

Development and characterization of simple sequence repeat markers for genetic analyses of *Sargassum horneri* (Sargassaceae, Phaeophyta) populations in Kyoto, Japan

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Simple sequence repeat (SSR) markers were developed for the brown alga *Sargassum horneri* (also known as “akamoku”) from an SSR-enriched genomic library. Of 22 SSR markers developed, 10 primer pairs produced clearly distinguishable DNA bands, indicating polymorphisms in *S. horneri* populations collected around Wakasa Bay, Kyoto, Japan. Ten primer pairs among the newly developed SSRs were also applicable to any of five other *Sargassum* species tested. To assess the utility of SSR markers for the classification of *S. horneri*, we genotyped 86 akamoku individuals from six populations (Naryu, Obase, Oshima, Satohami, Tai, and Taiza). We detected 148 alleles using 11 markers (10 new and 1 previously published). The allele number per locus ranged from 4 to 32 (average, 13.5). Based on the genotyping data for the 11 SSR markers, three of the six akamoku populations were separated on a phylogram. These results indicate that the SSR markers developed in this study are informative and useful for genetic analyses in *Sargassum* species.

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