

# **Yves Van de Peer**

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## **Areas of Research**

Plant phylogenetics, genome evolution, whole genome duplication.

## **Contact Information**

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## **Research Interests**

As an evolutionary biologist and a bioinformatician, I'm interested in using bioinformatics approaches to study the evolution of genes, genomes, and organisms. Regarding genome structure and evolution (which forms a major part of our research), I'm particularly interested in the study of gene and genome duplications as well as in the evolution of novel gene functions after duplication. Gene and genome duplication events have been considered important mechanisms for increasing biological complexity or evolving novelty in biology. However, controversy still exists about how and how fast duplicated genes evolve new functions and on the importance of whole genome duplications. Although the number of sequence data that can provide us with answers to the significance of gene and genome duplication, mapping and interpreting (large-scale) gene duplication events remains difficult. We believe that whole genome duplications are often an evolutionary dead end, except under certain circumstances, for instance under times of environmental upheaval or changing environmental conditions.

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## **Education Background**

**Bachelor:** University of Antwerp, Belgium

**Doctor:** University of Antwerp, Belgium

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## Work experience

Postdoc, University of Konstanz, Germany, 1996-2000

Associate/Full Professor, Ghent University, 2001-

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## Part-time Academic Jobs:

Editorial Boards of five international journals (The Plant Journal, Peer J, Genome Biology and Evolution, Current Plant Biology, Frontiers in Genetics).

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## Selected Publication

Zhang, J., Fu, X.-X., Li, R.-Q., Zhao, X., Liu, Y., Li, M.-H., ... Chen, Z.-D. (2020). The hornwort genome and early land plant evolution. *NATURE PLANTS*, 6(2), 107–118. <https://doi.org/10.1038/s41477-019-0588-4>

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Bezuidt, O. K. I., Lebre, P. H., Pierneef, R., León-Sobrino, C., Adriaenssens, E. M., Cowan, D. A., ... Makhalaanyane, T. P. (2020). Phages actively challenge niche communities in Antarctic soils. *MSYSTEMS*, 5(3). <https://doi.org/10.1128/msystems.00234-20>

Pu, X., Li, Z., Tian, Y., Gao, R., Hao, L., Hu, Y., ... Song, J. (2020). The honeysuckle genome provides insight into the molecular mechanism of carotenoid metabolism underlying dynamic flower coloration. *NEW PHYTOLOGIST*, 227(3), 930–943. <https://doi.org/10.1111/nph.16552>

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