High satellite repeat turnover in allopolyploids Anemone multifida (2n = 32) and Anemone baldensis (2n = 48) (Ranunculaceae)

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Hybridization and genome doubling is accompanied by rapid and dynamic genetic and epigenetic changes, as well as changes in gene expression and phenotypic variation. How the emerging plant balances two coevolved genomes remains largely unknown. Here we focus on satellite DNA, aiming to trace its appearance, amplification and loss during plant speciation and allopolyploidisation. As a model, we used allotetraploid *Anemone multifida* (BBDD, 2n = 4x = 32) and allohexaploid *A. baldensis* (AABBDD, 2n = 6x = 48) originating from the crosses of diploids *A. sylvestris* (donor of the A subgenome), *A. cylindrica* (donor of the B subgenome) and *A. parviflora* (donor of the D subgenome). Using next generation sequencing, TAREAN integrated in the RepeatExplorer2 pipeline, Southern blot and fluorescence in situ hybridisation (FISH) we characterize three highly repetitive DNA sequences (AparSAT3, AcylSAT1 and AcylSAT2). AparSAT3 is highly abundant in the D subgenome of *A. multifida* and *A. baldensis*, as well as in its parental species *A. parviflora*. We detected dispersal of AparSAT3 between subgenomes B and D after allopolydisation. AcylSAT1 and AcylSAT2 occur in different but multiple, discontinuous tandem arrays scattered over all chromosomes of *A. multifida*, *A. baldensis* and their putative progenitors. FISH pattern of AcylSAT2 in each subgenome differs in comparison to its parental species suggesting events of intergenomic homogenisation after allopolyploidization. Our results illustrate complex evolutionary pathways of satellite repeats through *Anemone* speciation and allopolyploidization.

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