material.[7] One possible explanation proposed to account for the tetrol formation in the NMO system involves the "second cycle" process, a scenario in which the preferential oxidation of the ene diol over the parent diene is due to a rather strong affinity of the trioxo Os(VIII) glycolate for the ene diol.[8b,9,10] However, selective ene diol formation in the $K_3Fe(CN)_6$-based system appears to be determined only by the electronic nature of the ene diol and the corresponding parent diene, consistent with our earlier finding that using $K_3Fe(CN)_6$ as the stoichiometric oxidant in place of NMO excludes the "second cycle" in the catalytic process.[11]

In conclusion, we have shown that the AD of dienes, and by implication higher polyenes, is highly selective and favors oxidation of the more electron-rich olefin when $K_3Fe(CN)_6$ is used as a stoichiometric oxidant. The high selectivity of this reaction makes effective control of the AD to a mono-dihydroxylation stage possible. The resulting chiral ene diol products should prove useful in asymmetric synthesis.

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Supplementary Material Available: Listings of experimental procedures and physical and analytical data (^1H NMR, ^{13}C NMR, HRMS, HPLC, and GLC retention times of the diols or their MTPA esters and the optical rotations) of the diols (6 pages). Ordering information is given on any current masthead page.

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Matrix-Assisted Laser Desorption/Ionization of Capillary Electrophoresis Effluents by Fourier Transform Mass Spectrometry

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Capillary electrophoresis (CE) is a powerful separation technique capable of rapid and efficient separation of complex biological mixtures.[1] With CE, separation efficiencies in excess of 10^6 theoretical plates have been achieved in times as short as a few minutes.[2] Additionally, the small sample volumes required make possible the investigation of many biological processes at the cellular level.[3] The major limitation of this method lies in detection of the eluted analytes.[4] Ideally, the detector should have sufficient sensitivity to record the passage of an analyte zone as it migrates through the capillary. Sub-attomole detection limits can be achieved using laser-induced fluorescence[5–7] or electrochemical detection.[8–10] Unfortunately, both techniques lack specificity. An ideal complement, capable of providing the desired molecular specificity, is mass spectrometry. Zare and co-workers[11] have demonstrated on-line CE matrix-assisted laser desorption/ionization (MALDI)[12,13] using an ice/nicotinic acid matrix and time-of-flight (TOF) mass analysis for the analysis of unspecified quantities of bovine insulin, albeit with exceptionally poor mass resolution. Off-line CE-MALDI, for picomole quantities of bovine trypsinogen, with TOF analysis has also been reported.[14]

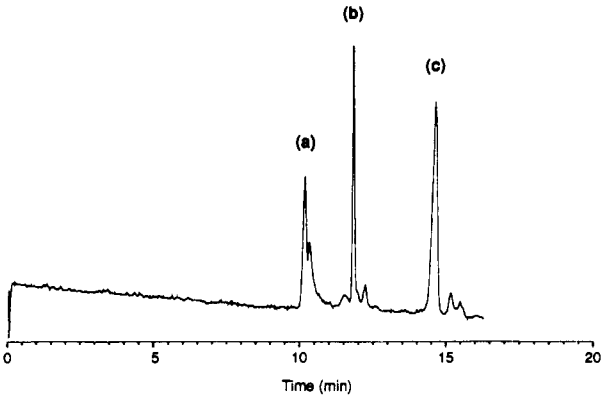

Figure 1. Ultraviolet detector electropherogram for the capillary zone electrophoresis of (a) somatostatin; (b) equine myoglobin; and (c) bovine insulin.

A previously unexplored alternative is to employ a Fourier transform mass spectrometer (FTMS) as the mass analyzer. The high-resolution spectra made available by this device (typically between 10^4 and 10^6, even for high-mass species[15,16]) and the potential for performing high-resolution MS/MS experiments offer the promise of dramatic improvements in the determination of structures of high molecular weight compounds separated by CE. Although high mass resolution has not yet been obtained (typically 50–100 for the CE application), nevertheless, off-line CE-MALDI with Fourier transform mass spectrometry analysis can provide highly accurate mass measurements for large biomolecules at the sub-picomole level. Until recently,[17] it was thought[18] that MALDI analysis of large molecules would be difficult with FTMS, possibly requiring unusually high trapping voltages to succeed at all. After the recent successful development of a means for accomplishing MALDI-FTMS, it seemed logical to explore its promising potential for off-line CE analysis. Accordingly, a concentric flow deposition interface with post-column matrix solution introduction was designed and fabricated. This device permits deposition of CE effluents *concurrently with matrix solution* upon an indexed stepper-motor-controlled laser desorption probe tip, which can be transferred to the FTMS system for mass spectrometric analysis.[19]

