

Full Length Article

Residue-specific radical-driven dissociation of peptides using matrix-assisted laser desorption/ionization in-source decay with hydrogen-donating and -abstracting matrices



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dedicated to Professor Shuying Liu in honor of her 75th birthday.

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ABSTRACT

Radical-driven dissociation (RDD) of peptides was examined by MALDI-ISD with hydrogen-donating and -abstracting matrices. The observed fragment ions could be explained by the RDD of carbonyl-carbon (C_{CO})-centered hydrogen-excess radical ions $[M + H_{CO} + H]^+$ and β -carbon ($C\beta$)-centered hydrogen-deficient radical ions $[M - H\beta + H]^+$. The ISD spectra with hydrogen-abstracting and -donating matrices yielded C-terminal $[x]^+$, $[y]^+$ and $[z]^+$ ions and C-terminal $[x + 2H]^+$, $[y + 2H]^+$ and $[z + 2H]^+$ ions, respectively, indicating the formation of MALDI plume devoid or rich in hydrogen radicals H. The residue-specific cleavages of the hydrogen-deficient radical ions $[M - H + H]^+$ gave $[d]^+$ ions for Asp and Met, $[b]^+$, $[y]^+$ and $[w]^+$ ions for Pro, and relatively intense $[a]^+$ ions for aromatic residues (Tyr and Phe). We suggest that $[y_m + 2H]^+$ ions are produced from transient radical ions $[z_{m+1} + H]^+$.

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1. Introduction

The importance of radical-driven dissociation (RDD) has long been recognized in the structural elucidation of organic compounds using mass spectrometry (MS) because of the specific cleavage initiated by a radical (unpaired electron) site [1]. Recent RDD researches on peptides and proteins utilize electron-capture dissociation (ECD) [2], electron-transfer dissociation (ETD) [3], ultraviolet photo-dissociation (UVPD) [4–7], and in-source decay (ISD) [8–10] combined with matrix-assisted laser desorption/ionization (MALDI) [11,12] and electrospray ionization (ESI) [13,14]. Traditionally, RDD employs electron ionization (EI) to form radical cations $[M]^+$ of volatile compounds. In modern RDD, the peptide radical ions can be generated by electron attachment to protonated analytes $[M + nH]^{n+}$ [2,3], short wavelength UV photon irradiation to analyte ions [4–6], and hydrogen atom binding to carbonyl oxygens of peptide backbones [9]. The structures of hydrogen-abundant protonated and hydrogen-deficient peptides $[M \pm H + H]^+$ are shown in Scheme 1a. RDD of peptides characteristically give amino (N)-terminal $[a]^+$, $[c + 2H]^+$, and $[d]^+$ ions and carboxyl (C)-terminal $[x]^+$, $[z + 2H]^+$, and $[w]^+$ ions [2,9,10]. In

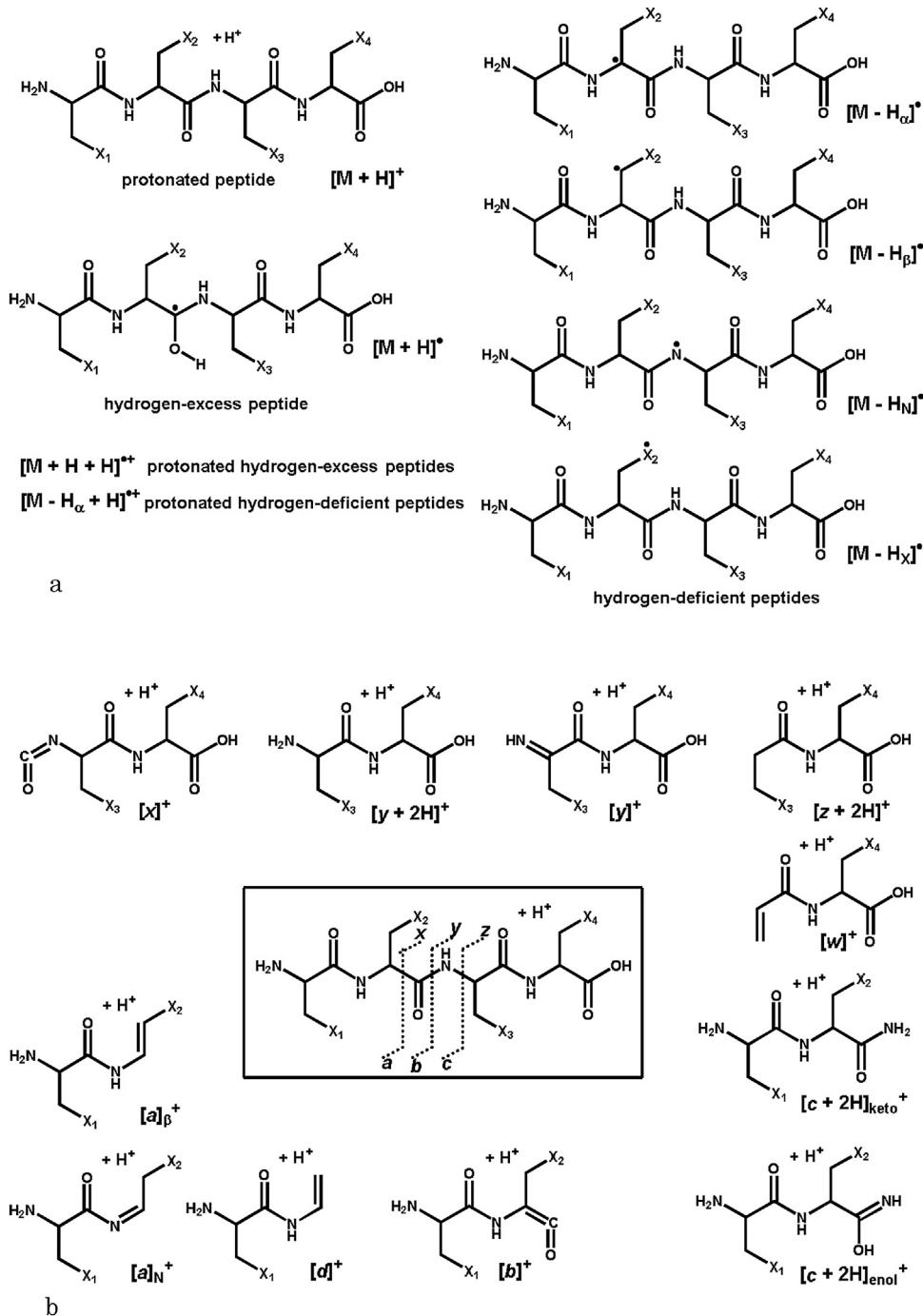
contrast, conventional low-energy collision-induced dissociation (low-E CID) of peptides results in $[b]^+$ and $[y + 2H]^+$ ions [15]. Herein we use the peptide fragment ion nomenclature proposed by Chu et al. [16] based on Biemann's nomenclature [17] (Scheme 1b).

