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Analysis of two different satellite DNA subfamilies in the complex sex-chromosome system of *Rumex acetosa* (*Polygonaceae*)

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Although satellite DNAs normally evolve concertedly, resulting in intra-specific sequence homogenization and inter-specific divergence, the existence of several mechanisms leading to satellite DNA subfamilies formation has been largely reported. Among the proposed causes, the existence of higher-order repeats, the population size and recombination disruptions are supposed to be the major factors.

Sex chromosomes represent good examples not only of repetitive sequence accumulation sites, but also of systems with an almost complete lack of recombination, and as such, they are ideal candidates for subfamily formation.

Specifically, in this study we analysed the sex-chromosome system of the dioecious species *Rumex acetosa* (*Polygonaceae*) paying special attention to a Y-specific satellite DNA family, RAYSI. *Rumex acetosa* is a classical model in sex-determining mechanisms research due to the presence of a complex sex system comprising of females 2n=14 (XX + 12 autosomes) and males 2n=15 (XY_1Y_2 + 12 autosomes). The two Y chromosomes appear not to recombine during male meiosis and both of them will only pair with the ends of each X chromosome arm. In this study, by means of molecular as well as fluorescent *in situ* hibridization techniques, we demonstrate the existence of two subfamilies of the RAYSI family (called RAYSI-S and RAYSI-J) looking at both fixed positions (homogenizated positions) and also their differential chromosome location. Causes and implications are discussed as well.