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**Use of complete chloroplast genomes as phylogenetic markers for investigation of the origin and evolution of domesticated apple**

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**Abstract:** Despite a wide number of recent studies, phylogenetic affinities of the domesticated apple remain not well-resolved. A number of authors tried to address the issue using individual gene markers or genetic fingerprinting techniques; however, these studies did not converge on any particular outcome. Wising to test the performance of the phylogenomic approach in resolving infrageneric relationships within *Malus*, we built a 134,553 position long alignment including two previously published cpDNAs and 45 *de novo* sequenced, fully co-linear chloroplast genomes from cultivated apple varieties and wild apple species. The data produced were determined to be free from compositional heterogeneity and from substitutional saturation, which can adversely affect phylogeny reconstruction. Phylogenetic analyses based on this alignment recovered a branch, having the maximum bootstrap support, subtending a large group of the cultivated apple sorts together with all analysed European wild apple (*Malus sylvestris*) accessions. One apple cultivar was embedded in a monophylum comprising wild *M. sieversii* accessions and other Asian apple species. The data demonstrate that *M. sylvestris* has contributed chloroplast genome to a substantial fraction of domesticated apple varieties, supporting the conclusion that different wild species should have contributed the organelle and nuclear genomes to domesticated apple.