In UVPD experiments, photo-induced homolytic cleavage of peptides at the $C\alpha$ -C bond and consecutive RDD reactions can explain the formation of N-terminal $[a]^+$ and $[d]^+$ ions and C-terminal $[x]^+$ and $[w]^+$ ions. The mechanism is attributable to the Norrish type I photochemical reaction [5,18] (Scheme 2). However, it is likely that $[a]^+$ ions preferentially form from β -carbon ($C\beta$)-centered hydrogen-deficient peptide radical ions $[M - H\beta + H]^+$ [19–22]. Indeed, we also recently reported that $[a]^+$ ions are produced from the ($C\beta$)-centered radical ions $[M - H\beta + H]^+$ when MALDI-ISD is performed with a hydrogen-abstracting matrix 4-nitro-1-naphthol (4,1-NNL) [23] (Scheme 3). The Brodbelt group pointed out that $[a]^+$ ions generated by UVPD are useful for characterizing hydrogen-bonding motifs of proteins [24]. In UVPD, product ions originating from residue-specific cleavages at aromatic side chains, backbone $C=O$ chromophore [22,25,26], at acidic Asp/Glu/Cys, and Pro effects in low-E CID [15] give structural information. Therefore, it is important to examine residue-specific cleavage of peptides from the standpoint of radical-driven dissociation (RDD).

Here, we examine the residue-specific cleavage of peptides containing Arg, Tyr, Phe, Asp, Pro, deuterated-Gly, and deuterated-

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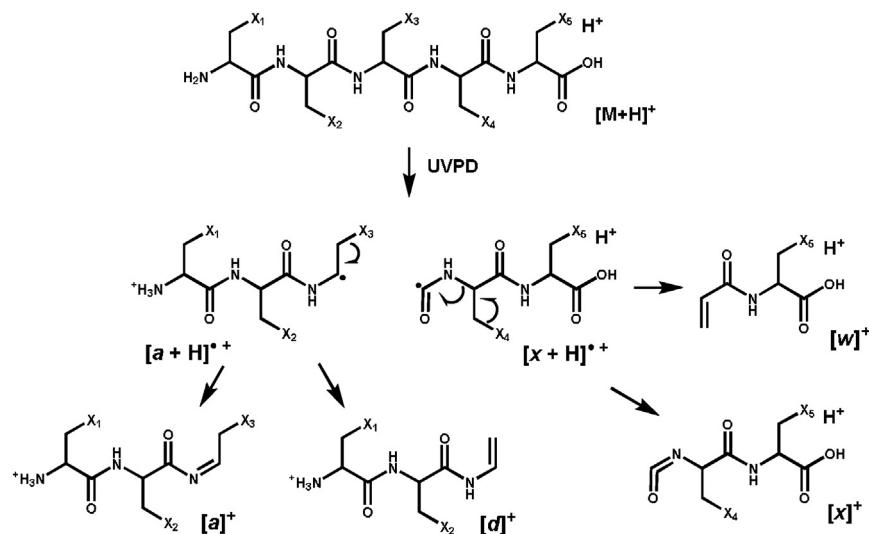
Scheme 1. a. Nomenclature of protonated peptide and hydrogen-excess/deficient peptides. b. Nomenclature of peptide product ions [16,17].

Ala residues using MALDI-ISD. The radical species, such as hydrogen-abundant and -deficient peptide ions, $[M \pm H + H]^+$, were generated with hydrogen-donating matrices 5-amino-1-naphthol (5,1-ANL) and 2,5-dihydroxybenzoic acid (2,5-DHB) and, hydrogen-abstracting matrices 4,1-NNL and 5-aminosalicylic acid (5-NSA), respectively. We also discuss the formation mechanisms of the product ions, especially $[y]^+$ and $[y + 2H]^+$ ions, in the different plume conditions and consecutive radical-driven dissociations of transient radical species.

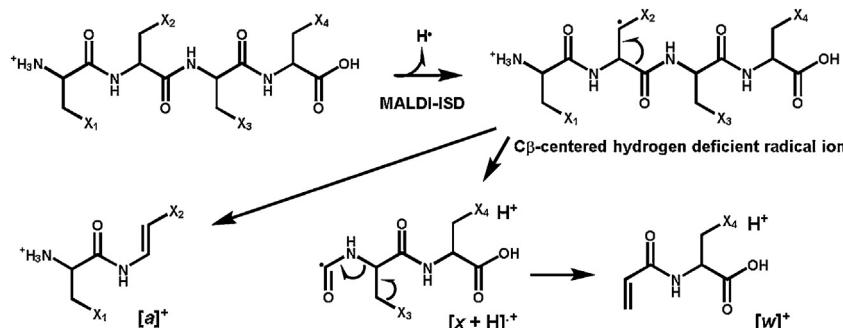
2. Experimental

2.1. Materials

Matrix materials 5,1-ANL, 2,5-DHB, 4,1-NNL, and 5-NSA were purchased from Tokyo Chemical Industry (Tokyo, Japan). Synthetic peptides RGV-d5 (RGVKVDYG(d2)PAMAFA(d3)PADLAAEF, Mr 2301.6) and EGV-d5 (EGVKVDYG(d2)PAMAFA(d3)PADLAARF, Mr 2301.6) were obtained from Peptide Institute (Minoh, Osaka, Japan). Acetonitrile was purchased from Wako Pure Chemicals



Scheme 2. The mechanism for the formation of $[a]^\bullet$, $[d]^\bullet$, $[x]^\bullet$ and $[w]^\bullet$ ions proposed from UVPD experiments of peptides [4–7,18–22].



Scheme 3. The mechanism for the formation of $[a]^\bullet$ and $[w]^\bullet$ ions proposed from MALDI-SD experiments of peptides with hydrogen-abstrating matrix [23].

