

عنوان مقاله:

Mapping QTLs for Aluminum Tolerance in wheat

محل انتشار:

سومین کنگره بین المللی و پانزدهمین کنگره ملی ژنتیک ایران (سال: 1397)

تعداد صفحات اصل مقاله: 10

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خلاصه مقاله:

Genetic improvement of aluminum (Al) tolerance is one of the cost-effective solutions to improve wheat productivity in acidic soils. In this study, QTLs for Al-tolerance were determined in 167 of the Seri/Babax recombinant wheat inbred lines (RIL) grown in control and Al-treated soil in field. This investigation was conducted using alpha lattice design with two replications during 2014-2015 and 2015-2016. In general, 46 QTLs including 22 major and 24 minor QTLs were detected for the traits (25 and 21 QTL under control and aluminum stress condition, respectively). 26 QTLs (56.52%), 19 QTLs (41.31%) and one QTLs (2.17%) were in the A, B and D genomes, respectively. For most identified QTLs, alleles decreasing or increasing traits were derived from Babax parental lines. Phenotypic variations that were explained by these QTLs changed from 5.90% to 12.11%. The highest and the lowest R² were related to SD and PHT QTLs in normal and stress conditions, respectively. LOD values ranged from 2.51 to 4.88. The lowest and the highest LOD scores were attained for the QTLs of GYLD (QGYLD9H.y2s) and PHT (QPHT18H.y2s) under Al stress. Results showed co-located QTLs for DHE with GSP, CTm with TGW and SPAD with TSN in normal and Al trials, which suggested pleiotropic or linkage gene effects for these traits. QTLs QTGW5H.y2n and QTGW5H.y2s is ranged from 0.00 cM of chromosome 5H, controlling TGW was quite stable. 22 major QTLs controlling traits in this study can be used in breeding programs to improve wheat grain yield.

کلمات کلیدی:

Aluminum stress, Bread wheat, QTL mapping

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