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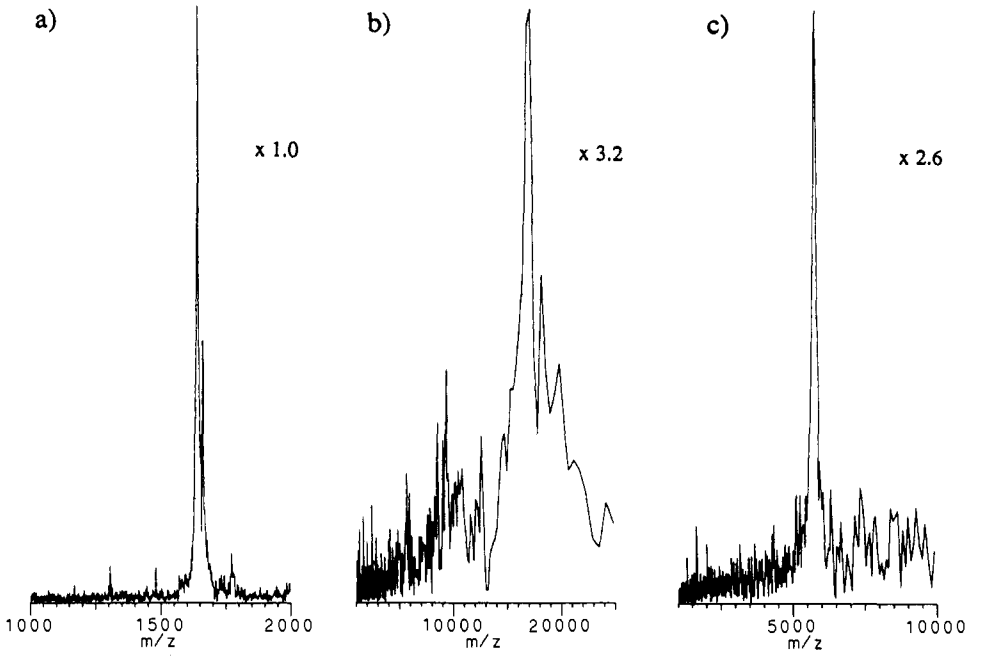

Figure 2. Matrix-assisted laser desorption Fourier transform mass spectra (355 nm) of (a) somatostatin; (b) equine myoglobin; and (c) bovine insulin.

A 200-nm UV detector senses the presence of component peaks and directs the entire peak volume of each component onto a separate probe tip position. Otherwise, effluent flow is diverted from the probe tip. For the first experiment, a 6 mM aqueous sodium bicarbonate solution containing a mixture of myoglobin and insulin was injected onto the CE column, introducing 4.9 pmol of myoglobin and 75.8 pmol of bovine insulin, subjected to electrophoresis,[20] and deposited, along with a 10^4 molar excess of 2,5-dihydroxybenzoic acid, upon a clean stainless steel probe tip. Following separation, the probe tip was transferred to the FTMS for analysis, where the single shot method, with the 308-nm laser beam impinging upon ca. 5% of the total sample surface area for each sample position, produced excellent spectra with signal to noise ratios in excess of 10:1. Up to five or six such spectra could be obtained for each spot, suggesting that a single spectrum corresponds to desorption of as little as 50 fmol of sample. As a second test of the method, a three-component mixture containing bovine insulin, somatostatin, and equine myoglobin in aqueous buffer solution was separated using similar CE conditions and the same column. Samples of 28, 16.2, and 6.2 pmol, respectively, were introduced onto the column. Figure 1 is the UV electropherogram for that separation, and Figure 2 shows the spectra obtained for these samples after transfer of a loaded Pyrex probe tip to the FTMS. Here, using the same considerations as described for the first sample, we estimate that between 60 and 300 fmol of sample were consumed per laser shot. Furthermore, on the basis of recent results with samples in a similar matrix,[16] it is expected that much higher mass resolution, with mass measurement accuracy better than the 0.01% commonly found[21] for MALDI-TOF, may be possible.

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(19) Spectra were recorded with a 7-T Millipore Extrel FTMS-2000 dual-cell mass spectrometer, equipped with an autoprobe. For laser desorption, a Lambda Physik EMG-201 MSC excimer laser (operating at 308 nm, 180 mJ/28 ns pulse) was used to pump a Lambda Physik FL-2001 dye laser. The 355-nm radiation was produced by pumping the dye laser cell containing a 0.60 g/L of dioxane solution of 2,2‴-dimethyl-*p*-quaterphenyl (BMQ, Lambda Physik), resulting in a maximum output energy of 5 mJ/pulse. For MALDI, the 355-nm laser light is attenuated by an iris and focused as a 0.06 mm^2 beam upon the probe tip. Alternatively, the 308-nm laser beam was used directly. Spectra were obtained using experimental parameters as described in ref 17.

(20) Electrophoresis was carried out using a 99-cm fused silica capillary column (Polymicrotechnologies, 360 μm o.d., 50 μm i.d.) connected to the UV detector (Model 500, Scientific Systems Inc.) via an additional 11 cm of column at 25 kV (Glassman High Voltage, Inc.) A solution of 30 mM aqueous sodium biocarbonate (pH 9.0) was used as the running buffer.

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High-Resolution Matrix-Assisted Laser Desorption/Ionization of Biomolecules by Fourier Transform Mass Spectrometry

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Since the introduction of matrix-assisted laser desorption/ionization (MALDI) mass spectrometry,[1-3] its applicability to a large number of organic molecules, primarily proteins and polymers, has been investigated. Unfortunately, mass resolution employing time-of-flight (TOF) mass spectrometers typically used with MALDI rarely exceeds 1000.[4] However, by using a Fourier transform mass spectrometer (FTMS), and a new approach to MALDI, it is now possible to obtain high mass resolution of protein molecular ions. This communication presents the first demonstration of this new technique, which appears to have great promise.

The present work builds upon the earlier results of Castoro and co-workers[5] who successfully demonstrated the adaptation of MALDI to Fourier transform mass spectrometry for analysis of molecular ion species of polymers and biomolecules with masses

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