(Osaka, Japan). Water used in all experiments was purified using a MilliQ water purification system from Millipore (Billerica, MA, USA). All reagents were used without further purification.

2.2. Mass spectrometry

MALDI-SD experiments were performed with a time-of-flight mass spectrometer AXIMA-CFR (Shimadzu, Kyoto, Japan) equipped with a nitrogen laser (337 nm wavelength, 4 ns pulse width) operating at a pulse rate of 10 Hz. The laser spot size on the target substrate was *ca.* 100 μm in diameter. The ions generated by MALDI were accelerated using 20 kV with delayed extraction. The analyzer was operated in reflectron mode, and ions were detected using a microchannel plate detector. A total of 500 shots were accumulated for each mass spectrum acquisition.

2.3. Sample preparation

Analyte peptide was dissolved in water at a concentration of 100 pmol/ μL . The matrix material was dissolved in water/acetonitrile (1:1, v/v) without any additives and the matrix solution was prepared at 10 mg/mL. A sample solution was prepared by mixing 10 μL of the dissolved analyte with 10 μL of matrix solution. A volume of 1.0 μL of the sample solution was deposited onto a stainless-steel MALDI plate, and the solvents were removed by evaporation in air at room temperature.

3. Results and discussion

3.1. Specific peptide fragment ions are generated in MALDI-SD acquired with hydrogen-donating matrix

Positive-ion MALDI-SD spectra of peptide RGV-d5 with an N-terminal Arg obtained with hydrogen-donating matrices 5,1-ANL and 2,5-DHB are shown in Fig. 1. The ISD spectrum acquired with 5,1-ANL only contained N-terminal $[c + 2\text{H}]^+$ ions except for $[c8 + 2\text{H}]^+$ and $[c14 + 2\text{H}]^+$ ions owing to the presence of Pro9 and Pro15 residues (Fig. 1a). The spectrum with 2,5-DHB showed preferential formation of $[c + 2\text{H}]^+$ ions and weak $[a]^\bullet$ and $[y + 2\text{H}]^+$ ions, and some $[b]^\bullet$ and $[d]^\bullet$ ions (Fig. 1b). The ISD spectra of peptide EGV-d5 with a C-terminal Arg obtained with 5,1-ANL and 2,5-DHB are shown in Fig. 2. In contrast to the RGV-d5 spectrum with 5,1-ANL, the ISD spectrum of EGV-d5 mainly yielded $[z + 2\text{H}]^+$ product ions. The ions, $[z8 + 2\text{H}]^+$ and $[z14 + 2\text{H}]^+$, were not observed due to the presence of Pro9 and Pro15 residues (Fig. 2a). This spectrum also has $[c + 2\text{H}]^+$, $[z\text{-matrix} + \text{H}]^+$ and $[y + 2\text{H}]^+$ ions. Interestingly, when 5,1-ANL was employed, the intensity of $[y16 + 2\text{H}]^+$ ion originating from cleavage at the C–N bond of Asp6-Tyr7 residues was higher than that of $[z16 + 2\text{H}]^+$, while the intensity of $[z_n + 2\text{H}]^+$ ions was more intense than that of the corresponding $[y_n + 2\text{H}]^+$ ions (Fig. 2a). In contrast, the ISD spectrum with 2,5-DHB demonstrated preferential production of $[y + 2\text{H}]^+$ rather than $[z + 2\text{H}]^+$ ions (Fig. 2b). It is noteworthy that $[z + 2\text{H}]^+$ ions were not observed due to the lack of strong protonation sites in z-fragments (Fig. 1b), whereas both Fig. 2a and b showed the C-terminal pair of $[y + 2\text{H}]^+$ and $[z + 2\text{H}]^+$ ions because of the presence of an Arg residue.

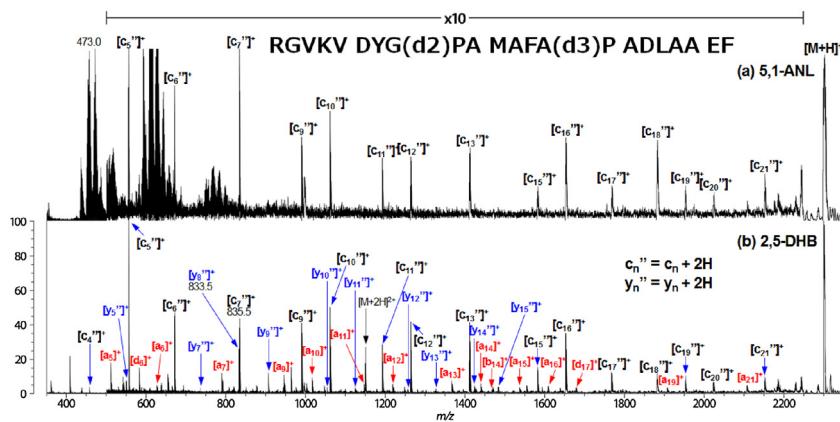


Fig. 1. MALDI-ISD spectra of peptide RGV-d5 containing an N-terminal Arg obtained with hydrogen-donating matrices (a) 5-amino-1-naphthol (5,1-ANL) and (b) 2,5-dihydroxybenzoic acid (2,5-DHB).

