

Full Length Research Paper

New evidence of QTLs attributed to salinity tolerance in rice

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An F_{2:3} population derived from the cross between Taromahalli (*indica*) and Khazar (*indica*) was used to mapping salt tolerance in rice. The linkage map constructed by 74 simple sequence repeat (SSR) molecular markers covered a total of about 1231.50 cM rice genome. Plant stand, chlorophyll content, root and shoot length, fresh weight of root and shoot, dry weight of root and shoot, Na⁺ uptake, K⁺ uptake, Na⁺/K⁺ ratio related to uptake ions and green leaf area were mapped. Four QTLs for root length under salt stress were detected on chromosomes 1, 4, 7 and 9. Also, two QTLs (on chromosome 9) for dry weight root and three QTLs for ion exchanges (on chromosome 3 and 10) were identified. Taromahalli alleles in these loci increased salt tolerance. Of these QTLs, the five major QTLs with the very large effect, qRL-7 for root length, qDWRO-9a and qDWRO-9b for dry weight root, qBI-1a and qBI-1b for biomass explained 16.21, 27.43, 25.50, 22.24 and 26.83% of the total phenotypic variance, respectively. All these results reinforced the idea that, new QTLs of this study play an important role in the growth of rice at seedling in Iranian local population under salinity condition.

Key words: Composite interval mapping, ion exchange, molecular markers, salt tolerance, simple sequence repeat.

INTRODUCTION

Rice (*Oryza sativa* L.) is salt sensitive, particularly at a seedling stage. It is important to breed new varieties with raised tolerance to salinity thus the normal approach is to expose a wide range of the crop to the stress and identify tolerant individuals for use in a breeding program. Salt-tolerance related traits are complex and to facilitate the development of new varieties with a high level of salinity tolerance, it will be required to understand the genetic control mechanisms for salt tolerance. This can be done by using molecular markers technology and mapping QTLs controlling salt tolerance-related traits.

QTL analysis of salt tolerance has been conducted by several researchers (Zhang et al., 1995; Koyama et al., 2001; Lin et al., 2004; Ming et al., 2005; Lee et al., 2007). Flowers et al. (2000) detected 16 QTLs related to ion

concentration of sodium and potassium in rice shoots using amplified fragment length polymorphism (AFLP) analysis and RIL mapping population. They found that 12 QTLs affected shoot concentration, dry weight production on chromosome 6, one QTL for high sodium uptake on chromosome 1, two QTLs for potassium uptake found on chromosome 9 and 6 and another on chromosome 4 which is responsible for Na⁺/K⁺ discrimination. Prasad et al. (2000) using a double haploid (DH) mapping population, found seven QTLs for seedling traits, two QTLs for seed germination, one for seedling root length, three for seedling dry matter and one for seedling vigor. Of the total seven QTLs, four QTLs were located on chromosome 6. Lang et al. (2001a, b) identified single sequence repeat (SSR) and restriction fragment length polymorphism (RFLP) markers associated to QTLs for seedling survival in saline condition, shoot and root dry mass, Na⁺ and K⁺ absorption and for Na⁺/K⁺ ratio on chromosomes 1, 2, 3, 7, 9, 11 and 12. Koyama et al. (2001) identified 11 QTLs on 4 different chromosomes, 1, 4, 6 and 9 for different component trait related to salinity.

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