Investigation of Conformation-Dependent Properties of L-Phenylalanine in Neutral and Radical Cations by Using a Density Functional Taking into Account Noncovalent Interactions

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Conformation-dependent properties of L-phenylalanine in neutral and radical cations have been studied by using density functional theory (DFT) with a new density functional M05-2X, which is applicable to molecular systems with nonconvalent interactions. Adiabatic and vertical ionization energies and charge distributions in the cationic conformers in addition to optimized geometrical structures for both the neutral and the cationic conformers were evaluated. These results were compared with DFT (B3LYP) results. The M05-2X results can explain the correspondence between the observed and predicted conformers without ambiguity. The possibility of conformerization of neutral conformers is indicated from the results of IRC (intrinsic reaction coordinate) profiles.

Introduction

Small biomolecules, in particular amino acids, are known to have many conformers whose structures depend on internal charge distributions and external conditions.[1−3]

Noncovalent, long-range interactions between a partially charged backbone and a side chain in amino acids play an essential role in determining stable conformers, especially, ionic conformers.[4] A number of spectroscopic studies on identification of conformers of amino acids have been reported following the success of Levy's group in identifying multiple conformers in laser-induced fluorescence spectra of aromatic amino acids in a supersonic jet.[5−9]

Geometrical structures and their electronic properties of neutral and radical cationic conformers of L-phenylalanine, one of the aromatic amino acids, have been investigated in detail by means of laser spectroscopic techniques[10] combined with ab initio computational methods.[2−4,6,8,9,11,12] Most of the theoretical analyses of conformer spectra have been carried out by using DFT (B3LYP).[6,8,9] Some of the stable conformers predicted by B3LYP calculation could not be observed experimentally.[3,6,11,12]

The most widely used form of density functional, B3LYP, has some serious shortcomings, however, according to a new report.[13] This is due to the lack of noncovalent interactions in the functional. Recently, there have been theoretical efforts to develop new functionals with noncovalent interaction, which have better performance than B3LYP.[13−19] Therefore, it is worth applying a new DFT functional M05-2X to neutrals and, in particular, cationic conformers of L-phenylalanine in order to theoretically confirm their assignments[6,11] and clarify correspondence between observed and predicted conformers.

In this paper, we provide explicit structural assignment of neutral and cationic conformers of L-phenylalanine based on the M05-2X results of conformation-dependent properties:[14,17] geometrical structure, adiabatic and vertical ionization energies, and charge distributions. We also theoretically determine a most probable reaction path between neutral conformers belonging to the same subgroup by finding the corresponding transition state and the IRC (intrinsic reaction coordinate) profile.[20]

In the next section, theoretical methods and procedures are briefly described. In section A, M05-2X results of optimized geometrical structures and their relative energies for neutral and cationic conformers are shown and compared with the results obtained by B3LYP with the same basis set. A new grouping of the stable conformers into two subgroups I and II is given based on the calculated results together with the results of the charge distribution in cations described in section D.

In section B, the correspondence between the observed and the computed neutral conformers is discussed in terms of the transition state (TS) and corresponding IRC between two conformers. In section C, vertical and adiabatic ionization energies of conformers are calculated to provide further evidence to support the regrouping of subgroups I and II.

Delocalization of charge distributions between the amino and phenyl groups in L-phenylalanine on ionization is explained in terms of hyperconjugation in which the highest occupied molecular orbital (HOMO) of the phenyl group and the nonbonding molecular orbital (n-MO) of the amino group form new bonding and antibonding MOs.

Computational Methods

All calculations in this work were carried out using the Gaussian 03 Rev. E01 software package[20] to employ the M05-