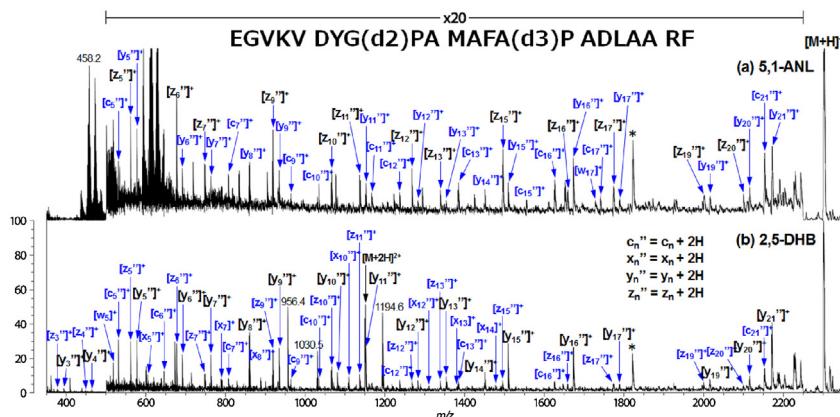
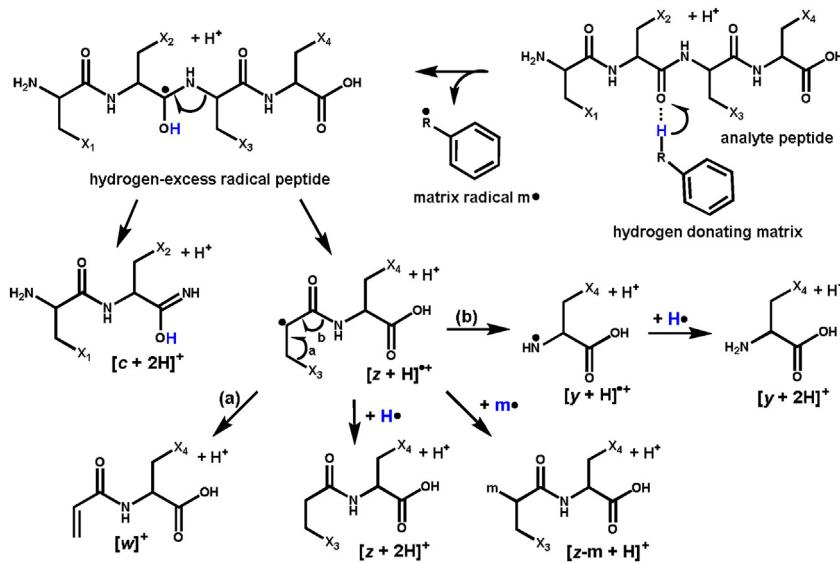


Fig. 2. MALDI-ISD spectra of peptide EGV-d5 containing a C-terminal Arg obtained with hydrogen-donating matrices (a) 5-amino-1-naphthol (5,1-ANL) and (b) 2,5-dihydroxybenzoic acid (2,5-DHB).



Scheme 4. Proposed MALDI-ISD mechanism of peptides with hydrogen-donating matrix.

The MALDI-ISD mechanism of peptides and proteins with hydrogen-donating matrix can be explained by a prompt (within several tens ns) and specific cleavage at the N-C α bond of the peptide backbone. It results from the generation of hypervalent radical species such as carbonyl-carbon (C CO)-centered hydrogen-

abundant radical peptides and proteins [M + H CO] $^\cdot$ (Scheme 4). In MALDI-ISD experiments, the prompt and specific cleavage takes place independently of ionization (protonation and deprotonation) [27,28]. The C CO -centered hydrogen-abundant radical peptides and proteins [M + H CO] $^\cdot$ are formed via hydrogen transfer from phe-

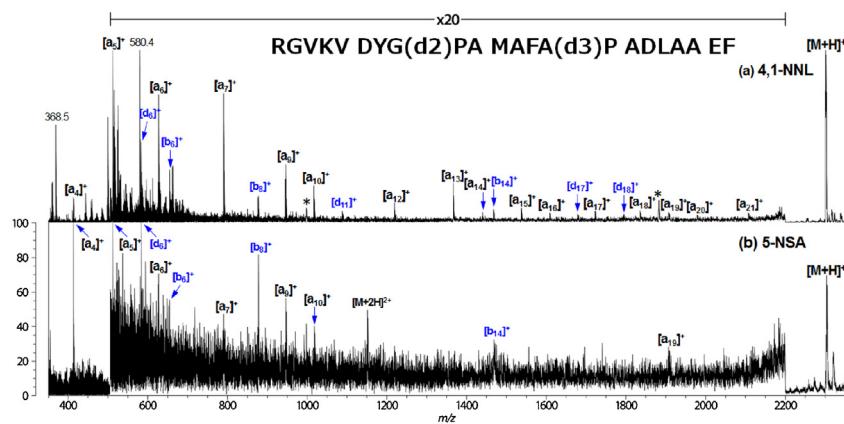


Fig. 3. MALDI-SD spectra of RGV-d5 with hydrogen-abstrating matrices (a) 4-nitro-1-naphthol (4,1-NNL) and (b) 5-nitro-salicylic acid (5-NSA). The asterisk indicates a metastable peak.

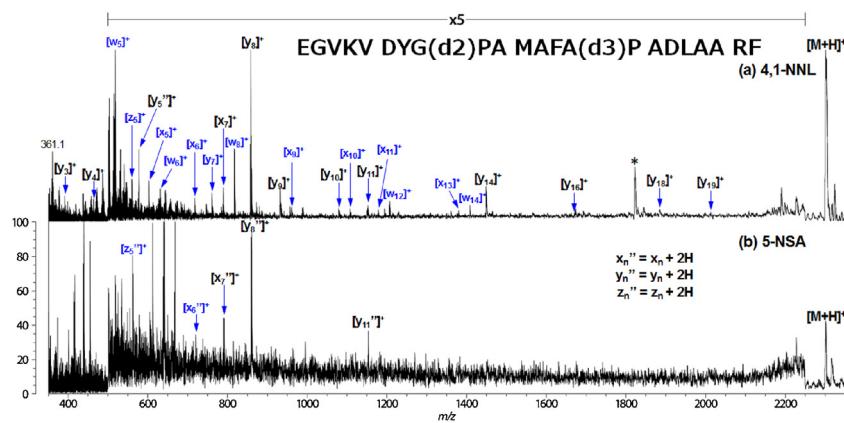


Fig. 4. MALDI-SD spectra of EGV-d5 with hydrogen-abstrating matrices (a) 4-nitro-1-naphthol (4,1-NNL) and (b) 5-nitro-salicylic acid (5-NSA). The asterisk indicates a metastable peak.

