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## **Analysis of ‘QTL-seq’ associated with allelopathic potential in rice**

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### **Abstract**

In this study, QTL analysis of allelopathy was conducted. A total of 171 of F8 RILs developed from the cross between Nongan(low allelopathic cultivar) and Sathi(high allelopathic cultivar) were used . the performance of allelopathy were evaluated using ‘ECAM(Equal Compartment Agar Method)’, where the root length of lettuce cultivated with the RILs were measured. The distribution of the performance was followed as normal distribution. In order to identify the location of QTLs related to allelopathy, QTL-seq with BSA(Bulked-segregant analysis) was performed with 20 highest and 10 lowest RILs. As a result, Two Sliding window coordinate region of candidate QTLs were detected on Chr4 (5,050,001 - 14,800,000 , 18,650,001 - 22,500,000), Chr8 (2,550,001 - 8,250,000 , 21,150,001 - 26,800,000) and One region on Chr7 (1 - 3,300,000), Chr9 (1 - 13,300,000) respectively.

Keywords: rice, allelopathy, QTL, QTL-seq, BSA

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