ORIGIN AND EVOLUTION OF THE SEX-DETERMINING CHROMOSOMAL SYSTEM OF *RUMEX ACETOSA* USING REPETITIVE DNA SEQUENCES

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Rumex acetosa is a classical model for research on sex-determining mechanisms. Females have 2n=14 (XX + 12 autosomes) and males 2n=15 (XY_1Y_2 + 12 autosomes). The origin and the evolution of this sex system remains puzzling. In this study, we have investigated about repetitive sequences (satellite DNAs and ribosomal ITS sequences) in the genome of *Rumex acetosa* and in related *Rumex* species in order to elucidate part of this enigma.

With respect to the origin, we have analysed three different satellite DNA families. One of these is RAYSI (930 pb), a specific male repetitive sequence which occurs in both Y chromosomes while the second one, RAE730 (730 bp) appears in supernumerary segments of a variable number of chromosomes, and in Spanish populations it is fixed in a pair of autosomes. We demonstrate that both of these satellites have a common origin in a 120 bp repetitive sequence through an intermediary 360 pb satellite. Independent amplification processes have led a separate evolution of the two satellite DNA families from the 360 pb sequence. The third family, the 180 bp satellite RAE180, is in the first and in the second pair of autosomes as well as in both Y chromosomes, and, according to our data, it is not related to the other two satellite DNA families. Here, we demonstrate that explosive accumulation processes have occurred in two heterochromatic regions of the genome: the Y chromosomes and the supernumerary segments.

With respect to the evolution, firstly, we have demonstrated that these three satellite DNA families are present at least in the dioecious relatives *Rumex acetosa* and *Rumex papillaris* of the Acetosa group of species, while they are absent in the other hermaphroditic or polygamous representatives. On the other hand, data based on the molecular analysis of ITS ribosomal sequences has led us to estimate that the divergence between *Rumex acetosa* and *Rumex papillaris* occurred 2 million of years ago. Thus it has been feasible to develop a comparative study between satellites evolving in sex chromosomes and those evolving in autosomes. In this sense, we have provided satisfactory proof of the idea that the evolutionary change and concerted evolution rates are lower for satellite DNAs in the sex chromosomes than for the satellite DNAs in autosomes. Furthermore, despite that recombination is avoided between Y_1 and Y_2 sex chromosomes, there is a remaining homogenization rate in them, probably related to intrachromosomal exchanges and gene conversion. Finally, that two RAYSI subfamilies exist in separate clusters supports the idea that Y_1 and Y_2 evolve separately.