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Microfluidic capillary electrophoresis-mass spectrometry for analysis of monosaccharides, oligosaccharides and glycopeptides

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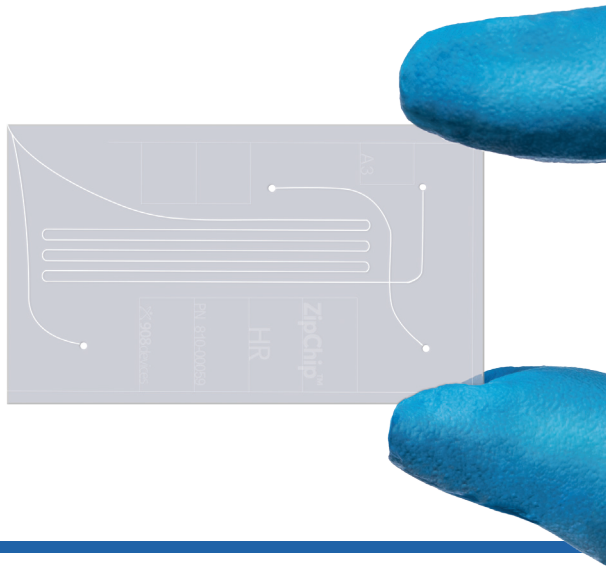

ABSTRACT: Glycomics and glycoproteomics analyses by mass spectrometry require efficient front-end separation methods to enable deep characterization of heterogeneous glycoform populations. Chromatography methods are generally limited in their ability to resolve glycoforms using mobile phases that are compatible with online liquid chromatography-mass spectrometry (LC-MS). The adoption of capillary electrophoresis-mass spectrometry methods (CE-MS) for glycomics and glycoproteomics is limited by the lack of convenient interfaces for coupling the CE devices to mass spectrometers. Here, we describe the application of a microfluidics-based CE-MS system for analysis of released glycans, glycopeptides and monosaccharides. We demonstrate a single CE method for analysis three different modalities, thus contributing to comprehensive glycoproteomics analyses. In addition, we explored compatible sample derivatization methods. We used glycan TMT-labeling to improve electrophoretic migration and enable multiplexed quantitation by tandem MS. We used sialic acid linkage-specific derivatization methods to improve separation and the level of information obtained from a single analytical step. Capillary electrophoresis greatly improved glycoform separation for both released glycans and glycopeptides over that reported for chromatography modes more frequently employed for such analyses. Overall, the CE-MS method described here enables rapid setup and analysis of glycans and glycopeptides using mass spectrometry.

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