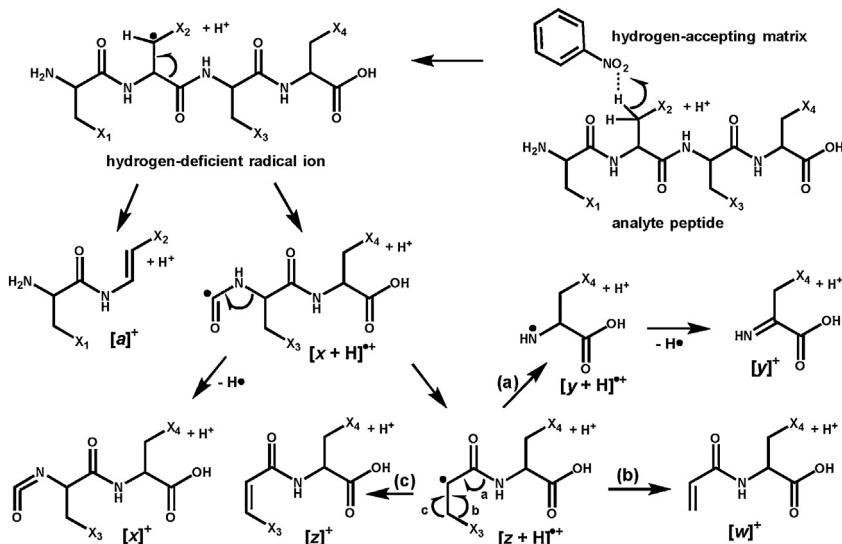
nolic (Ph-OH) and anilinic (Ph-NH₂) matrix active hydrogens to the carbonyl oxygens of backbone by intermolecular hydrogen-bonding [9]. The salient characteristic of positive-ion ISD spectra of peptides is the production of N-terminal [c + 2 H]⁺ ions. In contrast, C-terminal [z + 2 H]⁺ and [z-m + H]⁺ ions are formed by hydrogen H-and matrix radicals m-binding to transient radical species [z + H]⁺ in MALDI plumes [29,30], as depicted in Scheme 4. Although the formation of [c + 2 H]⁺, [z + 2 H]⁺, and [z-m + H]⁺ ions observed in Figs. 1a and 2a can be rationalized by radical-initiated reactions shown in Scheme 4, the detailed mechanism for the formation of [y + 2 H]⁺ ions is not yet clear. A possible mechanism of [y + 2 H]⁺ ion formation may be hydrogen attachment to transient radical ions [y + H]⁺ (Scheme 4), as described in section 3.3.

The ISD spectra of RGV-d5 and EGV-d5 obtained with 2,5-DHB differ from those acquired with 5,1-ANL (Figs. 1 and 2b). The ISD spectrum of RGV-d5 showed C-terminal [y + 2 H]⁺ ions but no [z + 2 H]⁺ and [z-m + H]⁺ ions, while that of EGV-d5 contained [y + 2 H]⁺, [z + 2 H]⁺, and [z-m + H]⁺ ions. The lack of [z + 2 H]⁺ and [z-m + H]⁺ ions in Fig. 1b may be due to the absence of an NH₂ group or Arg residue in those fragments (Scheme 4). In contrast, the ISD spectra of EGV-d5 clearly showed [z + 2 H]⁺ and [z-m + H]⁺ ions because an Arg residue is located on the C-terminus (Fig. 2b). The formation of [a]⁺, [d]⁺, and [x + 2 H]⁺ ions observed in the ISD spectra of RGV-d5 and EGV-d5 ions obtained with 2,5-DHB (Figs. 1 and 2b) are described in next section.

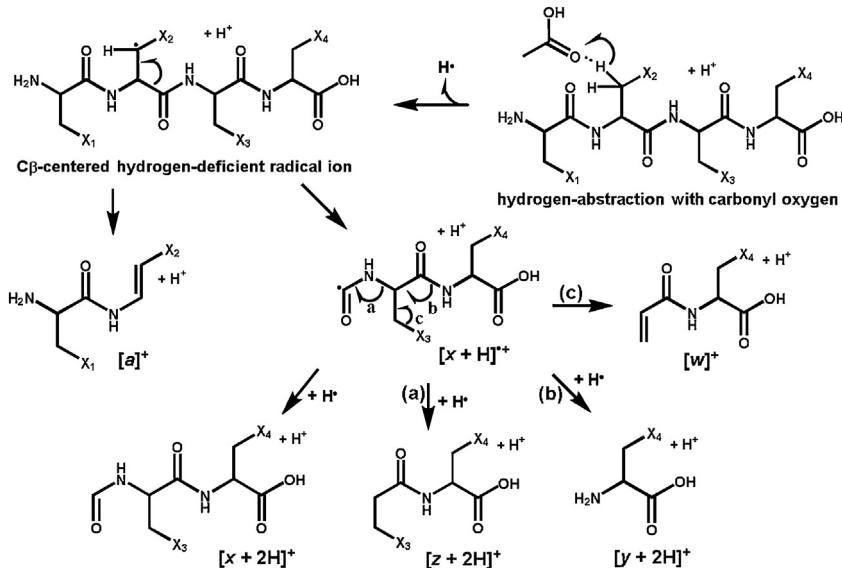
3.2. Specific peptide fragment ions are generated in MALDI-SD with hydrogen-abstrating matrix

The MALDI-SD spectra of peptide RGV-d5 obtained with hydrogen-abstrating matrices 4,1-NNL and 5-NSA are shown in Fig. 3. The ISD spectrum with 4,1-NNL mainly showed N-terminal [a]⁺ ions, except for [a8]⁺ and [a11]⁺ ions arising from cleavage at the Cα-C bond of Gly8-Pro9 and Met11-Ala12 residues, respectively (Fig. 3a). The spectrum with 5-NSA also contained some [a]⁺ and [b]⁺ ions (Fig. 3b). In Fig. 3a, it should be noted that [a7]⁺ and [a13]⁺ ions originating from cleavage at the Cα-C bond of aromatic side chains Tyr7-Gly8 and Phe13-Ala14 residues have a significantly high intensity. On the other hand, ISD of EGV-d5 with 4,1-NNL mainly yielded [y]⁺, [x]⁺ and [w]⁺ ions. Particularly noteworthy are the high intensities of [y8]⁺ and [y14]⁺ ion peaks that originate from cleavage at the C-N bond of Xxx-Pro residues (Fig. 4a). Conversely, the spectrum acquired with 5-NSA only resulted in few [y + 2 H]⁺ and [x + 2 H]⁺ ions (Fig. 4b). The mechanism of MALDI-SD with hydrogen-abstrating matrix can be rationalized by the RDD reactions of the β-carbon (Cβ)-centered radical peptide ions [M - Hβ + H]⁺, as shown in Scheme 5 [23]. The RDD reactions of Scheme 5 can also explain the lack of [a]⁺ ions arising from the cleavage of Gly-Xxx residues.

