve. Those α-amino acids, for which thermal processes in the first stage of decomposition were missing, are following: L-aspartic acid, DL-aspartic acid, L-asparagine, D-glutamine, L-tyrosine, D-tyrosine and DL-tryptophan. For these compounds, only two stages of decomposition were noticed, the second and the third ones.

The second stage of decomposition of the α-amino acids depends much on chemical constitution of the analysed compounds. At this stage, which runs with several dozen per cent of the loss of mass, partial degradation of anhydrous substance with the formation of intermediate products of decomposition occurs, and it goes through two or three unseparable substages. The data compiled in Table 2 show that it is particularly evident in the case of thermal degradation of L-aspartic acid, L-asparagine and DL-lysine (Figs. 2 and 3), which form three substages of decomposition within the second stage. In each of the substages, the endothermic effect in the DTA curve commences the decomposition.

In the third stage, the decomposition products of partial degradation of the analysed compounds are subjected to final decomposition accompanied by total combustion of the coked organic residue. The overall thermal effect of this stage is exothermic as indicated by the extensive peak in the DTA curve.

Multivariate analysis

The data sets determined based on the DTA, TG and DTG analyses of decomposition of the α-amino acids were used for PCA and CA calculations [20, 21]. PCA calculations led towards reduction of dimensionality of the complex multivariate data by deriving a new set of variables describing the data in order to decrease the variance. New variables labelled as principal components (PC's), were calculated as columns in the new matrix, which reflects main relations among the α-amino acids and enables their classification.

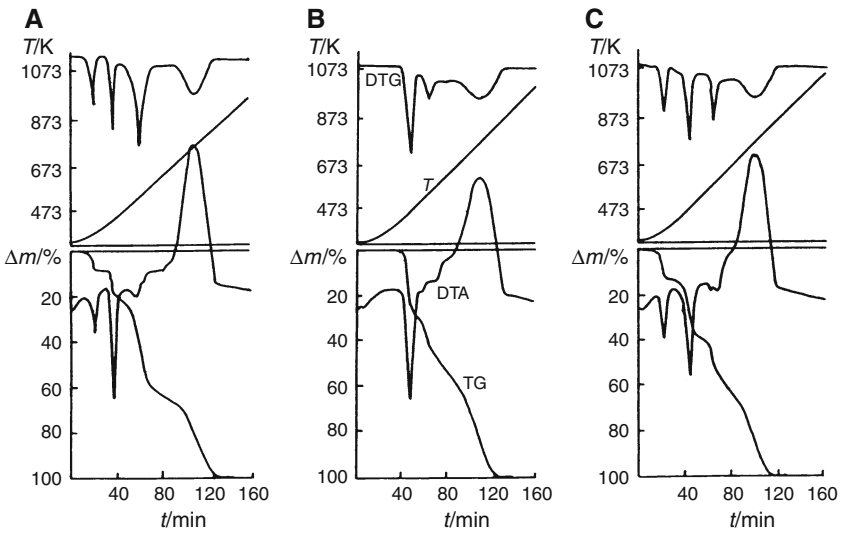

Fig. 3 DTA, TG and DTG curves of thermal decomposition of: **a** DL-glutamic acid hydrate (3), **b** L-asparagine (4), **c** DL-asparagine hydrate (5). 100 mg samples were heated at 5 K min^{-1} heating rate

Table 3 Values of variances and eigenvalues for the DTA, TG and DTG data sets for α-amino acids

Decomposition stage thermoanalytical data sets	PC1		PC2		PC3	
	Variances/ %	Eigenvalues	Variances (cumulative variances)/%	Eigenvalues	Variances (cumulative variances)/%	Eigenvalues
II (DTA)	51.8	12.4	37.7 (89.6)	9.1	4.6 (94.2)	1.1
II (TG–DTG)	45.1	13.5	29.4 (74.5)	8.8	16.3 (90.8)	4.9
III (DTA)	52.5	12.6	29.8 (82.3)	7.2	6.6 (88.9)	1.6
III (TG–DTG)	52.9	15.9	25.5 (78.4)	7.6	7.0 (85.4)	2.1
II (DTA, TG, DTG)	46.5	25.1	31.0 (77.5)	16.8	10.4 (87.9)	5.6
III (DTA, TG, DTG)	49.8	26.9	27.4 (77.2)	14.8	6.6 (83.8)	3.6

