
عنوان مقاله:

Genetic structure of Fe toxicity tolerance in Iranian rice (Oryza sativa L.) inbred lines population at seedling stage

محل انتشار:

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خلاصه مقاله:

Rice is the world's most important staple food and will continue to be so in the coming decades. Ferrous iron is essential for rice growth. A mapping population of ۹۶ rice inbred lines derived by Neda (NAD) and Ahlemitarom (ATM) cross, was used to detect quantitative trait loci (QTLs) for fresh biomass (FB), root length (RL), shoot length (SL), root number (RN), leaf width (LW), root fresh weight (RFW), root dry weight (RDW) and Fe content (FC) under Fe toxicity condition in rice. Two parents and ۹۶ inbred lines were evaluated for the traits by growing them under normal and Fe toxicity nutrient solution. Under stress condition, two QTLs were detected for FB on chromosome ۱۰, with LOD of ۲.۸۵۹, and ۲.۴۶۵. Twelve QTLs were identified for RL on chromosomes ۲, ۴, ۵, ۶, ۷, ۸, ۹, ۱۰, and ۱۲. Three QTLs were detected on chromosomes ۶, ۷, and ۸ for RN, and two QTLs for RDW on chromosomes ۲ and ۹. One QTL controlling LW, RFW, and FC was located on chromosomes ۱۰, ۹, and ۱, respectively. The other QTLs for FB, SL, and RN was located on chromosomes ۱۲, ۱۲, and ۳ under normal condition, with respective contributions of ۹.۷, ۱۰, and ۹.۹, respectively. qLWN-۲, qLWN-۷, and qLWN-۱۲ were located for LW on chromosomes ۲, ۷, and ۱۲. These QTLs, due to the high percentage of explanation after validation, are a good candidate for marker-assisted selection programs with the help of markers in the rice population.

کلمات کلیدی:

Rice, Fe toxicity, Mapping, QTL, marker assisted selection

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