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An Integrated Systems Approach to Deconstructing Glycosylation

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**AN INTEGRATED SYSTEMS APPROACH TO DECONSTRUCTING GLYCOSYLATION**

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**GOAL:** To deconstruct the regulation of the complex, non-template driven synthesis of carbohydrates using high-throughput microarray methods

**STRATEGY:** Isolate matched glycomic and transcriptomic samples from the NCI-60 panel, or metabolically perturbed cell lines and subject to a “systems biology” approach of lectin and genomic microarray followed by the decomposition and integration of the data sets

**CONCLUSION:** The lectin microarray platform is suitable to identify distinct, carbohydrate-based cell surface features which differentiate certain cancer tissue types.

**CONCLUSION:** Decomposing the lectin and gene expression data reveals 3 unique glycosylation patterns. N-linked expression is inversely correlated, O-linked positively. Each eigen-celltype has process specific gene/glycosylation patterns (not shown).

**Future Directions**
- We have used a “systems” approach to identify regulatory effects on the glycome
- We are now expanding our analysis to include glycomic analysis of the entire NCI-60 panel and genomic analysis with our custom designed arrays
- We are perturbing the metabolic state of select cell lines in order to determine the effect on glycome expression