

A draft genome sequence of European pear (*Pyrus communis* L. 'Bartlett')

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We have sequenced the genome of European pear, *Pyrus communis* cultivar 'Bartlett'/'William Bon Chrétien' using second generation sequencing technology (Roche 454). A draft assembly was produced from single end reads, 2 kb, and 8 kb insert paired end reads using Newbler (version 2.7). The assembly contained 142,083 scaffolds greater than 499 bases (maximum scaffold length of 1.29Mb) covering a total of 577.3 Mb, representing 96.1% of the expected 600 Mb *Pyrus* genome. Preliminary analysis indicated that 549 SNP markers anchored 105 Mb (17.5%) of the assembled genome to a consensus genetic map of 'Old Home' x 'Louise de Bonne Jersey' and P019R054T042 x P037R048T081 segregating populations. Synteny with the apple genome primary assembly of 'Golden Delicious', and other rosaceous genomes is being used to extend putative anchoring. Gene prediction was performed and the use of the gene family of expansins will be reported as an example of assessment of the quality of the gene prediction. This 'Bartlett' genome sequence is a unique tool for identifying the genetic control of key horticultural traits and developing better pear cultivars, enabling wide application of marker-assisted (MAS) and genomic selection (GS).