The analysis of the data compiled in Table 3 has shown that the first two main principal components explain totally about 90 and 75 % of variances, respectively, for the DTA and TG–DTG curves of the second stage of decomposition, and eigenvalues of PC1 and PC2 are greater than 1. This meets a sufficient condition for investigation of the relation between these compounds in the two-dimensional space, PC1 against PC2, which is graphically represented in Fig. 4a (results of DTA) and in Fig. 4b (results of TG–DTG).

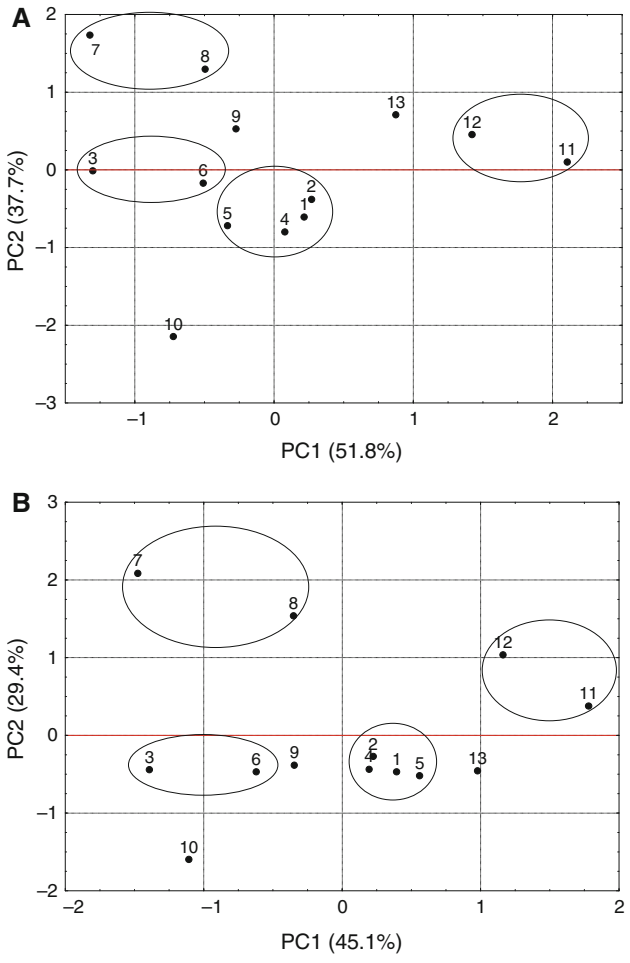

Fig. 4 PCA score plots for the second stage of thermal decomposition of α-amino acids based on the: **a** DTA, **b** TG–DTG data sets

By analysing location of the 13 α-amino acids in the two-dimensional space it was established that compounds 1, 2, 4 and 5 (Arabic digits denote numbers, by which α-amino acids are labelled in the first column of Tables 1 and 2), can be found in a similar range of the PC1 and PC2 values. These are the aliphatic α-amino acids with the same number of carbon atoms. Their common feature is the presence of the amine $–NH_2$ and carboxylic –COOH functional groups, and compound 1 (L-aspartic acid) and 2 (DL-aspartic acid) have an additional carboxylic group. Moreover, L-asparagine (4) and DL-asparagine hydrate (5) contain an amide group.

In the range of very similar PC2 values, there are also α-amino acids numbered 7 and 8. This pair is formed by the hydrates of L-lysine (7) and DL-lysine (8). The former is an L stereoisomer, whereas the latter is an equimolar mixture of the D and L isomers. In addition, in the similar range of the PC1 and PC2 values, fall two other compounds, namely L-tyrosine (11) and D-tyrosine (12). A very close range of the PC2 values is also characteristic for DL-glutamic acid hydrate (3) and D-glutamine (6). Their common feature is the presence of two carboxylic groups, but in D-glutamine the additional carboxylic group is in the amide form.

