

## Glycosylation Fingerprints of Normal, Metastatic and Developmental Cells

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As a consequence of genomic expression, cell milieu, and temporal factors, molecular glycosylation represents an unsurpassed chemical fingerprint for tissue or cell characterization. Differential mass profiles of released glycans (N-, and O-linked) provide a door to such evaluation, but the details of cellular specificity are buried under the major “housekeeping” structures common in all cells. Thus, a structural evaluation must constitute digging into the minor isomeric components and the details of linkage and branching to gather a comprehensive assessment of each monomer. In an effort to evaluate this specificity in metastatic tissue a murine cell model has been used. The model manifests all the hallmarks of metastatic disease; spontaneous development, local invasion, intravasation, immune system survival, extravasation, and secondary tumor formation involving liver, kidney, spleen, lung, and brain. Using astrocyte cell lines from this model, we compared N-linked glycosylation from a non-metastatic brain tumor cell line and two different metastatic brain tumor cells. Selected ions in each profile were disassembled by ion trap mass spectrometry (MS<sup>n</sup>) which exhibited multiple structural differences between each tissue. These unique structures were identified within isomeric compositions as pendant non-reducing termini of di-, and trisaccharide fragments, probably transparent to a tandem MS approach but distinctively not to sequential ion trap MS<sup>n</sup> detection. Similar evaluations have proceeded on stem cell lines and individual glycoproteins with particularly unique results. Although numerous analytical strategies have been introduced to identify selected components of carbohydrate structure, it has been the continued focus of this and previous efforts to only build upon protocols that can be integrated into a high throughput strategy consistent with automation. Such protocols could bring an important analytical focus to carbohydrate sequencing that is greatly lacking.

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