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TARGETED DEVELOPMENT AND MAPPING OF FUNCTIONAL MOLECULAR MARKERS IN AN APPLE ROOTSTOCK (*Malus pumila*) MAPPING PROGENY

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The cultivated apple (*Malus pumila* Mill.) is an economically important crop, which is widely grown throughout the world. The identification of genes involved in traits of agronomic importance and the development of molecular markers for these genes is the key to the development of marker-assisted selection in breeding programs. Several genetic maps have been reported for apple, but the focus of these maps has been mainly on scion (fruit variety) crosses. In this investigation we aim to use information from the published apple genome sequence to develop intron-spanning primer pairs from the exons of Malus genes identified from within genetic regions of low marker density on a pre-existing SSR-based linkage map of an apple rootstock cross M.27 x M.116 (M432). Eighteen 'gaps' – regions larger than 10 cM containing no genetic markers - were identified for gene-specific primer design. BLAST analysis produced 2536 possible contig matches. The most significant 319 matches were selected and identified on 249 scaffolds. A total number of 165 gene-specific primers have been designed around the introns of genes located in these scaffolds. A set of 78 primers amplified single products in the parental genotypes whereas 33 amplified two products. Polymorphic markers developed within these scaffolds will increase marker density within regions. This communication details targeted development of markers for the improved saturation of the M432 apple rootstock linkage map.