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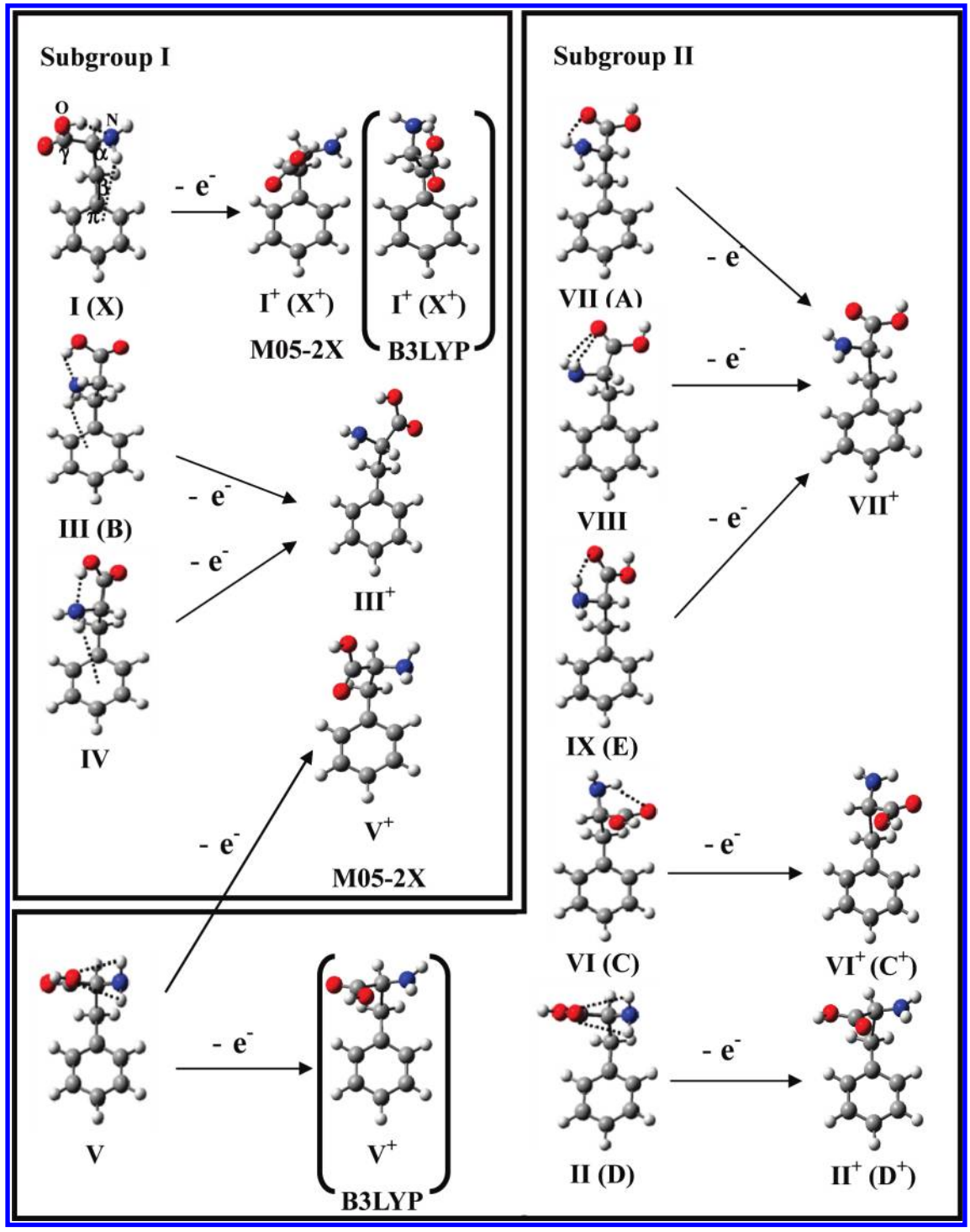

Figure 1. Nine most stable structures of L-phenylalanine conformers in neutrals and cations. All structures were determined at the M05-2X/6-311+G* level of theory. Alphabetic capital letters represent the conformers observed experimentally, and Roman numerals were adopted from the report by L. G. Snoek et al.[6] The nine neutral conformers were converged at six optimized cationic structures on the right-hand side. Conformers I and V in cations gave different structures between M05-2X and B3LYP. They are marked as M05-2X and B3LYP, respectively. The others lead to almost the same conformers regardless of the methods used.

2X method.[14] The geometries of conformers of L-phenylalanine in the ground state were optimized at the M05-2X/6-311+G* level with scanning for five dihedral angles rotation: $C_\gamma-O = 0°, 180°$; $C_\pi-C_\beta = 60°, 120°, 180°$; $C_\beta-C_\alpha = -120°, -60°, 0°, 60°, 120°, 180°$; $C_\alpha-N = -120°, -60°, 0°, 60°, 120°, 180°$; $C_\alpha-C_\gamma = 30°, 90°, 150°, 210°, 270°, 330°$. A total of 1296 initial geometries of the multiconformer existed, and they were converged to 39 stable local minima and 38 local minima in B3LYP with 6-311+G*.

The optimized structure in the corresponding transition state (TS) was obtained for the most probable reaction path between two neutral conformers belonging to the same subgroup, which was confirmed using IRC profiles.[20] The vertical ionization potential of each conformer was calculated by single-point energy calculation at the optimized neutral in the ground state by setting the charge and spin multiplicity to +1 and 2, respectively. We also carried out geometry optimization of each conformer of L-phenylalanine radical cation in the ground state

