

Dissertation Defense

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“COMPOUND SPECIFIC ISOTOPE ANALYSIS OF AMINO ACIDS IN FRESHWATER ECOSYSTEM: INSIGHTS AND APPLICATIONS”

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Abstract -Investigation of the $d^{13}C$ and $d^{15}N$ of individual compounds, commonly referred to as compound specific isotope analysis (CSIA), along with traditional techniques such as stomach content, dietary tracers, and bulk stable isotopic analysis (BSIA), provide a detailed description of trophic dynamics of organisms. CSIA analysis of amino acids (CSIA-AA) in particular, has been used successfully in marine, estuarine, and more recently, terrestrial systems to estimate trophic position (TP) among organisms. Despite the analytical potential of this technique, its application in freshwater systems has remained limited. The goal of this dissertation is to bridge this knowledge gap by assessing the validity and efficacy of the CSIA-AA technique, through studies ranging from laboratory microcosm experiments, to natural freshwater ecosystems in Alabama. In Chapter 2, patterns of trophic enrichment were investigated in a freshwater phytoplankton-grazer model through a controlled feeding experiment in microcosms. Trophic fractionation among amino acids was consistent with previously published results from similar marine studies. TP determined by CSIA-AA provided a better estimate of trophic status than BSIA, extending the potential of this technique in freshwater systems. Chapter 3 examined the isotopic underpinnings of the phenotypic plasticity in bluegills from the Sipsey River main channel and its backwater habitats, thereby extending CSIA-AA to fluvial and lacustrine environments. BSIA of $d^{13}C$ indicated that the main channel bluegills were subsidized by allochthonous detrital carbon, compared to bluegills from the two floodplain lakes that relied on submerged macrophytic vegetation. Estimates of trophic length using CSIA placed bluegills from all three sites at comparable TP, between trophic levels 3 and 4, suggesting some degree of omnivory. In Chapter 4, the biotic factors affecting the significant difference in mercury concentrations between the largemouth bass from the Sipsey and Black Warrior Rivers were identified, using dual CSIA of triglyceride fatty acids (TGFA; $d^{13}C$) and amino acids ($d^{15}N$). Results indicate that increased presence of sulfate-reducing bacteria, coupled with detritus based food web, was the primary driver of the elevated mercury levels in the Sipsey bass. Data presented in this dissertation clearly demonstrate the potential of CSIA-AA and CSIA-TGFA to provide high-resolution insights into complex food web interactions.