



The genome of the domesticated apple (*Malus × domestica* Borkh.)

Submitted by Elisabeth Chevreau on Tue, 05/26/2015 - 18:34

Titre The genome of the domesticated apple (*Malus × domestica* Borkh.)

Type de publication Article de revue

Auteur Velasco, Riccardo [1], Zharkikh, Andrey [2], Affourtit, Jason [3], Dhingra, Amit [4], Cestaro, Alessandro [5], Kalyanaraman, Ananth [6], Fontana, Paolo [7], Bhatnagar, Satish K [8], Troggio, Michela [9], Pruss, Dmitry [10], Salvi, Silvio [11], Pindo, Massimo [12], Baldi, Paolo [13], Castelletti, Sara [14], Cavaiuolo, Marina [15], Coppola, Giuseppina [16], Costa, Fabrizio [17], Cova, Valentina [18], Dal Ri, Antonio [19], Goremykin, Vadim [20], Komjanc, Matteo [21], Longhi, Sara [22], Magnago, Pierluigi [23], Malacarne, Giulia [24], Malnoy, Mickael [25], Micheletti, Diego [26], Moretto, Marco [27], Perazzolli, Michele [28], Si-Ammour, Azeddine [29], Vezzulli, Silvia [30], Zini, Elena [31], Eldredge, Glenn [32], Fitzgerald, Lisa M [33], Gutin, Natalia [34], Lanchbury, Jerry [35], Macalma, Teresita [36], Mitchell, Jeff T [37], Reid, Julia [38], Wardell, Bryan [39], Kodira, Chinnappa [40], Chen, Zhoutao [41], Desany, Brian [42], Niazi, Faheem [43], Palmer, Melinda [44], Koepke, Tyson [45], Jiwan, Derick [46], Schaeffer, Scott [47], Krishnan, Vandhana [48], Wu, Changjun [49], Chu, Vu T [50], King, Stephen T [51], Vick, Jessica [52], Tao, Quanzhou [53], Mraz, Amy [54], Stormo, Aimee [55], Stormo, Keith [56], Bogden, Robert [57], Ederle, Davide [58], Stella, Alessandra [59], Vecchiotti, Alberto [60], Kater, Martin M [61], Masiero, Simona [62], Lasserre, Pauline [63], Lespinasse, Yves [64], Allan, Andrew C. [65], Bus, Vincent G. M. [66], Chagné, David [67], Crowhurst, Ross N. [68], Gleave, Andrew P [69], Lavezzo, Enrico [70], Fawcett, Jeffrey A [71], Proost, Sebastian [72], Rouzé, Pierre [73], Sterck, Lieven [74], Toppo, Stefano [75], Lazzari, Barbara [76], Hellens, Roger P [77], Durel, Charles-Eric [78], Gutin, Alexander [79], Bumgarner, Roger E [80], Gardiner, Susan E [81], Skolnick, Mark [82], Egholm, Michael [83], Van de Peer, Yves [84], Salamini, Francesco [85], Viola, Roberto [86]

Pays Etats-Unis

Editeur Nature Publishing Group

Ville New-York

Type Article scientifique dans une revue à comité de lecture

Année 2010

Langue Anglais

Date Oct. 2010

Numéro 10

Pagination 833-839

Volume 42

Titre de la revue Nature Genetics

ISSN 1546-1718

Résumé en
anglais

We report a high-quality draft genome sequence of the domesticated apple (*Malus × domestica*). We show that a relatively recent (>50 million years ago) genome-wide duplication (GWD) has resulted in the transition from nine ancestral chromosomes to 17 chromosomes in the Pyreae. Traces of older GWDs partly support the monophyly of the ancestral paleohexaploidy of eudicots. Phylogenetic reconstruction of Pyreae and the genus *Malus*, relative to major Rosaceae taxa, identified the progenitor of the cultivated apple as *M. sieversii*. Expansion of gene families reported to be involved in fruit development may explain formation of the pome, a Pyreae-specific false fruit that develops by proliferation of the basal part of the sepals, the receptacle. In apple, a subclade of *MADS-box* genes, normally involved in flower and fruit development, is expanded to include 15 members, as are other gene families involved in Rosaceae-specific metabolism, such as transport and assimilation of sorbitol.

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DOI

[10.1038/ng.654](https://doi.org/10.1038/ng.654) [88]

Lien vers le
document

<http://dx.doi.org/10.1038/ng.654> [88]

Titre abrégé

Nat Genet

Liens

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