TABLE 1: Molecular Constants for Nine Conformers in Neutrals and Those for Cations in Parentheses[a]

subgroup	experiment assignment	conformer	dihedral angle (deg) $C_\pi-C_\beta-C_\alpha-N$	dihedral angle (deg) $C_\alpha-NH_2$	bond length (Å) $C_\alpha-C_\beta$	bond length (Å) $C_\alpha-N$	bond length (Å) $C_\beta-C_\pi$
			(a) 05-2X, neutral (cation)				
I	X	I	52(**88**)	123(131)	1.54(1.57)	1.46(1.44)	1.51(1.49)
	B	III	−63(−86)	122(137)	1.54(1.59)	1.46(1.42)	1.51(1.46)
		IV	−60(−86)	121(137)	1.53(1.59)	1.46(1.42)	1.51(1.46)
II(I)		V	62(64)	**120(127)**	1.54(**1.56**)	1.45(1.44)	1.51(1.48)
II	A	VII	−60(−69)	122(176)	1.55(1.77)	1.45(1.36)	1.50(1.45)
	C	VI	178(171)	120(168)	1.54(1.79)	1.45(1.36)	1.51(1.44)
	D	II	62(73)	119(178)	1.54(1.78)	1.45(1.36)	1.51(1.44)
	E	IX	−62(−69)	123(176)	1.54(1.77)	1.45(1.36)	1.51(1.44)
		VIII	−73(−69)	120(176)	1.54(1.77)	1.45(1.36)	1.51(1.45)
			(b) B3LYP, neutral (cation)				
I	X	I	52(**172**)	123(133)	1.55(1.56)	1.47(1.44)	1.51(1.50)
	B	III	−64(−84)	122(143)	1.55(1.58)	1.47(1.42)	1.51(1.48)
		IV	−64(−84)	122(143)	1.54(1.58)	1.47(1.42)	1.51(1.48)
II(I)		V	61(72)	**121(179)**	1.55(**1.70**)	1.45(1.39)	1.51(1.47)
II	A	VII	−61(−72)	122(176)	1.57(1.70)	1.45(1.39)	1.51(1.47)
	C	VI	−175(177)	121(165)	1.54(1.70)	1.46(1.39)	1.51(1.47)
	D	II	62(73)	120(178)	1.55(1.70)	1.45(1.39)	1.51(1.46)
	E	IX	−63(−73)	123(176)	1.55(1.70)	1.46(1.39)	1.51(1.46)
		VIII	−73(−72)	120(176)	1.56(1.70)	1.45(1.39)	1.51(1.47)

[a] These were evaluated at the optimized geometries shown in Figure 1. (a) Results obtained by M05-2X; (b) results obtained by B3LYP. Values that are considerably different between these two functionals are written in bold.

TABLE 2: Relative Energies (in kcal/mol) of the Nine Most Stable Conformers in the Neutral (Cationic) Ground State Calculated by M05-2X and B3LYP with a 6-311+G* Basis Set Including Zero-Point Energy Correction[a]

Subgroup	Experimental Assignment	Conformer	Neutral M05-2X	Neutral B3LYP	Cation M05-2X	Cation B3LYP
I	X	I	0.00	0.11	6.29	1.68
	B	III	0.62	0.00	10.03	7.29
		IV	0.79	0.17	10.03	7.29
		V	1.15	1.64	1.46	0.96
II	A	VII	1.50	1.00	0.71	0.00
	C	VI	1.56	1.08	0.17	0.04
	D	II	0.47	0.87	0.00	0.22
	E	IX	1.71	1.22	0.71	0.00
		VIII	2.06	1.09	0.71	0.00

[a] The value of conformer I(X) calculated by M05-2X is the origin of the relative energy.

at the M05-2X/6-311+G* level. The charge distribution for cations was obtained using natural bond orbital (NBO) analysis.

Results and Discussion

A. Geometrical Structures of Stable, Neutral, and Cationic Conformers. Figure 1 shows the L-phenylalanine models for the nine most stable neutral conformers and six cationic ones in their ground states, the structures of which were calculated by using M05-2X optimization. Conformers obtained by using the popular (DFT) B3LYP, which were different from the M05-2X results, are also shown in Figure 1. A comparison of M05-2X and B3LYP results is shown in Table 1. Here, dihedral angles, $C_\pi-C_\beta-C_\alpha-N$ and $C_\alpha-NH_2$, and bond lengths, $C_\alpha-C_\beta$, $C_\alpha-N$, and $C_\beta-C_\pi$, which characterize each conformer, are listed in Table 1. The two functionals, M05-2X and B3LYP, gave almost the same results regarding geometrical structures for other groups such as the phenyl ring and the carboxyl groups in both the neutrals and the cations.

The neutral conformers of six alphabetic capital letters, A, B, C, D, E, and X, in Figure 1 are quoted from ref 6 in which their assignment was carried out based on a combination of UV−UV and IR−UV double-resonance spectroscopy of jet-cooled L-phenylalanine and coupled with ab initio computations. The nine Roman numerals I, II, ..., VIII, and IX are numbered in order of relative energies calculated using the MP2/6-311G** level of theory.[6] Neutral conformers IV, V, and VIII, which were predicted by B3LYP results, have not been experimentally identified.

For the neutral conformers, the geometrical structures calculated with M05-2X and those calculated with traditional (DFT) B3LYP are almost the same, as can be seen in Figure 1 and Table 1. For the cations, two cations, I and V, converged into different ones.

