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**The Thesis Submitted for M. Sc. Degree in the field of
Agricultural Biotechnology**

Identification and mapping of QTLs controlling seed quality related traits in barley

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Abstract

Barley is an important crop, both in terms of malt production and livestock nutrition. In order to identify the locus for several quantitative traits, and the correlation between the QTL and the traits, 72 doubled haploid barely lines, together with their parents (Steptoe and Morex) were selected and examined under normal condition with three replications. The studied traits include the quantity of alpha-amylase, peroxidase, polyphenol oxidase, catalase, gayocole peroxidase, ascorbat peroxidase, diastatic power and malt extract quantity. The statistical analysis consist of analysis of variance and correlation between the traits, done by SAS, QTL analysis, done by QTL Cartographer, and genetic linkage map of 327 RFLP markers resulted based on combined interval mapping and cluster analysis was done by software NTSYS. The results of analysis of variance revealed significant difference among lines. The effect of genotype was significant for alpha-amylase, peroxidase, polyphenol oxidase, gayocole peroxidase, ascorbat peroxidase, diastatic power ($p < 0.01$) as well as the catalase enzyme and malt extract ($p < 0.05$). The diastatic power with alpha amylase enzyme had the highest correlation (0.67). Principal component analysis showed that three eigenvelues were higher than 1, which the first factor justified 30.14% of the variation and the second and third factor justified 18.98% and 16.66%, respectively. For all of the studied traits, a total of 27 QTLs were idenfied. The justified variance of genotype by these QTLs varied from 6.8 to 27.1%. The extreme values for variance of phenotype for the trait of diastatic power in mean was get. All of The justified variances of phenotype by these QTLs from 6.6 to 88% were getting for the diastasic power. LOD was in range of 1.96-8.35. The highest and lowest LOD was obtained for QTLs in the diastatic power and trait malt extract, respectively.

Key words: QTL, Identify the locus of trait quantities, lines doubled haploid, barely.