

## Publications Etienne Bucher

**28 publications** in international peer reviewed journals ([Google Scholar](#))  
3 reviews, 3 book chapters, 1 patent  
**3520 citations, h-index: 20**

### 5 selected publications:

Thieme, M., Lanciano, S., Balergue, S., Daccord, N., Mirouze, M., and **Bucher, E.** (2017). Inhibition of RNA polymerase II allows controlled mobilisation of retrotransposons for plant breeding. **Genome Biol** 18, 134. citations 18

- ✓ **This work describes the key findings that lead to the ERC Consolidator project (BUNGEE) and a patent.**



Daccord, N., Celton, et al. and **Bucher, E.** (2017) High quality *de novo* assembly of the apple genome and methylome dynamics of early fruit development. **Nature Genet** 49, 1099–1106. citations **229**

- ✓ **I was leading a large consortium to generate a high-quality reference apple genome and epigenome. We found that important traits such as fruit size can be epigenetically regulated.**



Ito, H.\*, Gaubert, H.\*, **Bucher, E.\***, Mirouze, M., Vaillant, I., and Paszkowski, J. (2011). An siRNA pathway prevents transgenerational retrotransposition in plants subjected to stress. **Nature** **472**, 115–119. **\*authors contributed equally. citations: 405**

- ✓ **Key paper. I played a crucial role in this work, since I initially discovered the heat induced TE and supervised the work of my co-first authors (H. Gaubert, PhD student / H. Ito post-doc).**

Yokthongwattana, C.\*, **Bucher, E.\*<sup>1</sup>**, Caikovski, M., Vaillant, I., Nicolet, J., Mittelsten Scheid, O., and Paszkowski, J. (2010). MOM1 and Pol-IV/V interactions regulate the intensity and specificity of transcriptional gene silencing. **Embo J** 29, 340–351. citations: 57, **\*authors contributed equally, <sup>1</sup>corresponding author**

- ✓ **This paper shows that I contributed to the better understanding of the roles of the plant specific RNA polymerases to epigenetic silencing.**

Kanno, T.\*, **Bucher, E.\***, Daxinger, L., Huettel, B., Böhmendorfer, G., Gregor, W., Kreil, D.P., Matzke, M., and Matzke, A.J.M. (2008). A structural-maintenance-of-chromosomes hinge domain-containing protein is required for RNA-directed DNA methylation. **Nat Genet** **40**, 670–675. **\*authors contributed equally, citations: 176**

- ✓ **This paper shows that I made important contributions in the elucidation of epigenetic silencing mechanisms in plants.**



### **Full publication list**

Perrin, A., Daccord, N., Roquis, D., Celton, J.-M., Vergne, E., and Bucher, E. (2020). Divergent DNA Methylation Signatures of Juvenile Seedlings, Grafts and Adult Apple Trees. *Epigenomes* 4: 4. 10.3390/epigenomes4010004

Gully, K., Pelletier, S., Guillou, M.C., Ferrand, M., Aligon, S., Pokotylo, I., Perrin, A., Vergne, E., Fagard, M., Ruelland, E., Grappin, P., Bucher, E., Renou, J.P., and Aubourg, S. (2019). The SCOOP12 peptide regulates defense response and root elongation in *Arabidopsis thaliana*. *J Exp Bot* 10.1093/jxb/ery454

Ferrafiat, L., Pflieger, D., Singh, J., Thieme, M., Böhner, M., Himber, C., Gerbaud, A., Bucher, E., Pikaard, C.S., and Blevins, T. (2019). The NRPD1 N-terminus contains a Pol IV-specific motif that is critical for genome surveillance in *Arabidopsis*. *Nucleic Acids Res* 47: 9037–9052. 10.1093/nar/gkz618

Nyikó, T., Auber, A., and Bucher, E. (2019). Functional and molecular characterization of the conserved *Arabidopsis* PUMILIO protein, APUM9. *Plant Mol Biol* 10.1007/s11103-019-00853-7