In Figure 1, except for conformer V, the conformers in their neutrals and cations are classified into two subgroups, I (I, III, IV) and II (II, VI, VII, VIII, IX). It has already been understood qualitatively that each subgroup has two different types of intramolecular hydrogen bonding associated with the n-MO of the amino group: $-COOH \rightarrow -NH_2$ for subgroup I and $-NH_2 \rightarrow -OCOH$ for subgroup II.[6] There are significant changes in dihedral angle $C_\alpha-NH_2$ and bond length $C_\alpha-C_\beta$ between neutral and cationic conformers belonging to subgroup II, while there are no such differences in subgroup I.[2] The change from nonplanar $C_\alpha-NH_2$ in neutrals to planar in cations is due to breakdown of intramolecular hydrogen bonding $-NH_2 \rightarrow -OCOH$ on ionization. The mechanism of the lengthening of the $C_\alpha-C_\beta$ bond on ionization is explained in section C.

In previous papers on geometrical structures obtained by using the B3LYP method there was no clear difference in ionization energies or vibrational frequencies in the neutral ground state between V and VII conformers.[6,8,12] Furthermore, there were no deviations of cationic structures, that is, the two conformers commonly showed elongation of the $C_\alpha-C_\beta$ bond and planarity of $-NH_2$ (see Table 1). There has been heated debate about whether observed conformer A was to be assigned to conformer V[6] or VII.[11]

Experimentally, conformer V was assigned to A by Snoek et al.[6] Later, it was rationalized from UV rotational band contour analysis by Lee et al. that conformer A corresponds not to conformer V but to conformer VII.[11] The results obtained by using the M05-2X method, in contrast, show no elongation of

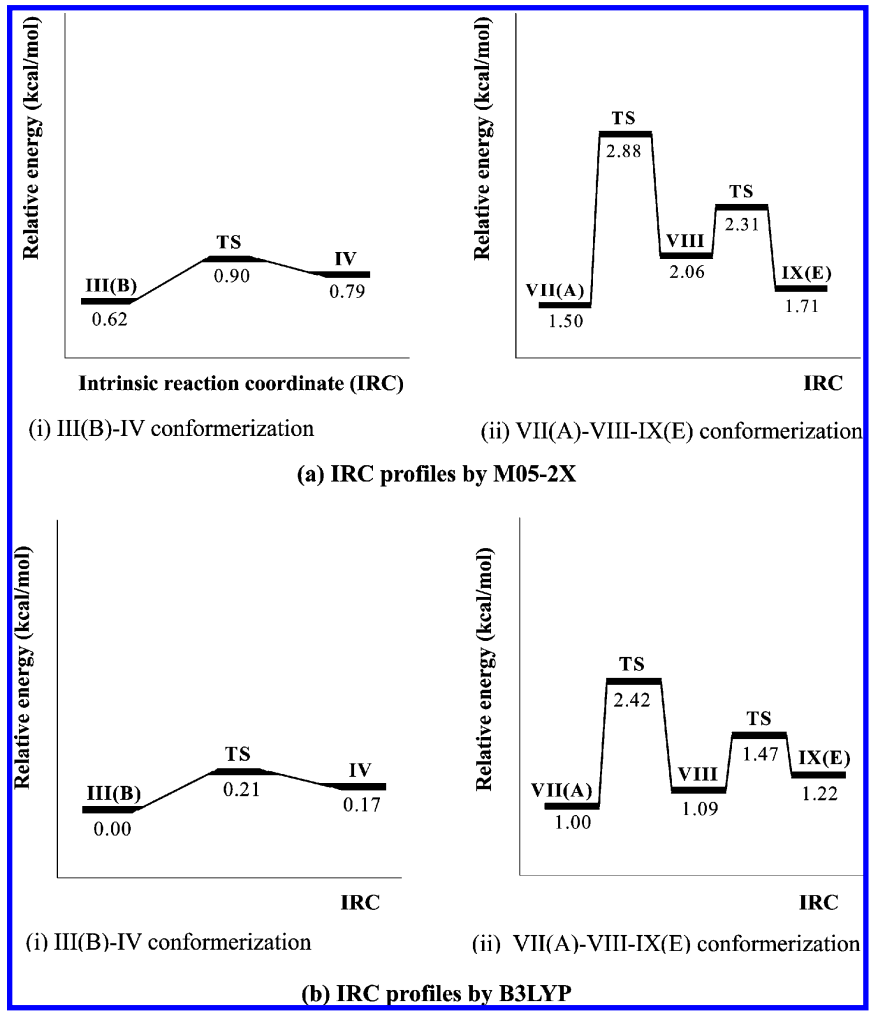

Figure 2. IRC profiles for conformerizations for neutral conformers: (i) III(B) and IV conformarization and (ii) VII(A), VIII, and IX(E) conformarization. (a) Results obtained by M05-2X; (b) results obtained by B3LYP. The origin of the relative energy is taken to be the energy of III(B), which was calculated by B3LYP. Rotation of $-NH_2$ keeping intramolecular hydrogen bonding with the carbonyl group is the reaction coordinate for (i), and rotation of $-NH_2$ is the reaction coordinate for (ii). Reaction paths through corresponding transition state are determined by IRC. Zero-point energy correction was taken into account.

the $C_\alpha-C_\beta$ bond and a nonplanar, pyramidal structure for $-NH_2$ on conformer V. This indicates that neutral conformer V belongs to subgroup II while cationic conformer V belongs to subgroup I.

