

W630

Recurrent Polyploidy in the Salt Marsh Genus *Spartina*: Lessons and Challenges

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Genus *Spartina* (Poaceae, Chloridoideae) is characterized by recurrent hybridization and genome duplication. Species introduction outside their native range had dramatic ecological and evolutionary consequences. This genus contains a notorious example of neopolyploidy, namely the invasive allododecaploid species *Spartina anglica*. This species formed in southern England during the 19th century, following genome duplication of the sterile F1 hybrid *S. x townsendii* which resulted from hybridization between two hexaploid species, the introduced *Spartina alterniflora* and the native *Spartina maritima*. *Spartina anglica* has larger ecological amplitude than its parents and has rapidly colonized the European saltmarshes and it is now introduced in several continents. Another sterile F1 hybrid (*S. x neyrautii*) was also formed independently from the same parents in South-West France. 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. It also allows distinguishing the effects of two important components of allopolyploid speciation: interspecific hybridization (in *S. x townsendii* and *S. x neyrautii*) and genome duplication (in *S. anglica*). We have employed various molecular approaches to decipher the evolutionary history of the genus, the genomic and transcriptomic effects of allopolyploidy. As *Spartina* belongs to one of the poorest investigated lineage in the Poaceae family from the genomic perspective, we have developed various genomic resources (massive parallel sequencing, reference transcriptomes, BAC sequencing) which are now employed for the challenging analysis of the evolution of such highly redundant genomes.

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