
Epigenetics and stress tolerance in polyploid *Spartina* (Poaceae)

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Abstract

Investigating epigenetic mechanisms in non-model species confronted to challenging environments is an important question in evolutionary ecology, but needs the development of adequate resources and methodologies. We present here the approach we developed in the salt-marsh genus *Spartina* (Poaceae) which is notorious for its recurrent hybridization and genome duplication events that resulted in highly successful invasive species. *Spartina* species play an important ecological role in the sedimentary dynamics of coastal saltmarshes in several continents where they are able to tolerate several hours of immersion under seawater. Some species exhibit particular tolerance and resilience to chemical pollution (e.g. heavy metals, polycyclic aromatic hydrocarbons PAHs) which make them excellent candidates for phytoremediation. The most complex genome (namely the invasive allo-dodecaploid *Spartina anglica*) arose recently in Europe *c.a.* 150 years ago, by genome duplication of the homoploid hybrid *S. x townsendii* resulting from an interspecific cross between the introduced *S. alterniflora* ($2n=6x=62$) as maternal parent and the European native *S. maritima* ($2n=6x=60$). Allopolyploidy was accompanied by significant DNA methylation alteration following hybridization, mostly in regions flanking transposable elements, and gene expression evolution. We used massive parallel sequencing technologies to explore the genomes and transcriptomes of these species, and we developed bioinformatic approaches and tools for detecting the different putative orthologous copies originating from the parents (duplicated homoeologs) in *S. anglica*. We also evaluated the repetitive compartments and annotated repeats, which allowed us to identify small RNAs (siRNAs and miRNAs) involved in epigenomic response to PAH-induced stress and/or in parental species, hybrid and the highly tolerant allopolyploid.

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