This is totally different from the results obtained by B3LYP: both the neutral and the cationic conformers of V were assigned to subgroup II. Such a hybrid type of conformer that has different characters between the neutral and ion is one of the newly found results using the new DFT functional that takes into account noncovalent interactions.

Table 2 shows relative energies including zero-point energy corrections (ZPE_{corr}) of the conformers, which were calculated by both methods. The original Roman numerals were used to avoid confusion even though their energy ordering is different from that of M05-2X in Table 2.

B. Correspondence between the Observed and Computed Conformers. It has remained to be determined why conformers IV, V, and VIII, which were predicted by B3LYP calculations, have not been identified experimentally. Conformer IV belonging to subgroup I has a relative energy ΔE of 0.17 kcal/mol (B3LYP) as shown in Table 2 and an activation energy E_a of 0.04 kcal/mol (see Figure 2) in its neutral state, which is efficient for IV to be produced in a chamber under experimental conditions at temperatures of 170−190 °C (kT= 0.88−0.92 kcal/mol).

Conformer VIII belonging to subgroup II has also not been assigned experimentally, though B3LYP calculation of ΔE = 1.09 kcal/mol shown in Table 2 indicates the possibility of its observation. The M05-2X value of ΔE = 0.79 kcal/mol for conformer IV is very close to that of conformer III(B), ΔE = 0.62 kcal/mol. Here, entropy effects were neglected since the change in dihedral angle $C_\pi-C_\beta-C_\alpha-C_\gamma$, which is associated with the backbone and side chain (residue) rotation, is very small between the two conformers.

Figure 2 shows the results of IRC profiles for two conformerizations, (i) III(B)−IV conformerization and (ii) VII(A)−VIII−IX(E) conformerization. Figure 2a shows M5-2X results, and Figure 2b shows B3LYP results. For (i) III(B)−IV conformerization, both the M05-2X and B3LYP results gave almost the same behaviors for IRC profiles with a transition state having one imaginary frequency: the E_a of IV is 0.11 kcal/mol for M05-2X and 0.04 kcal/mol for B3LYP; ΔE between III(B) and IV is 0.17 kcal/mol for both M05-2X and B3LYP.

It has been shown that complex molecules with multiple degrees of conformational flexibility need a barrier height of 600 cm^{-1} (1.72 kcal/mol) or higher to be trapped in jet expansion experiments.[22] This shows that under ordinary experimental conditions for a supersonic jet expansion experiment it is highly possible for III(B) and IV to be detected as the same conformer. The population ratio between III(B) and

