Genome merger and duplication as springboards for plant invasion: lessons from Spartina

Malika Ainouche^{*†1}, Armand Cave-Radet , Delphine Giraud , Alex Baumel , Blanca Gallego-Tevar , Jesus Castillo , Mathieu Rousseau-Gueutin , Julien Boutte , Julie Ferreira De Carvalho , Oscar Lima , Ales Kovarik , Andrew Leitch , Ilia Leitch , Abdelkader Ainouche , Francisco Cabello-Hurtado , Abdelhak El-Amrani , and Armel Salmon

¹UMR CNRS 6553 ECOBIO - Université de Rennes 1 – CNRS : UMR6553 – France

Abstract

During the last centuries, species introductions outside their native range have dramatically increased and have accelerated ecological changes, native species threat, but also biological diversification through rapid expansion of introduced plants, interspecific hybridization with natives and allopolyploid speciation. In evolutionary ecology, the polyploid grass genus Spartina provides one of the most fascinating examples with this respect, and it wellillustrates the multifaceted challenges of invasive population management. Spartina contains several species that have become highly successful invaders of intertidal mudflats and saltmarshes where they play an important ecological role as "ecosystem engineers". In Europe, such examples include (i) the cryptic introduction of the East-American tetraploid S. patens (which has until recently been considered as a Mediterranean endemic under the name of S. versicolor), (ii) introduction of the South-American heptaploid S. densifiora to the south-west coasts of the Iberian Peninsula and its subsequent hybridization with the native hexaploid S. maritima and (iii) introduction of the East-American hexaploid S. alterniflora to western Europe (UK, France, Spain) and its hybridization with S. maritima in England and in southwest France. In England, hybrid genome duplication resulted in a highly successful allododecaploid species, S. anglica that has now colonized European saltmarshes and is introduced in several continents. Spartina represents then an excellent model system to explore at various evolutionary time scales the genomic determinants of species expansion. Hybrid and polyploid genome dynamics, gene expression evolution in stressful conditions will be discussed in the light of their ecological implications

^{*}Speaker

[†]Corresponding author: malika.ainouche@univ-rennes1.fr