Development of Molecular Tools for Identification of Prairie Terrestrial and Wetland Algae

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ABSTRACT

Algae are a diverse group of photosynthetic protists. Green algae are typically unicellular, though some may occur as multicellular colonies, and they are found across a wide range of habitats, including marine, freshwater, and terrestrial environments. A photosynthetic producer and sometimes symbiont, algae can occupy important roles in an ecosystem; in other circumstances they can have negative impacts on environmental quality. Estimations of the number of green algal species range from eight thousand to over fifteen thousand. The identification of individual algal species can be problematic due to their small size and typically simple cell anatomy. For this reason, molecular tools may be employed to distinguish between algae. We have examined the utility of inter-simple sequence repeat (ISSR) analysis to generate a “bar code” molecular phenotype for the identification of different green algae. Environmental samples were collected from UNO’s Glacier Creek Preserve and from other local sites. Algae from these sites were cultured and isolated. Genomic DNA from these algae was used as the template for PCR amplification, both with and without initial purification from the algae. Amplification of the high-copy number ribosomal internal transcribed sequence was possible without initial DNA purification, yielding characteristic size products for different algae; this method did not reliably work for amplification using ISSR primers. Isolated algal DNA was tested with rDNA ISSR primers to identify primers that could generate distinct amplification patterns that might be useful for rapid identification of algal species.

Conclusions and Future Directions

Several morphologically distinct algae could be cultures from the Glacier Creek Prairie Preserve, suggesting a diverse community. Amplification of the ribosomal Internal Transcribed Spacer from isolated algal genomic DNA yielded differently diverse community. Amplification of the ribosomal Internal Transcribed Spacer (ITS) from isolated algal genomic DNA yielded differently diverse community. Amplification of the ribosomal Internal Transcribed Spacer (ITS) from isolated algal genomic DNA yielded differently diverse community. Amplification of the ribosomal Internal Transcribed Spacer (ITS) from isolated algal genomic DNA yielded differently diverse community. Amplification of the ribosomal Internal Transcribed Spacer (ITS) from isolated algal genomic DNA yielded differently diverse community.