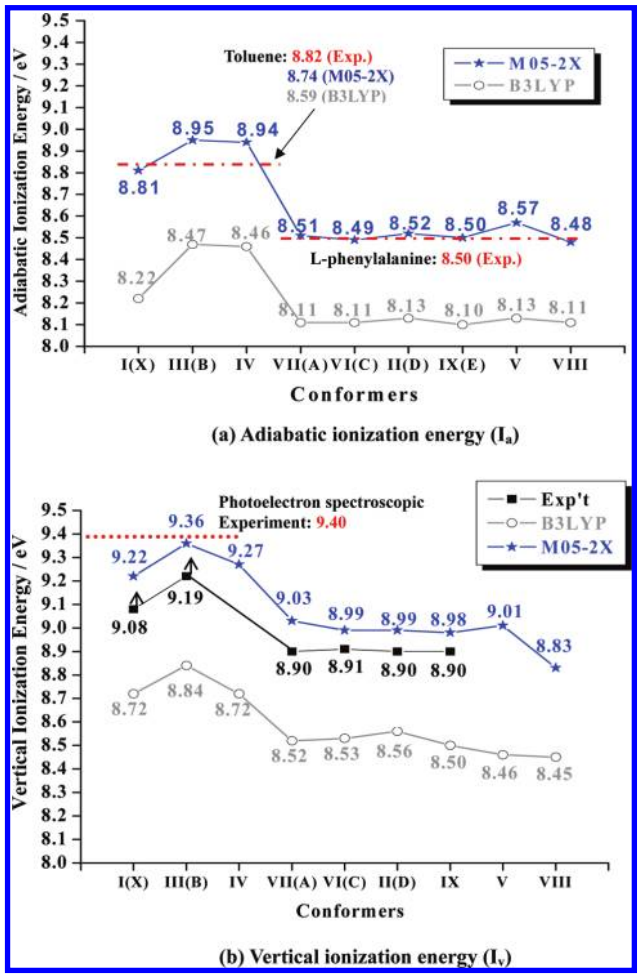

Figure 3. M05-2X and B3LYP results for (a) adiabatic and (b) vertical ionization energies for the nine most stable conformers. Zero-point energy corrections are included. Experimental values are also shown for comparison. For adiabatic ionization energies, ionization energies of aromatic molecules with the corresponding chromophore are shown. For (b) Experimental values denoted by black rectangles were estimated from photoionization efficiency (PIE) curves in resonant two-photon ionization experiments (see text). A dotted line denotes vertical ionization values obtained by one-photon photoelectron spectroscopic measurement of mixed conformers of L-phenylalanine.[26]

IV is roughly estimated to be 1:0.21 using a vibrational temperature of $T = 57$ K, which was adopted from rotational band-counter analyses of conformers in a supersonic jet expansion experiment by J. P. Simons et al.[6] The ratio obtained by assuming that conformers retain thermal equilibrium is approximate, and detailed discussions are needed on cooling and trapping processes in supersonic jet expansion experiments in order to obtain more reliable population ratios.[22,23]

Although it is difficult to find clear evidence of the coexistence of the two conformers from the corresponding band in UV spectra, the possibility of coexistence is indicated by comparison of experimental rotational band contours with theoretically predicted results.[11] Here, the experimental band contours cannot be fitted well to the theoretical ones within one conformer III(B) model. For (ii) VII(A)−VIII−IX(E) conformerization, two results are totally different: the B3LYP cannot explain the fact that VIII have not been observed. On the other hand, its M05-2X calculation showed $\Delta E = 2.06$ kcal/mol = $\sim$700 cm^{-1}, indicating that the energy is too high for it to be observed. The population of conformer VIII, which was estimated in the same way as described above, is too small to be observed, while VII(A) and IX(E) can be observed.

C. Vertical and Adiabatic Ionization Energies. Figure 3a and b shows calculated adiabatic (vertical) ionization energies of nine L-phenylalanine conformers. Here, zero-point energy corrections were taken into account. Both the adiabatic and vertical ionization energies calculated with M05-2X are higher than those calculated with B3LYP by $\sim$0.5 eV for all of the conformers. There have been no experimental reports on adiabatic ionization energies except for photoelectron measurements.

This is because Franck−Condon factors for 0−0 transitions are negligibly small, which are due to large geometrical changes between the neutral and the cationic states, that is, elongation of the $C_\alpha-C_\beta$ bond and dihedral angle of $C_\pi-C_\beta-C_\alpha-N$ and pyramidal structure for $-NH_2$ on ionization as shown in Table 1. Photoelectron spectroscopic values of toluene (8.82 eV)[24] and L-phenylalanine (8.50 eV)[25] are plotted in Figure 3a. The theoretical values I_a (M05-2X and B3LYP) for toluene are also plotted to estimated a possible error in the calculations.

The M05-2X adiabatic ionization energies of the subgroup I conformers, I (X), III(B), and IV, are close to that of toluene, and the adiabatic ionization energies of the subgroup II conformers, VII(A), VI(C), II(D), and IX(E), are close to that

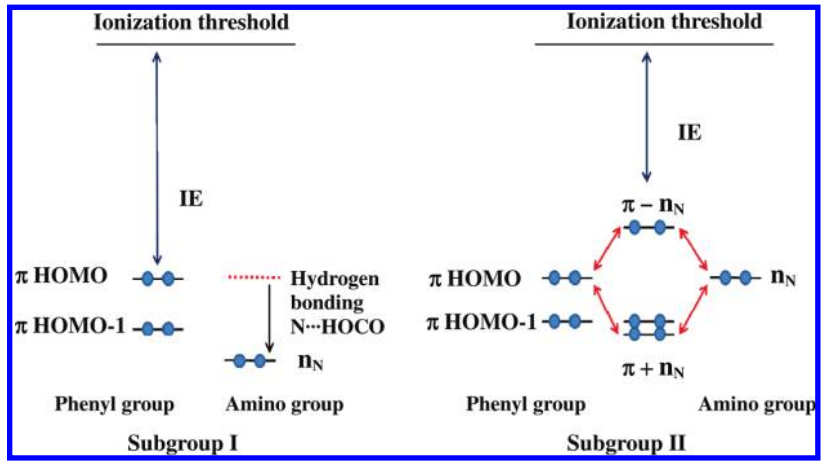

Figure 4. MO picture showing the differences in ionization energies between conformers belonging to subgroup I and those belonging to subgroup II. (a) For subgroup I, intramolecular hydrogen bonding from carboxylic hydrogen to lone pair electrons induced stabilization for the nonbonding orbital of nitrogen. (b) For subgroup II, the nonbonding orbital of the amino group and a π MO of the phenyl ring interact to form new bonding and antibonding MOs. The antibonding MO is destabilized, and these results in lower ionization energy are compared with noninteracting cases.

