

DENITRIFIER COMMUNITY COMPOSITION AND GEOMORPHOLOGY INFLUENCE
RATES OF DENITRIFICATION IN A LARGE RIVER

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ABSTRACT

Humans have drastically altered the global nitrogen (N) cycle by increasing reactive N loading to the environment, resulting in negative ecological consequences. One permanent sink for this excess N is denitrification, a microbially-mediated process by which nitrate (NO_3^-) is reduced by stepwise reactions to dinitrogen gas (N_2) by heterotrophic facultative anaerobes. Previous studies have shown that as N loads to small streams increase, denitrifying communities reach saturation with regard to their uptake kinetics, resulting in the export of NO_3^- to larger rivers. Our goal was to identify factors influencing rates of sediment-associated denitrification in a larger river, including variation in seasonal water chemistry, sediment characteristics, and changes in the community structure of denitrifiers. We used an analysis of nitrite reductase-encoding functional genes (*nirS* and *nirK*) coupled with measured potential denitrification rates to potentially link denitrifier diversity with ecosystem function in the Cahaba River, a 6th order river that flows 305 km through three distinct geomorphic units (Valley Ridge, Fall Line, Coastal Plain). We found that denitrification rates varied seasonally in response to in-stream primary production, and had a positive relationship with the percentage of fine sediment, resulting in different rates between geomorphic units and suggesting that the geomorphic structure of the river strongly influenced the location of denitrification hotspots. The composition of *nirS* and *nirK* communities appeared to be responding differently to changes in the dissolved oxygen regimen and organic carbon supply, and *nir* gene composition was distinct between two of the three geomorphic units that also had different rates of denitrification. This shift in denitrifier gene composition coincident with an increase in rates of N removal via denitrification suggests a linkage between microbial diversity and ecosystem function, but our study design did not allow for controlled experimentation to clearly distinguish between environmental and genetic controls on denitrification. This study marks the first attempt to link denitrifier community structure to denitrification rates in a high order river, and has documented rates of N removal that suggest large rivers are not conduits through which materials simply pass on their route to coastal ecosystems, but are important sites for retention of excess N.