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Fruit texture plays a major role in apple fruit quality, and it has been the major driving factor in the selection process carried out by breeders. The economic importance of texture relies on the fact that some aspects of this multi-trait feature (crispness in particular) are the reason for not liking a particular fruit, and thus it represents the principal aspect sensorially perceived by consumers. Texture, which changes significantly during storage, can only be evaluated many years after from the crossing, and it has been established that it is regulated by a considerable number of genes. In this work a candidate gene driven association mapping approach has been employed in order to define valuable new markers suitable to predict the dissected fruit texture subtraits in apple. LD mapping was carried out in an apple collection, ad hoc assembled, and a candidate gene was targeted over a comprehensive QTL investigation based on two bi-parental maps. Finally we also present a preliminary functional genomic investigation addressed to target novel putative candidate genes to further unravel the complex control of fruit texture in apple.

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