TABLE 3: Partial Charge Distributions of Cationic Conformers, which were Obtained by M05-2X and B3LYP (in parentheses) with a 6-311+G* Basis Set Through NBO Analysis[a]

Subgroup	Experimental Assignment	Conformer	M05-2X (B3LYP)			
			Phenyl group		Amino group	
I	X	I	0.79	(0.62)	0.04	(0.09)
	B	III	0.73	(0.53)	0.09	(0.17)
		IV	0.73	(0.54)	0.09	(0.16)
		V	**0.81**	(0.42)	0.06	(0.33)
II	A	VII	0.34	(0.41)	0.34	(0.35)
	C	VI	0.38	(0.44)	0.33	(0.34)
	D	II	0.39	(0.44)	0.31	(0.34)
	E	IX	0.34	(0.41)	0.34	(0.35)
		VIII	0.33	(0.40)	0.34	(0.35)

[a] Results obtained by M05-2X show that the charge is localized on the phenyl ring for subgroup I, while it is delocalized into two chromophores, phenyl and amino groups, for subgroup II.

of L-phenylalanine, and their energy differences are within 0.1 eV. The adiabatic energies calculated B3LYP, on the other hand, are far from the experimental values by ~0.6 eV for the subgroup I conformers and ~0.4 eV for the subgroup II conformers.

Concerning vertical ionization energies, conformational-dependent ionization energies have been reported by Lee et al.[21] They measured photoionization efficiency (PIE) curves as a function of the wavelength of the ionization laser while fixing the wavelength of the excitation laser at the S_1 band origin of each conformer in mass-resolved resonant two-photon ionization (R2PI) experiments. The spectra exhibit a start up in PIE curve at ~8.8 eV for all the subgroup II conformers (VII(A), VI(C), II(D), and IX(E)) and at ~9.0 eV for I(X) and 9.15 eV for III(B) of subgroup I conformers.

We estimated the vertical ionization energy corresponding to the maximum Franck−Condon overlap between the initial and the ionized states from each PIE spectrum by noting that the PIE curve corresponds to ionization yield as a function of the wavelength of the ionization laser. The values thus estimated are indicated by the solid squares in Figure 3b.

The estimated values for the vertical ionization energies of subgroup I conformers are marked by solid squares with an arrow, which represent lower bounds for the vertical ionization energies observed because of restriction in the wavelength ranges in the PIE measurement.[21] Only one experimental value of 9.4 eV, which was obtained from a photoelectron spectrum[26] of a mixture of L-phenylalanine conformers, is given in Figure 3b.

Figure 3b demonstrates that the M05-2X functional satisfactorily reproduces vertical ionization energies, being close to both the PIE and the photoelectron experimental values, while the B3LYP functional could not quantitatively reproduce these experimental values. It has already been pointed out that there is a tendency in ionization energy differences between subgroup I and II conformers, that is, the ionization energies of subgroup I conformers are higher than those of subgroup II.[21]

As shown in Figure 4, the tendency can be explained in terms of intramolecular hydrogen bonding between lone pair electrons of the amino group and hydrogen of the carboxyl group for subgroup I conformers. The n-MO of the amino group is stabilized as a result of hydrogen bonding, and interactions between the π-HOMOs of the phenyl group and the n-MO become negligibly small.

For subgroup II conformers, on the other hand, the energy levels of π-MOs and n-MO are close to each other as can be seen in Figure 4, and a pair of MOs is formed between a π -MO and a n-MO. This newly formed MOs are called hyperconjugative MOs.[27]

Ionization from one of the hyperconjugative MOs with an antibonding character results in lowering of ionization energies of subgroup II conformers. $C_\alpha-C_\beta$ elongation of the subgroup II conformers on ionization can qualitatively be explained in