The matrix effect on the ISD spectrum of EGV-d5 is of significant interest. The ISD spectrum of this peptide obtained with 4,1-NNL contains C-terminal [x]⁺, [y]⁺ and [z]⁺ ions (Fig. 4a), whereas the



Scheme 5. MALDI-ISD mechanism of peptides with hydrogen-abtracting matrix.



Scheme 6. MALDI-ISD reactions in the plume with 2,5-DHB matrix.

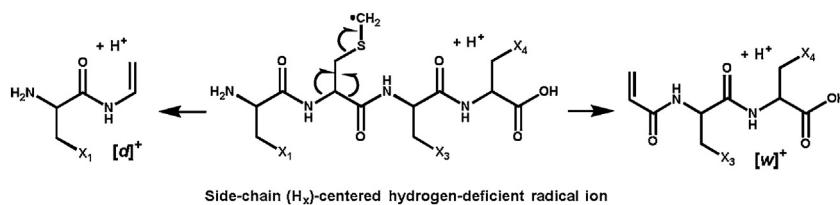
spectrum acquired with 2,5-DHB had $[x + 2H]^+$, $[y + 2H]^+$, and $[z + 2H]^+$ ions (Fig. 2b). Use of the hydrogen-abstracting matrix 4,1-NNL may form a dense gas-like MALDI plume devoid of hydrogen radicals H. Conversely, hydrogen-donating matrices 5,1-ANL and 2,5-DHB form a MALDI plume abundant in hydrogen and matrix radicals ($H\cdot$ and $m\cdot$). In fact, $[c + 2H]^+$, $[x + 2H]^+$, $[y + 2H]^+$, $[z + 2H]^+$ and $[w]^+$ fragment ions observed in the ISD spectra of RGV-d5 and EGV-d5 with 5,1-ANL can be perfectly rationalized by the binding processes of hydrogen and matrix radicals ($H\cdot$ and $m\cdot$) with the transient radical species $[z + H]^+$ and $[y + H]^+$ (Scheme 4). In contrast, the fragment ions $[a]^+$, $[x]^+$, $[y]^+$, $[z]^+$, and $[w]^+$ were observed in the ISD spectra acquired with hydrogen-abstracting matrix 4,1-NNL, (Figs. 3 and 4a). This observation can be explained by the loss of hydrogen from the transient radicals $[x + H]^+$ and $[y + H]^+$ (Scheme 5) that may occur in plumes lacking hydrogen radicals.

Regarding the ISD spectrum of EGV-d5 with 2,5-DHB (Fig. 2b), it should be noted that this matrix has both hydrogen-donating and -abstracting properties, due to the presence of phenolic hydroxyl (Ph-OH) and carboxyl carbonyl (COOH) groups, respectively. The

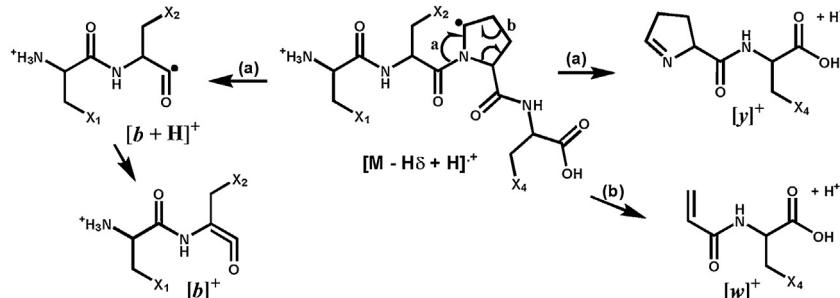
presence of a carbonyl oxygen in MALDI matrix results in $[a]^+$ ions, as well as $[c + 2H]^+$, $[y + 2H]^+$, and $[z + 2H]^+$ ions [31]. Therefore, the $[a]^+$, $[x + 2H]^+$, $[y + 2H]^+$, $[z + 2H]^+$, and $[w]^+$ fragment ions observed in the ISD spectra of RGV-d5 (Fig. 1b) and EGV-d5 (Fig. 2b) obtained with 2,5-DHB can be explained by the formation of the C β -centered hydrogen-deficient radical ions $[M - H_B + H]^+$ and subsequent RDD reactions leading to $[a]^+$ and $[x + H]^+$ ions (Scheme 6). The resulting transient radical ions $[x + H]^+$ may produce $[x + 2H]^+$, $[y + 2H]^+$, and $[z + 2H]^+$ ions via hydrogen binding in the hydrogen atom rich plume.

3.3. $[Y_m + 2H]^+$ ions are produced from $[z_{m+1} + H]^+$ radical ions

When hydrogen-donating matrices 5,1-ANL and 2,5-DHB were used, the ISD spectra of EGV-d5 showed preferential production of C-terminal $[z + 2H]^+$ and $[y + 2H]^+$ ions (Fig. 2), respectively. Although the formation of $[z + 2H]^+$ ions (and also $[z-m + H]^+$) can be explained by binding of hydrogen H-and matrix radical m-to the transient radical ions $[z + H]^+$ in MALDI plumes (Scheme 4)



Scheme 7. xxx.



Scheme 8. xxx.

[29,30], the mechanism of $[y + 2 H]^+$ ion production has not previously been described. Interestingly, the ISD spectrum of EGV-d5 gave a relatively intense peak corresponding to $[y_{16} + 2 H]^+$ ion originating from cleavage at the C–N bond of Asp6-Tyr7 residues, while other $[y_m + 2 H]^+$ ion intensities were lower than $[z_m + 2 H]^+$ ions (Fig. 2a). The reason why the intensity of the $[y_{16} + 2 H]^+$ ion is high may be because the ISD fragments $[c + 2 H]^+$ originating from cleavage at the N–C α bond of Xxx-Asp residues of peptides and proteins give rise to discontinuous intense peaks [32]. In fact, the $[c_5 + 2 H]^+$ and $[c_{16} + 2 H]^+$ ions originating from the cleavage of Xxx-Asp yield non-sequential intense peaks compared to the other $[c + 2 H]^+$ ions (Fig. 1). According to the specific N–C α bond cleavage (Scheme 3) as for Val5-Asp6, the relatively abundant radical ion $[z_{17} + H]^+$ is formed as a pair of abundant $[c_5 + 2 H]^+$ ion in Fig. 1. The resulting $[z_{17} + H]^+$ ion may occur by consecutive radical-driven dissociation (RDD) leading to the formation of the transient radical ion species $[y_{16} + H]^+$. However, these transient radical ions could not be observed in the ISD spectra. Similar consecutive RDD reactions have been reported in a study on the cascade dissociation of peptide-radical cations $[z + H]^+$ [33]. Therefore, the $[y_{16} + 2 H]^+$ ion could be formed by binding hydrogen to the radical y-ion $[y_{16} + H]^+$ resulting from the transient radical z-ion $[z_{17} + H]^+$. Therefore, the most likely mechanism of $[y_{m-1} + 2 H]^+$ formation in Fig. 2a can be explained by the competitive reactions of the $[z_m + H]^+$ ions, as shown in Scheme 4.

