
MALIKA AINOUCHE

CV

PARTICIPANT AT:

EVOLUTION OF PLANT PHENOTYPES FROM GENOMES TO TRAITS



March, 17th-18th, 2015, Barcelona

Malika Ainouche, Professor, University of Rennes, Rennes, France

Malika Ainouche's research aims at exploring the mechanisms generating biodiversity with particular focus on the role of interspecific hybridization and genome duplication (polyploidy) in the formation of successful, invasive species. They are using the saltmarsh grass genus *Spartina* as a model of recurrent hybridization and polyploidy, to study allopolyploid genome evolution at various evolutionary time scales. In the last years her lab has contributed to decipher the phylogenetic history of polyploid *Spartina* species, and analyzed the genetic, epigenetic and transcriptomic consequences of allopolyploidy in recently formed homoploid hybrids and the neopolyploid *Spartina anglica*. They are now more specifically interested in integrating genomic approaches to understand the role of polyploid genome evolutionary dynamics in the evolution of phenotypes and adaptive traits.

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ABSTRACT

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**March, 17th-18th, 2015, Barcelona****Malika Ainouche**, Professor, University of Rennes, Rennes, France**Polyploidy, Genome Evolution and Functional Novelty in Genus *Spartina* (Poaceae)**

Polyploidization has major effects on the evolution of genome structure and gene expression. It can also lead to the emergence of new functions and phenotypic novelties, which may affect the adaptive success of polyploids. Genus *Spartina* is characterized by recurrent hybridization and genome duplication. This polyploid genus evolved through two main lineages, containing respectively tetraploid and hexaploid species. Hybridization and / or genome duplication within and between these lineages resulted in various ploidy levels (7x, 9x, 12x), including a notorious example of recent allopolyploid speciation (the invasive allododecaploid *Spartina anglica* formed during the 19th century). *Spartina* species play an important ecological role in the sedimentary dynamics of coastal saltmarshes in several continents. This system allows examining the consequences of polyploidy at various evolutionary time scales, and most particularly the consequences of recent polyploid speciation in natural populations in a well-understood historical and phylogenetic framework. We performed various molecular approaches to decipher the evolutionary history of the genus, the genomic and transcriptomic effects of allopolyploidy. The recent genomic resources gained from massive parallel sequencing, and construction of reference transcriptomes in *Spartina* allow exploring the role of polyploidy in the evolution of ecologically important traits. This will be illustrated on a remarkable function developed by some *Spartina* species, namely the ability to produce DMSP (Dimethylsulfoniopropionate), a molecule that has an analogous structure to the osmoprotectant glycine betaine, and for which degradation by micro-organisms plays an important environmental role in the global sulfur cycle.

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