



The improved assembly of the European Pear

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NOTE

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Gareth Linsmith^{1,2}, Luca Bianco², Chang Liu³, Stephane Rombauts¹, Jean-Marc Celton⁴, Sara Montanari⁵, Elio Schijlen⁶, Linda Bakker⁶, Cecilia Deng⁷, Charles-Eric Durel⁴, François Laurens⁴, David Chagne⁷, Riccardo Velasco², David Neale⁵, Yves Van de Peer¹ and Michela Troggio².

¹VIB / Ghent University, Bioinformatics & Systems Biology, Technologiepark 927, B-9052 Gent, Belgium.; ²Fondazione Edmund Mach, San Michele all'Adige (TN), Italy; ³ZMBP, Allgemeine Genetik, Universität Tübingen, Auf der Morgenstelle 32, D-72076 Tübingen, Germany; ⁴Institut de Recherche en Horticulture et Semences - UMR1345, Institut National de la Recherche Agronomique (INRA), SFR 4207 Quasav, 42 rue Georges Morel, F-49071 Beaucozéz, France.; ⁵University of California Davis, Department of Plant Sciences, Davis, CA USA; ⁶Wageningen UR - Bioscience P.O. Box 16, 6700AA, Wageningen, The Netherlands; ⁷The New Zealand Institute for Plant & Food Research Limited (PFR), Palmerston North Research Centre, Palmerston North, New Zealand.

Abstract: Apple and Pear diverged from each other between 5.4 and 21.5 MYA and are believed to share a common whole genome duplication event between 35 and 50 MYA (Velasco et al. 2010, Wu et al. 2012). Size differences have been observed between the Apple and Pear genomes which are estimated at 527Mb (*Pyrus x Bretschneideri* Rehd) and 700Mb (*Malus x Domestica* Borkh) respectively (Wu et al. 2013, Li et al. 2016). The difference in genome size has been accounted for primarily by the proliferation of transposable elements, with the gene space thought to be fairly similar between the two species (Wu et al 2012). Comparative genomics of the lineage has however, been hampered by the fragmented nature of the reference assemblies. A new chromosome scale apple assembly was recently produced (Daccord et al. 2017) and now also a chromosome scale assembly of the European Pear (this study), which shows strong collinearity with Apple, greatly facilitating the comparative study of these genomes.

Key words: *Pyrus communis*; pear; *Malus domestica*; apple; genome assembly; comparative genomics; Hi-C; Bionano; Pacbio

Plaza DB | Asian pear
Europ. pear
Apple
bioinformatics . psb . ugent . be / plaza