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Data Article

Data on the peptide mapping and MS identification for phosphorylated peptide

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ABSTRACT

This article contains peptides mapping, mass spectrometry and processed data related to the research "Identification and quantification of the phosphorylated ovalbumin by high resolution mass spectrometry under dry-heating treatment" [1]. Fourier transform ion cyclotron mass spectrometry (FTICR MS) was used to investigate the specific phosphorylation sites and the degree of phosphorylation (DSP) at each site. Specifically, phosphorylated peptides were monitored through mass shift on the FTICR MS spectrum. DSP was evaluated through the relative abundance levels of the FTICR MS spectrometry. From these data, the calculation method of DSP was exemplified.

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Specifications Table

Subject area	Chemistry, Biology
More specific subject area	Mass spectrometric analysis of the phosphorylation sites and degree
Type of data	Table, figures
How data was acquired	Mass spectrometry data were collected on FTDoc Viewer

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Data format	Analyzed
Experimental factors	Phosphorylated ovalbumin under dry-heating at 85 °C for 1, 2, and 5 days. Pepsin was used to digest the protein
Experimental features	Identification of the phosphorylation sites and degree of the phosphorylation
Data source location	Nanchang University, Nanchang, China
Data accessibility	Data is provided within this article

Value of the data

- Precise mass shift in FTICR Mass Spectrum could characterize of the phosphorylated protein.
- The abundance of the phosphorylated peptide was used to calculate the degree of phosphorylation (DSP) at each site.
- Method to calculate the DSP from the mass peak abundance.

1. Data

The data include table and figures, which help analyze the phosphorylated peptides and DSP. The peptic peptides detected by LC FTICR MS after 5 min digestion of natural ovalbumin as control are listed in Supplementary Table 1. Compared with the control, the phosphorylated peptides were directly determined from the mass increases of 79.9663 or its multiples. From these data, we

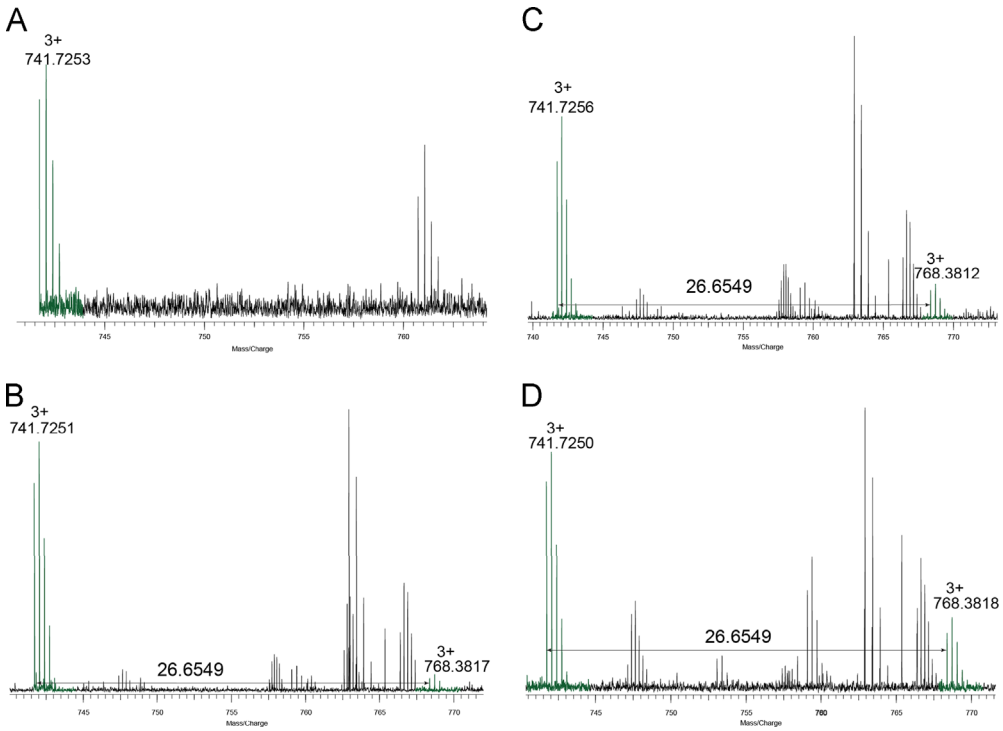

Fig. 1. FTICR MS of peptide 366–385 (^{366}FCIKHIATNAVLFFGRC VSP^{385}) at m/z 741.72^{3+} from natural Oval (A) and P-Oval incubated for 1 day (B), 2 days (C), and 5 days (D). Phosphorylation is indicated by a mass increase of 79.9663 Da.

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