Gully, K., Celton, J.-M., Degrave, A., Pelletier, S., Brisset, M.-N., and Bucher, E. (2019). Biotic Stress-Induced Priming and De-Priming of Transcriptional Memory in *Arabidopsis* and Apple. *Epigenomes* 3: 3. 10.3390/epigenomes3010003

Peace, C.P., Bianco, L., Troglio, M., van de Weg, E., Howard, N.P., Cornille, A., Durel, C.E., Myles, S., Migicovsky, Z., Schaffer, R.J., Costes, E., Fazio, G., Yamane, H., van Nocker, S., Gottschalk, C., Costa, F., Chagné, D., Zhang, X., Patocchi, A., Gardiner, S.E., Hardner, C., Kumar, S., Laurens, F., Bucher, E., Main, D., Jung, S., and Vanderzande, S. (2019). Apple whole genome sequences: recent advances and new prospects. *Hortic Res* 6: 59. 10.1038/s41438-019-0141-7

Zhang, P., Fan, Y., Sun, X., Chen, L., Terzaghi, W., Bucher, E., Li, L., and Dai, M. (2019). A large-scale circular RNA profiling reveals universal molecular mechanisms responsive to drought stress in maize and *Arabidopsis*. *Plant J* 98: 697–713. 10.1111/tbj.14267

Thieme, M., and Bucher, E. (2018). Transposable Elements as Tool for Crop Improvement. In *Advances in Botanical Research: Plant Epigenetics Coming of Age for Breeding Applications*, Elsevier), pp. 165–202.

David, W., and Bucher, E. (2018). The 5'-3' Exoribonuclease XRN4 Regulates Auxin Response via the Degradation of Auxin Receptor Transcripts. *genes* 9: 638. 10.3390/genes9120638

Ed. Gallusci, P., Bucher, E., Mirouze, M. (2018). *Plant Epigenetics Coming of Age for Breeding Applications*. *Advances in Botanical Research*. ISBN 9780128154038, 472 pages

Hibrand Saint-Oyant, L., Ruttink, T., Hamama, L., Kirov, I., Lakhwani, D., Zhou, N.N., Bourke, P.M., Daccord, N., Leus, L., Schulz, D., Van de Geest, H., Hesselink, T., Van Laere, K., Debray, K., Balzergue, S., Thouroude, T., Chastellier, A., Jeauffre, J., Voisine, L., Gaillard, S., Borm, T.J.A., Arens, P., Voorrips, R.E., Maliepaard, C., Neu, E., Linde, M., Le Paslier, M.C., Bérard, A., Bounon, R., Clotault, J., Choisne, N., Quesneville, H., Kawamura, K., Aubourg, S., Sakr, S., Smulders, M.J.M., Schijlen, E., Bucher, E., Debener, T., De Riek, J., and Foucher, F. (2018). A high-quality genome sequence of *Rosa chinensis* to elucidate ornamental traits. *Nat Plants* 10.1038/s41477-018-0166-1

Thieme, M., Lanciano, S., Balzergue, S., Daccord, N., Mirouze, M., and Bucher, E. (2017). Inhibition of RNA polymerase II allows controlled mobilisation of retrotransposons for plant breeding. *Genome Biology* 18: 1–10. 10.1186/s13059-017-1265-4

Daccord, N., Celton, J.M., Linsmith, G., Becker, C., Choisne, N., Schijlen, E., Van De Geest, H., Bianco, L., Micheletti, D., Velasco, R., Di Pierro, E.A., Gouzy, J., Rees, D.J.G., Guérif, P., Muranty, H., Durel, C.E., Laurens, F., Lespinasse, Y., Gaillard, S., Aubourg, S., Quesneville, H., Weigel, D., Van De Weg, E., Troglio, M., and Bucher, E.

(2017). High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. *Nature Genetics* 49: 1099–1106. 10.1038/ng.3886

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