# CURRICULUM VITAE

Marie-Claude Marsolier-Kergoat
Née le 8 septembre 1966 à Paris

Laboratoire d'Éco-anthropologie et Ethnobiologie
UMR 7206 CNRS/MNHN/Université Paris Diderot
Muséum National d'Histoire Naturelle
Site du Musée de l'Homme
17 place du Trocadéro
F-75116 Paris
mckergoat@mnhn.fr

## FORMATION

**2009-2010** : année sabbatique comme chercheur invité à Rockefeller University (New-York) dans le Center for Studies in Physics and Biology.

**2005** : Habilitation à Diriger des Recherches (Université Paris XI)

**1988-1992** : Doctorat en Biologie Moléculaire et Cellulaire des Plantes (Université Paris XI)

**1985-1989** : Ecole Normale Supérieure, Paris (admission en Biologie).

## PARCOURS SCIENTIFIQUE

**Depuis 2015** : Mise à disposition au Muséum National d'Histoire Naturelle (site du Musée de l'Homme)
Laboratoire d'Éco-Anthropologie et Ethnobiologie
UMR 7206 CNRS/MNHN/Université Paris Diderot
Dir. : S. Bahuchet
Thèmes de recherche : paléogénomique, études bioinformatiques sur la recombination

**2013-2015** : Chef de l'équipe "Bioinformatique et Biophysique de l'ADN"
Service de Biologie Intégrative et de Génétique Moléculaire (CEA/Saclay)
Dir. : A. Harel-Bellan
Thèmes de recherche : études bioinformatiques sur la recombination et la réplication

**2006-2013** : Chef du Laboratoire "Métabolisme de l'ADN et Réponses aux génotoxiques"
Service de Biologie Intégrative et de Génétique Moléculaire (CEA/Saclay)
Dir. : M. Werner, C. Carles, A. Harel-Bellan
Thèmes de recherche : les checkpoints de l'ADN, la ribonucléotide reductase, études bioinformatiques sur la recombination et la réplication

**1996-2006** : Chercheur
Service de Biochimie et de Génétique Moléculaire (CEA/Saclay)
Dir. : A. Sentenac.
Thèmes de recherche : les checkpoints de l'ADN chez *Saccharomyces cerevisiae*.

**1994-1995** : Chercheur

Laboratoire du Métabolisme et de la Nutrition des Plantes (INRA Versailles)
Dir. : J.-F. Morot-Gaudry
Thèmes de recherche : études des gènes codant la glutamine synthétase chez les légumineuses.

**1992- 1994** : Post-doctorante

Service de Biochimie et de Génétique Moléculaire (CEA/Saclay)
Dir. : A. Sentenac.
Thèmes de recherche : transcription du gène *SNR6* chez *Saccharomyces cerevisiae*.
Responsable : A. Sentenac.

**1988-1992** : Etudiante en thèse

Laboratoire du Métabolisme et de la Nutrition des Plantes (INRA Versailles)
Dir. : J.-F. Morot-Gaudry
Thèmes de recherche : études des gènes codant la glutamine synthétase chez le soja (*Glycine max* L.).
Directeur de thèse : B. Hirel.

## ENCADREMENT D'ÉTUDIANTS ET DE POST-DOCTORANTS

**2005-2007 :** Willy Aucher (post-doctorat)

**2003-2007** : Céline Clémenson (DEA et thèse)

**2002-2004** : Ghislaine Guillemain (post-doctorat)

**1999-2003** : Christophe Leroy (DEA et thèse)

## PUBLICATION LIST


[1] G.H. Miao, B. Hirel, M.C. Marsolier, R.W. Ridge and D.P. Verma. Ammonia-regulated expression of a soybean gene encoding cytosolic glutamine synthetase in transgenic *Lotus corniculatus*, **Plant Cell** (1991), 3, 11-22.

[2] B. Hirel, M.C. Marsolier, A. Hoarau, J. Hoarau, J. Brangeon, R. Schafer and D.P. Verma. Forcing expression of a soybean root glutamine synthetase gene in tobacco leaves induces a native gene encoding cytosolic enzyme, **Plant Mol Biol** (1992), 20, 207-218.

[3] A.F. Burnol, F. Margottin, P. Schultz, M.C. Marsolier, P. Oudet and A. Sentenac. Basal promoter and enhancer element of yeast U6 snRNA gene, **J Mol Biol** (1993), 233, 644-658.

[4] M.C. Marsolier, E. Carrayol and B. Hirel. Multiple functions of promoter sequences involved in organ-specific expression and ammonia regulation of a cytosolic soybean glutamine synthetase gene in transgenic *Lotus corniculatus*., **Plant J.** (1993), 3, 405-414.