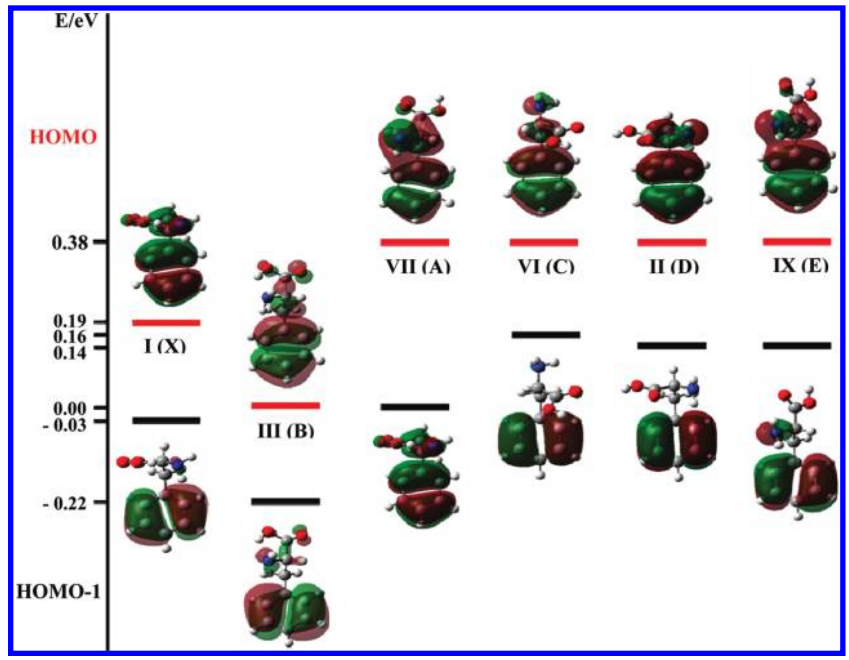

Figure 5. Molecular orbital phases and energies for HOMOs and HOMO-1 of six conformers. Orbital energies of the HOMOs of the conformers belonging to subgroup II were converged at almost the same value. It should be noted from their phases that these HOMOs form hyperconjugative MOs: electrons of nitrogen interact with the phenyl ring through space [VII(A), IX(E)] or bonds [VI(C), II(D)] on the HOMO. In contrast, I(X) and III(B) belonging to subgroup I do not form hyperconjugative MOs between the MO of the amino group and the phenyl group due to formation of the intramolecular hydrogen bond between the carboxylic hydrogen and the lone pair electrons of the amino group. This makes the HOMO energies lower than those of subgroup II.

terms of electron dynamics associated with hyperconjugative MO. The C_α-C_β elongation is mainly brought about by an electron release from the antibonding hyperconjugative MO: after ionization, both chromophores, phenyl and amino groups, have a positive partial charge with equal weights and attract electrons in the $C_\alpha-C_\beta$ bond. As a result, elongation occurs.

D. Charge Distributions of Cationic Conformers. Accurate evaluation of conformation-dependent charge distributions is very important in studying the mechanisms of ionization-induced chemical reactions as well as determination of conformers.[1,2] Table 3 shows the M05-2X results for the charge distributions on two chromophores, the phenyl ring and amino groups of the nine conformers. For comparison, B3LYP results also are shown in Table 3. Both the M05-2X and B3LYP results indicate that the charge distributions of subgroup I conformers are localized on the phenyl ring, while for subgroup II conformers except conformer V they are qualitatively delocalized, that is, the charges are shared between the two chromophores. This feature was already revealed in a previous study in which the B3LYP functional was adopted.[2]

The newly calculated value of 0.81 for conformer V strongly suggests that the cationic conformer belongs to subgroup I. In addition, the newly obtained results for the charge distributions show remarkable contrast in charge distributions between the two subgroups compared with those obtained by the B3LYP method. In particular, charges of subgroup II conformers are almost equally distributed between the phenyl and the amine groups.

The differences in charge distributions between the two subgroups were explained as a result of intramolecular hydrogen bond formation.[6] In addition to intramolecular hydrogen bonding $-COOH \rightarrow -NH_2$ for subgroup I conformers I(X) and III(B), we should stress that hyperconjugation in subgroup II conformers VII(A), VI(C), II(D), and IX(E) is responsible for the delocalized charges as qualitatively indicated in Table 3.

Figure 5 shows the phases of HOMO and HOMO-1 of the observed conformers: It can be seen from Figure 5 that for subgroup II hyperconjugative HOMOs are formed through space interactions between the n-MO of the amino group and the π orbital of the phenyl ring [VII(A), IX(E)] or through bond interactions [(VI(C), II(D)].

Conclusions

We performed M05-2X calculations of adiabatic ionization and vertical ionization energies and of charge distributions in the cationic conformers in addition to optimized geometrical structures for both the neutral and the cationic conformers of L-phenylalanine. The two functionals, M05-2X and B3LYP, gave the same nine stable conformers in their neutral state. However, quantitatively, their relative energies were different, the magnitudes of which are sufficient to identify the conformers: the M05-2X results can unambiguously explain the correspondence between the observed and the predicted conformers in terms of the relative energy and activation energy between the two conformers.

We confirmed the classification of the conformers into two subgroups, I and II, as given before except for conformer V. Conformer V is of a hybrid character, belonging to subgroup I in its neutral form and belonging to subgroup II in its cation form. This character should be confirmed by experiments. The present results provide a reliable basis for analysis of ionization efficiency spectra and investigation of mechanisms of chemical reactions of aromatic amino acids. Ionization-induced conformational change is one of the examples of chemical reactions.[28,29]

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