3.4. Residue-specific dissociation in MALDI-ISD

In the ISD spectra of the analyzed peptides, specific cleavage was observed at Asp, Met, Pro, Phe, and Tyr residues. The $[d_6]^+$ and $[d_{17}]^+$ ions originating from cleavage at both C α -C and C β -C δ bonds of Asp-Xxx residues were detected (Figs. 1b and 3). The Asp effect on $[d]^+$ ion formation also occurs in ultraviolet photodissociation (UVPD) of peptides [34] as shown in Scheme 2. The specific effects of Asp on protein cleavage have also been observed at the N–C α bond cleavage of Xxx-Asp in MALDI-ISD [32] and selective/enhanced cleavage at the C–N bond of Asp-Xxx residues in low-energy CID [15,35]. The residue effect on the formation of $[d]^+$ ions was also observed at the cleavage of both N–C α and C β -C δ bonds of Met-Xxx residues (Fig. 3a). The $[w_{12}]^+$ fragment ion was formed as a consequence of the presence of Met (Fig. 4a). The effect of this amino acid results in side-chain loss without the

observation of $[a_{11}]^+$ and $[y_{12}]^+$ ions possibly due to the loss of hydrogen from the side-chain methyl group (Scheme 7). The characteristic peaks corresponding to $[b_8]^+$ and $[b_{14}]^+$ ions in Fig. 3a and $[y_8]^+$, $[y_{14}]^+$, $[w_8]^+$, and $[w_{14}]^+$ ions in Fig. 4a may be due to a Pro effect. RDD reactions of the δ -carbon (C δ)-centered radical peptide ions $[M - H\delta + H]^+$ can explain how this effect may occur (Scheme 8) [23]. Regarding $[a]^+$ ion formation, cleavage at the C α -C bond of the Tyr-Xxx and Phe-Xxx residues gave relatively intense $[a_7]^+$ and $[a_{13}]^+$ ions peaks (Fig. 3a). This aromatic residue effect is a characteristic of UVPD of peptides and proteins [22,25,26]. As described above, it should be recognized that the specific cleavage of hydrogen-deficient peptide ions $[M - H + H]^+$ strongly depends upon the amino acid residues and the sites of a radical (unpaired electron).

4. Conclusions

The peptide fragment ion types observed in MALDI-ISD spectra obtained with hydrogen-donating and -abstracting matrix can be explained by the radical-driven dissociation (RDD) of the hydrogen-abundant/deficient radical ions $[M \pm H + H]^+$. The ISD spectrum of EGV-d5 acquired with a hydrogen-abstracting matrix 4,1-NNL showed C-terminal $[x]^+$, $[y]^+$ and $[z]^+$ ions, while the spectrum obtained with a hydrogen-donating matrices 5,1-ANL and 2,5-DHB contained $[x + 2 H]^+$, $[y + 2 H]^+$ and $[z + 2 H]^+$ ions, depending upon the MALDI plume deficient or rich in hydrogen radicals H $^\bullet$. The ISD experiments with 4,1-NNL mainly resulted in $[a]^+$, $[x]^+$, $[y]^+$ and $[w]^+$ ions, explained by the RDD $[M - H\beta + H]^+$ radical ions, whereas the spectra with 5,1-ANL typically showed $[c + 2 H]^+$ and $[z + 2 H]^+$ ions. The ISD spectra obtained with hydrogen-abstracting matrix specifically had $[a]^+$, $[b]^+$, $[d]^+$, $[y]^+$ and $[w]^+$ ions, but this depended upon the presence of Asp, Met, Pro, Phe and Tyr residues. We suggest that $[y_m + 2 H]^+$ ions are produced from transient radical ions $[z_{m+1} + H]^+$.