In the third stage of decomposition, a single exothermic effect in the DTA curve is seen and also the mass loss occurs from several to several dozen per cent in the TG curve. From the data of Table 3 it appears that PC1 and PC2 for the third stage of decomposition explain totally only 82 and 78 % of variances in the case of the DTA and TG–DTG analysis, respectively.

The data obtained from the DTA curves (Fig. 5a) show that L-aspartic acid (1), DL-aspartic acid (2), L-asparagine (4) and DL-asparagine hydrate (5) fall in the range of a very similar PC1 and PC2 values. In a similar range of PC1 and PC2 there are also pairs of the following compounds: DL-

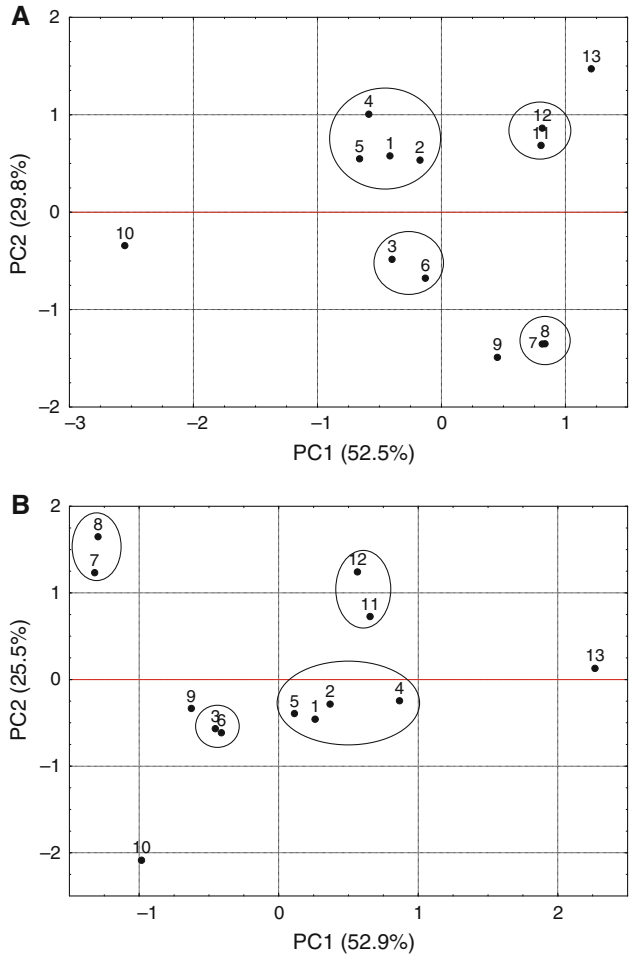

Fig. 5 PCA score plots for the third stage of thermal decomposition of α-amino acids based on the: **a** DTA, **b** TG–DTG data sets

glutamic acid hydrate (3) and D-glutamine (6), the hydrates of L-lysine (7) and DL-lysine (8), as well as L-tyrosine (11) and D-tyrosine (12).

A similar distribution pattern of the α-amino acids, obtained based on the data from the TG–DTG curves (Fig. 5b), has also been noticed. α-Amino acids numbered 1, 2, 4 and 5 can be found in a narrow range of PC2 values, and in a considerable larger range of PC1 values. DL-glutamic acid (3) and D-glutamine (6) are located in the range of very similar values both of PC1 and PC2. In a similar PC1 range, extending from −1.4 to −1.2, there are α-amino acids 7 and 8. Also in the close range of PC1 values, from 0.5 to 0.7, compounds having their molecules in an aromatic structure (11 and 12), can be found.

Analysis of PCA plots, developed based on the data from the DTA, TG and DTG curves, has shown that the compounds are located depending on their chemical structure in close ranges of the PC1 and PC2 values. However, several α-amino acids could not be localized within particular clusters, but were found in their vicinity, for instance DL-tryptophan (13), which is often localized close to the cluster containing α-amino acids 11 and 12. The reason for this can be the fact that in its molecule a heterocyclic ring is present, while in the molecules of D- and L-tyrosine an aromatic ring occurs in that position. DL-arginine hydrochloride (9) as well as DL-cysteine hydrate and hydrochloride (10) do not occur in any of the clusters because of the crucial difference in their structure as compared to that of remaining α-amino acids. Moreover, it has been found that addition of the two matrices resulted in an insignificant lowering of the variances per cent explained by first two main components. It means that PC1 and PC2 describe the relations between the compounds based on a smaller number of results than in the case of the matrices considered separately.

