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# A computational study of the thermodynamic properties of sinapic and ferulic acids and their corresponding radical cations

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#### **Abstract**

The gas-phase basicities and gas-phase proton affinities of sinapic acid and ferulic acid, which are common matrices used in matrix assisted laser desorption/ionization mass spectroscopy, have been calculated using density functional theory at the B3LYP/6-311+G(2df,p)//B3LYP/6-31G\*\* level. Respectively, the GBs of the two acids are 869.0 and 862.4 kJ/mol while the gas-phase PAs of the same systems are 903.4 and 896.0 kJ/mol. Our results indicate that the protonation in these systems takes place on the carboxylic sites. In addition, the GAs of the radical cations of these acids has also been calculated. The calculated GAs of SA and FA radical cations are 899.8 and 889.6 kJ/mol, respectively. Our results indicate that deprotonation in the two radical cations takes place on the phenol sites. We also provide the first estimates of the vertical ionization potentials (IPs) of the same systems at the B3LYP/6-311++G(2df,p)//B3LYP/6-31+G\*\* level using the lowest energy structure found for each acid. The calculated IPs of SA and FA are 7.54 and 7.82 eV, respectively.

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#### 1. Introduction

Matrix assisted-laser desorption and ionization mass spectrometry (MALDI-MS) is well known as a powerful ionization tool for mass analysis of large molecules [1–15]. In MALDI, the analyte is co-deposited onto a target surface with an excess of a small substituted aromatic compound called a matrix. Subsequent laser desorption and ionization of the mixture results in protonation of the analyte, making it amenable to mass spectrometric analysis. The mechanism of ionization and protonation involved in this technique is still not fully understood. In order to provide a fundamental understanding of this mechanistic problem, it is essential to understand thermodynamic properties of the relevant species in a MALDI event and the nature of the specific analyte/matrix interactions leading to proton transfer. We have previously studied, both computationally and experimentally, the specific analyte/matrix interactions between common MALDI matrices and several amino acids and tripeptides [16-18]. In an attempt to provide high quality thermodynamic database for species

acidities (GAs), gas-phase basicities (GBs), gas-phase proton affinities (PAs), and ionization potentials (IPs) of all isomers of dihydroxybenzoic acid (DHB) and the GAs of their radical cation species [19,20]. Here, we present a computational study of the GBs, PAs, and IPs of two common MALDI matrices: sinapic acid (SA) and ferulic acid (FA), and the GAs of their radical cations. The aim of this work is (1) to provide reasonable estimates of the GBs, PAs, and GAs of SA and FA, (2) to study the protonation process of the these matrices, and (3) to study the deprotonation process of the radical cation species of the same systems.

relevant to MALDI, we previously calculated the gas-phase

### 2. Computational methodology

The GB and PA of each matrix (M) are defined, respectively, as the negative of the free energy change and the negative of the enthalpy change for the reaction

$$M_{(g)} - H_{(g)}^+ \to MH_{(g)}^+$$
 (1)

while the GA of each matrix is defined as the free energy change for the reaction

$$M_{(g)} \rightarrow [M-H]_{(g)}^+ + H_{(g)}^+$$
 (2)

where  $[M-H]^-$  represents the deprotonated matrix. Similarly, the GA of each matrix radical cation  $(M \cdot^+)$  is defined as the

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free energy change for the reaction

$$M_{(g)}^{,+} \to [M - H]_{(g)}^{,} + H_{(g)}^{+}$$
 (3)

For the GB and PA calculations, we have examined all possible conformations of each matrix and its protonated species with significant hydrogen bonding. All geometries were optimized at the B3LYP/6-31G\*\* [21,22] level. Each stationary point was fully characterized as a true minimum by vibrational force constant analysis. Single point calculations were done on the lowest energy conformations of each matrix and its protonated form at the B3LYP/6-311+G(2df,p) level. The final  $\Delta E_{\rm elec}^0$  value using the lowest energy structures of each isomer and its protonated species was determined at the B3LYP/6-311+ G(2df,p)//B3LYP/6-31G\*\* level for each matrix. Basis set superposition error (BSSE) was calculated by standard procedures [23,24] for protonated benzoic acid, which was considered to be an adduct of benzoic acid and a proton. The relative energies of all protonated structures were assumed to be independent of BSSE. Thermodynamics properties, including zero-point energies, were obtained at the B3LYP/6-31G\*\* level and were used for the calculation of the GB and PA at 298 K and 1 atm (recommended scaling factors were taken from the literature) [25]. As recommended in this paper, the ZPE, enthalpy, and entropy were scaled individually. All thermodynamic properties, except the IPs, were Boltzmann averaged over all energetically competitive structures, as detailed in a previous publication [26].

