عنوان مقاله:

Mapping genomic regions associated with yield and drought tolerance indices in recombinant inbred lines of rice

محل انتشار:

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نویسنده:

مریم دانش گیلوایی - *Department of Agronomy and Plant Breeding, Faculty of Agricultural Sciences, University of Guilan, P. O. Box: ۴۱۶۳۵-۱۳۱۴, Rasht, Iran.*

خلاصه مقاله:

Mapping QTLs with molecular markers can be very useful for plant breeders in agricultural genomics. The identification and introgression of QTLs for grain yield and drought tolerance indicesis an efficient approach to improve the drought tolerance of rice varieties. In this study, QTLs controlling some traits associated with grain yield and drought tolerance indiceswere identified using ۱۵۰ F۸ lines derived from a cross between Sepidroud and Gharib, under non-stress and stress conditions. The genetic linkage map containing ۱۲ ISSR polymorphic markers, ۱۰۳ SSR, ۱ IRAP marker, ۱۱ REMAP markers and ۱۶ combinations of ISSR markers covered ۱۰۰۵.۲ cM of the rice genome and a mean distance between adjacent markers was ۴.۴۳ cM. In this experiment, two QTLs with main effects were mapped for SSI and YSI indices, three QTLs with main effects for grain yield under non-stress and stress conditions, TOL, STI, GMP, and YI, four QTLs with main effects for MP and HM. One epistatic QTL was mapped for grain yield under non-stress condition and STI index. The phenotypic variation explained by each main effect QTLs and epistatic QTLs ranged from ۳.۹۹ to ۲۵.۴۱% and ۶.۵۱ to ۱۸.۸۱%, respectively. Fifteen main effect QTLs, including, qGY۹, qGY۱۲a, qTOL۴,qTOL۵, qSSI۵, qSSI۶, qSTI۹, qSTI۱۲, qMP۹, qGMP۹, qGMP۱۲, qHM۱۲a, qYSI۵, qYSI۶, and qYI۱۲a as the major QTLs controlling these traits can be considered in rice breeding programs for improving grain yield and drought tolerance after validation. The markers UBC۸۱۶-۲, (Tos۲+UBC۸۲۷)-۴, (UBC۸۲۶+HB۱۲)-۶, RM۲۱۵ and RM۵۳۷۱ located near major QTLs could be used in MAS programs.

کلمات کلیدی:

Composite interval mapping, Drought resistance, Molecular markers

لینک ثابت مقاله در پایگاه سیویلیکا:

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