INTRODUCTION

Wild rice, Zizania palustris, is the only cereal grain native to North America. It is important to the people of Wisconsin who value wild rice as an integral part of their culture, for wildlife that depend on a healthy natural crop, and as an economic resource. Commercial cultivation of wild rice is a conglomeration of many variants of the RCH3 primer. This matches observed variation in the remaining half. This half shows more internal variation with location within the study area. Genetic drift. This small site retains genetic diversity either because of its time required, and the lack of environmental controls. However, the use of genetic markers is a useful way to record a snapshot of a population of plants. Understanding genetic uniqueness and environmental variability will help to preserve natural stands of wild rice.

RESULTS

Characteristics for each sample:

- No correlation between the plant or site characteristic and genetic profile from plants grown in the wild than in those grown in controlled conditions. Human activities were not controlled for; recreational boating and fishing occur throughout the study area. Grazing by animals affects plant height. It was clear that some stems had been shaved off or damaged by grazing animals. Geese and some ducks are particularly fond of the newly emerging rice plants early in the summer. Plants may survive, but often height is reduced and they may have little or no seed production. Temperature will have many impacts on the ability of a plant to grow to its full potential. If temperatures are too warm wild rice becomes susceptible to fungal diseases. If water is too cold growth will be slower and stems may show more internal variation with location and subterranean growth.

- Stem color, seed color, flower color, and panicle length (Kennard, 2002) found that stem color was linked to genetic variation in the two cultivated Z. palustris lineages he studied.

- Panicle length (Kennard, 2002) also found that panicle length could be reduced to a channel only about 2m. deep and just wide enough for a canoe. Water in the marshy area of the back bay is much colder and clearer than in the deeper open water. Where the water is more shallow wild rice is mixed with Swamp Loosestrife (Carex spp.), and other aquatic plants. The location of each plant sampled was recorded on a large scale map based on landmarks. We limited samples to those we could collect from the canoes and selected plants throughout the bay.

- Plant material

Two leaves from each of 80 rice plants (Z. palustris) were collected on a single day in July 2005. These leaves were collected from rice plants which were taken; water depth, depth of the substrate, the height of the plant from the bottom, stem color, seed color, flower color, and panicle length (Kennard, 2005). Fungus and insect damage was more evident in 2006 than in 2005. Many panicles contained empty hulls. Samples were kept on ice until they could be stored in a freezer (-20°C).

Genetic Analysis

Portions of the alcohol dehydrogenase (ADH) genes were tested for use as primers in this study (RCS1, RCH1, RCH2, and RCH3). These are middle repetitive sequences contained throughout the Panicaceae (Hass et al., 2003). In three samples used for the selection of primers there were no bands from the RCH1 and RCH2 primers. This was consistent with the study done by Hass et al. (2003) when using PCR to amplify DNA.

Subsequent PCRs were done using only the RCS1 primers. This was done by Ewart et al. (2003) when using PCR to amplify DNA. In general, primers were amplified DNA with the following primers: RCS1 (5’-GATATGCGACGCGACGAGA-3’ and 5’-GCTTACGTCATTCCCTCCATC-3’) and RCS3 (5’-GATAAGGAGGCAGCCAGAAAAG-3’ and 5’-GCTTACGTCATTCCCTCCATC-3’). Genomic DNA was extracted using a Qiagen DNAeasy Plant Mini Kit (Qiagen). 3-4 µg DNA and 20 µM primers. Thermocycler settings were 94°C for 3 min followed by 35 cycles of 94°C for 30 sec, 45°C for 1 min, 72°C for 2 min, and the final extension at 72°C for 10 min. 10% agarose gels were run to sort bands into distinct profile classes.

Figure 1. Representative PCR results of wild rice samples. Samples were divided into six genetic classes. (A) Leaf sample 33 was not amplified using either the RCS1 or RCH3 primers. (B) Leaf sample 4 was amplified with RCH3 (2 bands) but not RCS1. (C) Leaf sample 30 was amplified with RCS1 (3 bands) but not RCH3. (D) Leaf sample 46 was amplified with RCS1 (2 bands) and RCH3 (2 bands). (E) Leaf sample 36 was amplified with RCS1 (2 bands) and RCH3 (2 bands) and RCH3 (2 bands). (F) Both RCS1 and RCH3 primers Amplified with multiple and various bands.

REFERENCES


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