

Comparative citogenomic analysis of tandemly repeated DNA elements in four *Allium* species from the section *Cepa*

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J. Puizina^I, I. Šamanić^I, V. Besendorfer^{II}, Ž. Fredotović^I, J. Mlinarec^{II}, A. Jurković^{II}, J. McCann^{III}, H. Weiss-Schneeweiss^{IV}, N. Malenica^{II}, H. Kalinić^V

^IUniversity of Split, Faculty of Science, Department of Biology, Rudera Boškovića 33, Split, Croatia, ^{II}University of Zagreb, Faculty of Science, Department of Biology, Division of Molecular Biology, Horvatovac 101, HR-10000 Zagreb, Croatia, ^{III}University of Natural Resources and Biodiversity, Institute of Biotechnology, Gregor Mendel - Strasse 33, 1180, Vienna, Austria, ^{IV}University of Vienna, Department of Botany and Biodiversity Research, Renweg 14, 1030, Vienna, Austria, ^VUniversity of Split, Faculty of Science, Department of Computer Science, Rudera Boškovića 33, Split, Croatia

Allopolyploidy, which involves both polyploidy and inter-species hybridization, contributes to plant evolution and diversification. Most of the known allopolyploids are based on even-ploidy levels with very few odd-ploidy level taxa persisting in nature. One of such unusual cases is triploid onion, *Allium × cornutum* (Clementi ex Visiani, 1842), ($2n=3x=24$), an established minor garden crop, widespread in the northern hemisphere. By using molecular-phylogenetic approach we previously confirmed its unique triparental origin and successfully identified parental species. One of the ancestors was common onion, *Allium cepa* L., whereas the two other ancestral species were shown to originate from South-Himalayan regions, *Allium pskemense* B. Fedtsch and *Allium roylei* Stearn (Puizina et al. 1999, Fredotović et al. 2014). To better understand the genome evolution of allotriploid and its ancestral species, we performed de novo identification of repetitive DNA families by application of Next generation sequencing utilizing low-pass genome sequence data (~ 2%) and using the RepeatExplorer2 and TAREAN pipelines (Novak et al., 2020). The analyses showed that the genomes of all four species have a quite similar compositions, and that they are dominated by LTR-retrotransposons, making up 40-50% of nuclear DNA, with Tekay and Retand from Ty3 lineage and SIRE from Ty1 lineage being the most abundant. In contrast, satellite DNA was represented by only 0.1 - 1.6 % of nuclear DNA and ribosomal DNA on average by 0.3%. The results of comparative repeat analysis revealed shared and species specific repeats. By application of fluorescent *in situ* hybridization we mapped the two ribosomal and the three satellite DNA repeats from each parental species to the chromosomes of both diploid and allotriploid species. The mapped satellite and rDNA repeats provided useful chromosomal markers which allowed the individual identification of the majority of chromosomes within the analyzed karyotypes.