CA calculations were based on the measurements of similarity between objects and clusters of objects. The similarity was defined as Euclidean distance in the property space in which the objects were represented by points and

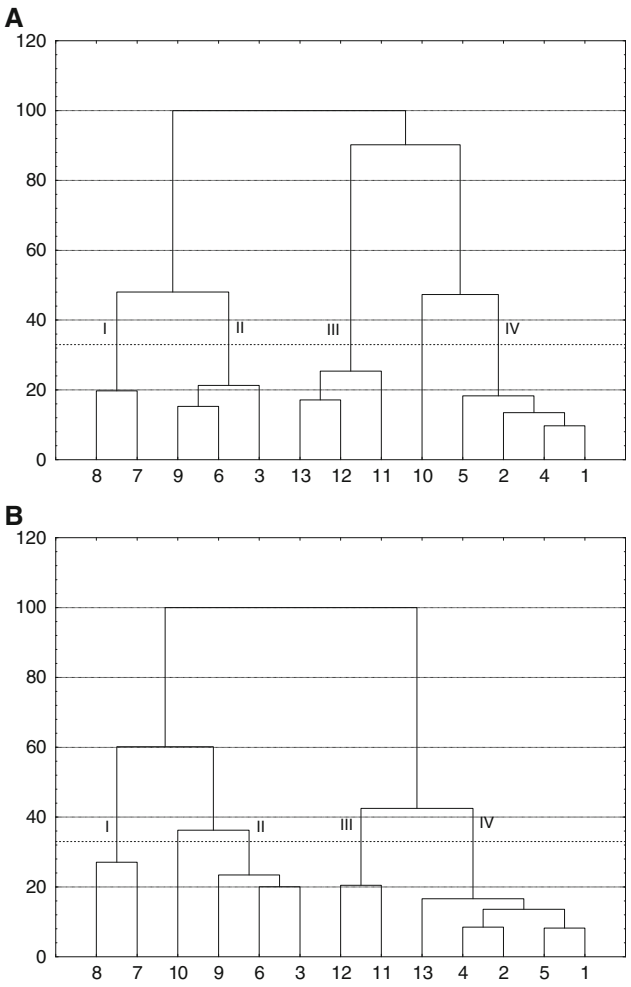

Fig. 6 CA dendrogram for the second stage of thermal decomposition of analyzed compounds based on the: **a** DTA, **b** TG–DTG data sets