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References

- [1] F.W. McLafferty, F. Turecek, *Interpretation of Mass Spectra*, 4th ed., University Science Books, CA, USA, 1993.
- [2] R.F. Zubarev, N.L. Kelleher, F.W. McLafferty, Electron capture dissociation of multiply charged protein cations. A nonergodic process, *J. Am. Chem. Soc.* 120 (1988) 3265–3266.
- [3] J.E.P. Syka, J.J. Coon, M.J. Schroeder, J. Shabanowitz, D.F. Hunt, Peptide and protein sequence analysis by electron transfer dissociation mass spectrometry, *Proc. Natl. Acad. Sci. U. S. A.* 101 (2004) 9528–9533.
- [4] M.S. Thompson, W. Cui, J.P. Reilly, Fragmentation of singly charged peptide ions by photodissociation at $\lambda=157$ nm, *Angew. Chem. Int. Ed.* 43 (2004) 4791–4794.
- [5] W. Cui, M.S. Thompson, J.P. Reilly, Pathways of peptide ion fragmentation induced by vacuum ultraviolet light, *J. Am. Soc. Mass Spectrom.* 16 (2005) 1384–1398.
- [6] J.A. Madsen, R.R. Cheng, T.S. Kaoud, K.N. Dalby, D.E. Makarov, J.S. Brodbelt, Charge-site dependent dissociation of hydrogen-rich radical peptide cations upon vacuum UV photoexcitation, *Chemistry* 18 (2012) 5374–5383.
- [7] F. Turecek, Peptide radicals and cation radicals in the gas phase, *Chem. Rev.* 113 (2013) 6691–6733.
- [8] R.S. Brown, J.J. Lennon, Sequence-specific fragmentation of matrix-assisted laser-desorbed protein/peptide ions, *Anal. Chem.* 67 (1995) 3990–3999.
- [9] M. Takayama, N-C_α bond cleavage of the peptide backbone via hydrogen abstraction, *J. Am. Soc. Mass Spectrom.* 12 (2001) 1044–1049.
- [10] J. Hardouin, Protein sequence information by matrix-assisted laser desorption/ionization in-source decay mass spectrometry, *Mass Spectrom. Rev.* 26 (2007) 672–682.
- [11] M. Karas, D. Bachmann, U. Bahr, F. Hillenkamp, Matrix-assisted ultraviolet laser desorption of non-volatile compounds, *Int. J. Mass Spectrom. Ion Proc.* 78 (1987) 53–68.
- [12] K. Tanaka, H. Waki, Y. Ido, S. Akita, Y. Yoshida, T. Yoshida, Protein and polymer analyses up to m/z 100000 by laser ionization time-of-flight mass spectrometry, *Rapid Commun. Mass Spectrom.* 2 (1988) 151–153.
- [13] C.M. Whitehouse, R.N. Dreyer, M. Yamashita, J.B. Fenn, Electrospray interface for liquid chromatographs and mass spectrometers, *Anal. Chem.* 57 (1985) 675–679.
- [14] J.B. Fenn, M. Mann, C.K. Meng, S.F. Wong, C.M. Whitehouse, Electrospray ionization for mass spectrometry of large biomolecules, *Science* 246 (1989) 64–71.
- [15] B. Paizs, S. Suhai, Fragmentation pathways of protonated peptides, *Mass Spectrom. Rev.* 24 (2005) 508–548.
- [16] I.K. Chu, J.C.-K. Siu, J.K.-C. Lau, W.K. Tang, X. Mu, C.-K. Lai, X. Guo, X. Wang, N. Li, Y. Xia, X. Kong, H.B. Oh, V. Ryzhov, F. Turecek, A.C. Hopkinson, Proposed nomenclature for peptide ion fragmentation, *Int. J. Mass Spectrom.* 390 (2015) 24–27.
- [17] K. Biemann, Contributions of mass spectrometry to peptide and protein structure, *Biomed. Environ. Mass Spectrom.* 16 (1988) 99–111.
- [18] F. Canon, A.R. Milosavljevic, L. Nahon, A. Giuliani, Action spectroscopy of a protonated peptide in the ultraviolet range, *Phys. Chem. Chem. Phys.* 17 (2015) 25725–25733.
- [19] J. Laskin, Z. Yang, C. Lam, I.K. Chu, Charge-remote fragmentation of odd-electron peptide ions, *Anal. Chem.* 79 (2007) 6607–6614.
- [20] L. Zhang, J.P. Reilly, Radical-driven dissociation of odd-electron peptide radical ions produced in 157 nm photodissociation, *J. Am. Soc. Mass Spectrom.* 20 (2009) 1378–1390.
- [21] J.P. Reilly, Ultraviolet photofragmentation of biomolecular ions, *Mass Spectrom. Rev.* 28 (2009) 425–447.
- [22] M. Xu, T. Song, Q. Quan, Q. Hao, D.-C. Fang, C.-K. Siu, I.K. Chu, Effect of the N-terminal basic residue on facile Ca-C bond cleavages of aromatic-containing peptide radical cations, *Phys. Chem. Chem. Phys.* 13 (2011) 5888–5896.
- [23] K. Nagoshi, M. Yamakoshi, K. Sakamoto, M. Takayama, Specific C_α-C bond cleavage of β-carbon-centered radical peptides produced by matrix-assisted laser desorption/ionization mass spectrometry, *J. Am. Soc. Mass Spectrom.* 29 (2018) 1473–1483.
- [24] L.J. Morrison, W. Chai, J.A. Rosenberg, G. Henkelman, J.S. Brodbelt, Characterization of hydrogen bonding motifs in proteins: hydrogen elimination monitoring by ultraviolet photodissociation mass spectrometry, *Phys. Chem. Chem. Phys.* 19 (2017) 20057–20074.
- [25] T. Ly, R.R. Julian, Residue-specific radical-directed dissociation of whole proteins in the gas phase, *J. Am. Chem. Soc.* 130 (2008) 351–358.
- [26] X. Mu, T. Song, M. Xu, C.-K. Lai, C.-K. Siu, J. Laskin, I.K. Chu, Discovery and mechanistic studies of facile N-terminal C_α-C bond cleavages in the dissociation of tyrosine-containing peptide radical cations, *J. Phys. Chem. B* 118 (2014) 4273–4281.
- [27] M. Takayama, A. Tsugita, Does in-source decay occur independent of the ionization process in matrix-assisted laser desorption? *Int. J. Mass Spectrom.* 181 (1998) L1–L6.
- [28] M. Takayama, A. Tsugita, Sequence information of peptides and proteins with in-source decay in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, *Electrophoresis* 21 (2000) 1670–1677.
- [29] T. Koehler, A. Engstroem, R.A. Zubarev, Fragmentation of peptides in MALDI in-source decay mediated by hydrogen radicals, *Anal. Chem.* 77 (2005) 172–177.
- [30] K. Demeure, L. Quinton, V. Gabelica, E. de Pauw, Rational selection of the optimum MALDI matrix for top-down proteomics by in-source decay, *Anal. Chem.* 79 (2007) 8678–8686.
- [31] M. Takayama, In-source decay characteristics of peptides in matrix-assisted laser desorption/ionization time-of-flight mass spectrometry, *J. Am. Soc. Mass Spectrom.* 12 (2001) 420–427.
- [32] M. Takayama, K. Nagoshi, R. Iimuro, K. Inatomi, Access of hydrogen-radicals to the peptide-backbone as a measure for estimating the flexibility of proteins using matrix-assisted laser desorption/ionization mass spectrometry, *Int. J. Mol. Sci.* 15 (2014) 8428–8442.
- [33] T.W. Chung, R. Hui, A. Ledvina, J.J. Coon, F. Turecek, Cascade dissociation of peptides cation-radicals. Part 1. Scope and effects of amino acid residues in penta-, nona-, and decapeptides, *J. Am. Soc. Mass Spectrom.* 23 (2012) 1336–1350.
- [34] N. DeGraan-Weber, S.A. Ward, J.P. Reilly, A novel triethylphosphonium charge tag on peptides, derivatization, and fragmentation, *J. Am. Soc. Mass Spectrom.* 28 (2017) 1889–1900.
- [35] C. Gu, G. Tsapralis, L. Breci, V.H. Wysocki, Selective gas-phase cleavage at the peptide bond C-terminal to aspartic acid in fixed-charge derivatives of Asp-containing peptides, *Anal. Chem.* 72 (2000) 5804–5813.