[5] M.C. Marsolier and B. Hirel. Metabolic and developmental control of cytosolic glutamine synthetase genes in soybean., **Phys. Plant.** (1993), 89, 613-617.

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[7] M.C. Marsolier, G. Debrosses and B. Hirel. Identification of several soybean cytosolic glutamine synthetase transcripts highly or specifically expressed in nodules: expression studies using one of the corresponding genes in transgenic Lotus corniculatus, **Plant Mol Biol** (1995), 27, 1-15.

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[9] M.C. Marsolier, M.N. Prioleau and A. Sentenac. A RNA polymerase III-based two-hybrid system to study RNA polymerase II transcriptional regulators, **J Mol Biol** (1997), 268, 243-249.

[10] R. Arrebola, N. Manaud, S. Rozenfeld, M.C. Marsolier, O. Lefebvre, C. Carles, P. Thuriaux, C. Conesa and A. Sentenac. Tau91, an essential subunit of yeast transcription factor IIIC, cooperates with tau138 in DNA binding, **Mol Cell Biol** (1998), 18, 1-9.

[11] O. Louvet, J. MacDougall and M.C. Marsolier. La levure: une cellule tube à essai., **Biofutur** (1999), 184, 82-83.

[12] M.C. Marsolier and A. Sentenac. RNA polymerase III-based two-hybrid system, **Methods Enzymol** (1999), 303, 411-422.

[13] O. Louvet and M.C. Marsolier A thermosensitive assay for RNA polymerase III-based two-hybrid system., in: L.Z.a.G. Hannon (Ed.), Yeast Hybrid Technologies, Eaton Publishing Co., 2000.

[14] M.C. Marsolier, P. Roussel, C. Leroy and C. Mann. Involvement of the PP2C-like phosphatase Ptc2p in the DNA checkpoint pathways of *Saccharomyces cerevisiae*, **Genetics** (2000), 154, 1523-1532.

[15] C. Leroy, C. Mann and M.C. Marsolier. Silent repair accounts for cell cycle specificity in the signaling of oxidative DNA lesions, **EMBO J** (2001), 20, 2896-2906.

[16] S. Lopez, M. Livingstone-Zatchej, S. Jourdain, F. Thoma, A. Sentenac and M.C. Marsolier. High-mobility-group proteins NHP6A and NHP6B participate in activation of the RNA polymerase III *SNR6* gene, **Mol Cell Biol** (2001), 21, 3096-3104.

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[19] C. Clemenson and M.C. Marsolier-Kergoat. The spindle assembly checkpoint regulates the phosphorylation state of a subset of DNA checkpoint proteins in Saccharomyces cerevisiae, **Molecular and Cellular Biology** (2006), 26, 9149-9161.

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[24] M. Oliva-Trastoy, V. Berthonaud, A. Chevalier, C. Ducrot, M.C. Marsolier-Kergoat, C. Mann and F. Leteurtre. The Wip1 phosphatase (PPM1D) antagonizes activation of the Chk2 tumour suppressor kinase, **Oncogene** (2007), 26, 1449-1458.

[25] C. Clemenson and M.C. Marsolier-Kergoat. DNA damage checkpoint inactivation: adaptation and recovery, **DNA Repair (Amst)** (2009), 8, 1101-1109.

[26] M.C. Marsolier-Kergoat* and E. Yeramian. GC content and recombination: reassessing the causal effects for the Saccharomyces cerevisiae genome, **Genetics** (2009), 183, 31-38.

* Corresponding author

[27] A. Goldar, M.C. Marsolier-Kergoat and O. Hyrien. Universal temporal profile of replication origin activation in eukaryotes, **PLoS One** (2009), 4, e5899.

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* Corresponding author

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[30] M.C. Marsolier-Kergoat. A simple model for the influence of meiotic conversion tracts on GC content, **PLoS One** (2011), 6, e16109.

[31] M.C. Marsolier-Kergoat. Asymmetry indices for analysis and prediction of replication origins in eukaryotic genomes, **PLoS One** (2012), 7, e45050.

[32] M.C. Marsolier-Kergoat* and A. Goldar. DNA replication induces compositional biases in yeast, **Mol Biol Evol** (2012), 29, 893-904.

* Corresponding author

[33] M.C. Marsolier-Kergoat. Models for the evolution of GC content in asexual fungi *Candida albicans* and *C. dubliniensis*, **Genome Biol Evol** (2013), 5, 2205-2216.

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[35] Y. Duroc, R. Kumar, L. Ranjha, C. Adam, R. Guérois, K. Md Muntaz, M.C. Marsolier-Kergoat, F. Dingli, R. Laureau, D. Loew, B. Llorente, J.B. Charbonnier, P. Cejka and V. Borde. Concerted action of the MutLβ heterodimer and Mer3 helicase regulates the global extent of meiotic gene conversion, **Elife** (2017), e21900.

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