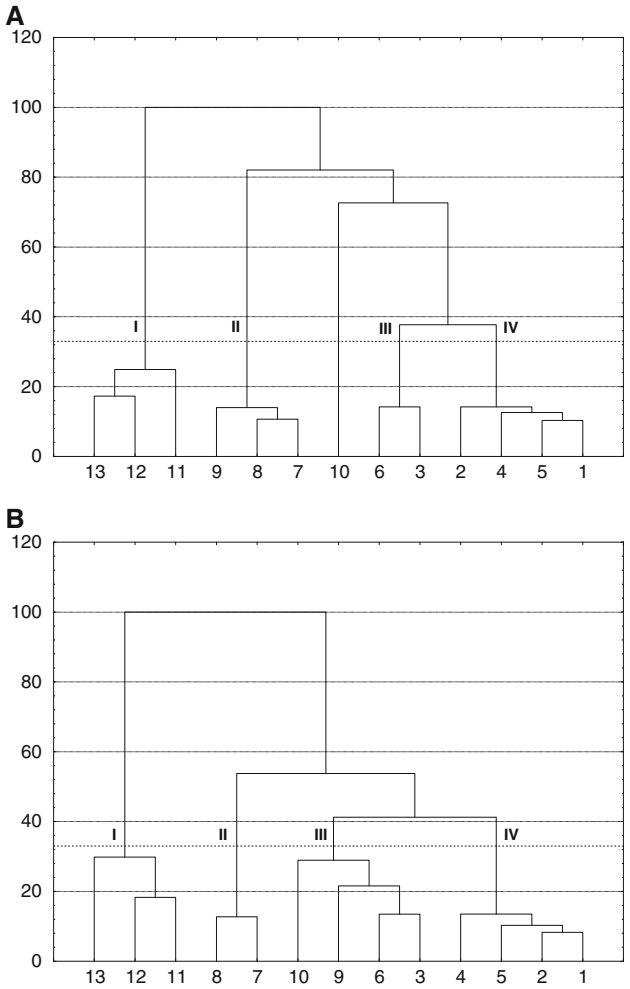

Fig. 7 CA dendrogram for the third stage of thermal decomposition of analyzed compounds based on the: **a** DTA, **b** TG–DTG data sets

the clusters by groups of points. From the multitude of algorithmic approaches to clustering, one of the most popular hierarchical agglomerative type of algorithms, the Ward's method, was employed. The agglomerative approach begins with a structure of *n* clusters, one per object, which grows a sequence of clusters until all *n* patterns are found in a single cluster.

Dendrograms illustrating the results of CA calculations are shown graphically in Fig. 6a (results of DTA) and in Fig. 6b (results of TG–DTG) for the second stage, and in Fig. 7a (DTA) and b (TG–DTG) for the third stage of decomposition. The results indicate that the compounds are grouped into the same clusters, as in the case of PCA results. This means that particular α-amino acids making up the given group; namely 1, 2, 4 and 5 (L-aspartic acid, DL-aspartic acid, L-asparagine, DL-asparagine hydrate), 3 and 6 (DL-glutamic acid hydrate, D-glutamine), 7 and 8 (the hydrates of L-lysine and DL-lysine), 11 and 12 (L-tyrosine, D-tyrosine), are characterized by a very similar course of their thermal decomposition caused by similar chemical structure of their molecules.

Independently, whether the DTA curves or the TG–DTG curves for the second or third stage of decomposition were analysed, always the lowest measure of Euclidean distance was characteristic for α-amino acids number 1, 2, 4 and 5, which could always be found in cluster IV (Figs. 6, 7). In a special way, other three compounds; DL-arginine hydrochloride (9), DL-cysteine hydrate and hydrochloride (10), and DL-tryptophan (13), are grouped. On the level below 33 % of the maximum distance measure, DL-cysteine does not form any cluster with any of the compounds studied. The probable reason for this is the presence of a sulfhydryl group, whose impact is decisive on the course of thermal decomposition of this amino acid. The degradation of DL-arginine containing a guanidine group shows the highest similarity with the thermal decomposition of D-glutamine (6), which is an amide (Fig. 6, cluster II; Fig. 7b, cluster III), and only in one case it is closely similar to the decomposition of compounds 7 and 8, which are amides, as well (Fig. 7a, cluster II). However, with the exception of the data obtained based on the TG–DTG curves for the second stage of the decomposition (Fig. 6b, cluster III), in all the remaining cases, α-amino acids containing aromatic ring in their molecule (11, 12 and 13), make up always a common cluster (Figs. 6a, cluster III, 7, cluster I).

Conclusions

It has been established that thermal decomposition of the α-amino acids takes place as the three-stage process. The first stage reflects the dehydration or release of hydrogen chloride by the majority of compounds, whereas in the second stage, partial degradation of the α-amino acids occurs, and it goes through two or three difficult substages for separation. The third stage is accompanied by burning of the charred residue of these compounds.

PCA and CA showed that there is a relation between thermal decomposition of the compounds and chemical structure of their molecules. With PCA, this relation is best illustrated by a two-dimensional plot of PC1 versus PC2. Two first PC's explain together more than 75 % of variance, and exceptionally, about 90 %. Higher values of the variance for the matrices based on the DTA, than on the TG–DTG analyses, can be obtained. On the other hand, the lowest variances are characteristic for the calculations performed for the pooled results of DTA, TG and DTG. The third decomposition stage correlates best with chemical structure of the compounds.

A similar course of thermal decomposition is characteristic for those compounds, whose molecules have similar chemical structure. The most important factor affecting

pathway of decomposition is the presence of functional groups and other substituents, both in the basic structure, and in the side chain.

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