Joëlle Amselem

Research Engineer Background in Computer science and Molecular Biology



Address: Paris, France

joelle.amselem@inrae.fr

Skills

Programming languages

- Shell, Perl, R, SQL

Bioinformatics

- Sequence analysis
- Transposable Element detection and analysis
- Gene prediction (structure and function)
- Variant detection

Project management

Education

- 1994: Master degree in « Computing applied to Life Sciences, Paris Descartes University, Paris
- **1990**: Diploma of « École Pratique des Hautes Études », Life and Earth Sciences, Paris Sorbonne university, Paris

Publications

ORCID 0000-0001-7124-3454

Google Scholar joelle.amselem	All	Since 2016
Citations	5825	2979

h-index 29 22 i10-index 36 28

Since 2003: INRA, Research Unit in Genomics Info, Versailles, France (<u>https://urgi.versailles.inrae.fr/</u>)

1986 -2002: INRA, Laboratory of Molecular and Cellular Biology, Versailles, France

Current activity

- **Bioinformatic projects management**
- Bioanalysis, Computing and Organization and animation of training session
 - Annotation of transposable elements
 - Genome information system around TEs

Research interest

After years of bioinformatic tools development (around transcriptomic and genome annotation), I carried out numerous bioinformatic analyzes in the frame of international genome sequencing and annotation projects including plants, fungi and insects. For over fifteen years, my research activities have covered the evolutionary dynamics and functional impact of repeats, genes and transposable elements annotation.

Main

Amselem J*, Cornut G, Choisne N, Alaux M, Alfama-Depauw F, Jamilloux V, et al. RepetDB: a unified resource for transposable element references. Mobile DNA. 2019;10:6.

- Plomion C¹, Aury J-M¹, Amselem J¹, Leroy T, Murat F, Duplessis S, et al. Oak genome reveals facets of long lifespan. Nature Plants. 2018;4:440.
- Perlin M, Amselem J, Fontanillas E, Toh S, Chen Z, Goldberg J, et al. Sex and parasites: genomic and transcriptomic analysis of Microbotryum lychnidis-dioicae, the biotrophic and plant-castrating anther smut fungus. BMC Genomics. 2015;16:461.
- Amselem J*, Lebrun M, Quesneville H. Whole genome comparative analysis of transposable elements provides new insight into mechanisms of their inactivation in fungal genomes. BMC Genomics. 2015;16:141.
- Amselem J, Vigouroux M, Oberhaensli S, Brown J, Bindschedler L, Skamnioti P, et al. Evolution of the EKA family of powdery mildew avirulence-effector genes from the ORF 1 of a LINE retrotransposon. BMC Genomics. 2015;16:917.

*Corresponding Author, ¹Co-first author



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