SERUM METABOLOMIC BIOMARKERS AND LUMBAR DISC DEGENERATION

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INTRODUCTION: It has been suggested that altered metabolism may contribute to lumbar disc degeneration (DD). Quantitative high-throughput serum nuclear magnetic resonance (NMR) metabolomics has recently been introduced as a cost-effective way to obtain comprehensive data on systemic metabolism. Here we report our preliminary work on the identification of serum metabolomic biomarkers in relation to lumbar DD, with a primary focus on small molecules and lipid extracts.

METHODS: A radiographic and clinical cross-sectional study of 810 Southern Chinese volunteers was performed. A serum NMR metabolomics platform was utilized to assess the systemic metabolic profiles (~150 metabolic measures for each individual). Sagittal MRIs were utilized to assess DD (Schneiderman criteria) from L1-S1. A summated degenerative disc disease (DDD) score of the lumbar levels was obtained. Subject demographics and environmental/lifestyle factors were also assessed. ROC analysis and multivariate logistic regression analysis were performed to determine the strength and risk of various metabolomic biomarkers in relation to DD.

RESULTS: There were 315 male and 495 females (mean age: 51 years). DD was noted in 77% of the subjects. Multivariate model adjusted for age, sex, BMI, smoking status, triglycerides, ESR, and hs-CRP where appropriate. Serum tyrosine: lactate (OR: 1.60; 95% CI: 1.03-2.49) and leucine:isoleucine (OR: 2.65; 95% CI: 1.01-6.92) were significantly associated with the overall presence of DD. Elevated serum biomarker ratio of valine to histidine (critical value$\geq$ 3.8; DDD Score $\geq$5; OR: 1.74; 95% CI: 1.07 -2.85) and lipid extracts (e.g. fatty acids; $p<0.05$) were significantly associated with moderate to severe DD.

CONCLUSIONS: This is the first study to report on a serum metabolomics approach in relation to DD. Novel serum biomarkers associated with early and moderate/severe lumbar DD were identified. Future studies are needed to validate the findings.