



Molecular genetic map construction and QTL analysis of fruit maturation period in grapevine

Y.H. Zhao¹, K. Su¹, Y.H. Guo¹, H.F. Ma² and X.W. Guo¹

¹Department of Pomology College of Horticulture,
Shenyang Agricultural University, Shenyang, China

²Dalian Academy of Agricultural Science, Dalian, China

Corresponding authors: Y.H. Guo / X.W. Guo

E-mail: guoyinshan77@126.com / guoxw1959@163.com

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ABSTRACT. In this study, we aimed at finding the genetic regularity of grape maturation period. Early-maturing grapevine, “87-1”, was used as the female parent and late-maturing, “9-22”, as the male parent, to create an F1 hybrid population. A total of 149 individual plants and their parents were selected as the mapping population. Sequence-related amplified polymorphism and simple-sequence repeat analyses were performed. We performed a linkage analysis and constructed a molecular genetic map. In the obtained map, the female and male parents each covered 19 linkage groups containing 188 and 175 maker loci, respectively. The total map distances for the female and male parents were 1074.5 and 1100.2 cM, respectively, whereas the average genetic distances between each two loci were 5.7 and 7.8 cM, respectively. The interval-mapping method was used in a quantitative trait locus (QTL) analysis for fruit maturation period. A total of 12 QTLs associated with fruit maturation period were detected. These included four QTLs in the male parent genetic map that were located in linkage groups M5, M11, M14-1, and M16, with a 62.6-75.7% rate of contribution of each QTL. Another three QTLs were found in the female parent genetic map, located in linkage groups F6, F14-1, and F18, with a 72.7-77.7%

rate of contribution of each QTL. Five more QTLs were detected in the consensus map, located in linkage groups LG11, LG14-1, LG16, LG17, and LG18, with 8.9-75.7% phenotypic variance explained by each QTL.

Key words: Grape; Fruit maturation period; QTL