The same methodology was used to calculate the GA of the radical cations of the two acids. However, the BSSE was calculated for the phenol radical cation and the same BSSE correction was used for both radical cations.

The vertical IP's were calculated at the B3LYP/6-311++ G(2df,p)//B3LYP/6-31+ $G^{**}$  level, using only the lowest energy structure for the neutral and cationic species of both systems.

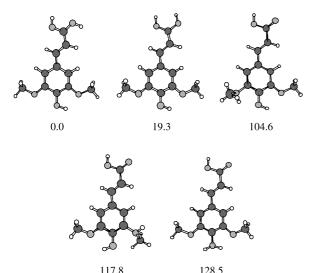


Fig. 1. All possible protonated conformations of one neutral conformation of SA with relative energies (kJ/mol) at the B3LYP/6 31G\*\* level.

All calculations were performed using the GAUSSIAN 98 [27] and 03 [28] suites of programs.

#### 3. Results and discussion

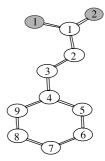
## 3.1. Gas-phase basicity and gas-phase proton affinity

To minimize the number of the conformations to be examined, all possible protonation sites were tested first for a limited number of conformations. Fig. 1 shows the protonated conformations of SA that resulted from protonating one neutral conformation of SA at the carboxylic group and at all phenolic groups (protonation at the carboxylic group's OH resulted in

Table 1
All calculated conformations of neutral SA and FA with their relative energies (kJ/mol) at the B3LYP/6 31G\*\* level<sup>a,b,c</sup>

Acid	COOH	6-OCH <sub>3</sub>	7-OH	8-OCH <sub>3</sub>	$\Delta E$ (kJ/mol)
SA	(C, T)	U	T	U	0.0
	(C, T)	U	C	U	0.1
	(C, C)	U	C	U	3.8
	(C, C)	U	T	U	4.0
	(C, T)	U	C	$D_p$	4.2
	(C, T)	$D^{b}$	T	U	4.5
	(C, C)	U	C	$D_p$	7.3
	(C, C)	$D^{b}$	T	U	8.8
FA	(C, T)	U	C	_	0.0
	(C, T)	_	T	U	1.1
	(C, C)	U	C	_	3.3
	(C, C)	_	T	U	5.3
	(C, T)	U	T	_	19.4
	(C, T)	_	C	U	20.9
	(C, C)	U	T	_	23.0
	(C, C)	_	C	U	24.8
	(C, T)	$D^{b}$	T	_	25.5
	(C, T)	_	C	$D_p$	26.6
	(C, C)	$D^{b}$	T	_	29.4
	(C, C)	_	C	$D_p$	30.0

<sup>&</sup>lt;sup>a</sup> The carbons in the parent structure of the SA and FA systems are numbered as shown below:



b The terms C, T, D, U and (,) represent the following: C, the C=O on  $C_1$  or 7 OH bond on  $C_7$  is cis to  $C_5$  or the C=O is cis to the OH on the COOH group; T, the C=O on  $C_1$  or 7 OH bond on  $C_7$  is trans to  $C_5$  or the C=O is 'trans' to the OH on the COOH group; U, the OH or OCH<sub>3</sub> points 'up' (toward the COOH group for a phenolic group or away from the benzene ring for a protonated carboxylic group); D, the OH or OCH<sub>3</sub> points 'down' (away from the COOH group for a phenolic group or toward the benzene ring for a protonated carboxylic group). The notation (C, T) means that the C=O on  $C_1$  is cis to the OH on the COOH group and the same C=O is 'trans' to  $C_5$ . Similar definitions hold for (T, C), (C, C) and (T, T).

<sup>&</sup>lt;sup>c</sup> OCH<sub>3</sub> is out of the plane of the benzene ring.

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