Sex determination and Flower Formation
Poster

THE SEX CHROMOSOME SYSTEM OF *RUMEX ACETOSA*: A STRUCTURAL AND FUNCTIONAL ANALYSIS

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Rumex acetosa is characterised by a múltiple chromosome system in which sex is determined by the ratio between X-chromosomes and autosomes sets, which is 2n=12+XX for females and 2n=12+XY_1Y_2 for males. For a better understanding of the sex chromosome molecular structure, as well as the genetic control of sex determination in this species, we have started a molecular study using two different approaches. On the one hand, we generated a sex chromosome specific library of *R. acetosa*, by microdissecting the trivalent that sex chromosomes form during male meiosis prophase. The screening of this library has allowed us to identify five repetitive DNA families that have been characterised in detail. One of these, family DOP-20, has shown no homology with other sequences in databases. Nevertheless, the putative proteins encoded by the other four families, DOP-61, DOP-47, DOP-60 and DOP-8, show homology with proteins from different plant retroelements, including polyproteins form GYPSY- and COPIA-like LTR retroelements, and reverse transcriptase from non-LTR retroelements. Southern blot hibridizations with the genomic DNA from males and females of *R. acetosa*, but also with DNA from different *Rumex* species, indicate that sequences from these five families are dispersed throughout the genome of both males and females of *R. acetosa*, although its accumulation seems to be more limited to dioecious species of the genus.

On the other hand, in order to isolate differentially expressed genes between female and male flowers that could be involved in sex determination of *R. acetosa*, we have carried out a cDNA subtraction experiment. cDNa from females floral buds was subtracted with male floral bud cDNA, and the resulting cDNA pool was cloned for further analysis. To date we have identified three clones whose expression level is higher in female than in male flowers. The protein encoded by one of these genes shows no homology with other proteins in the databases. Nevertheless, the other two encode for two proteins that show a significant similarity with either CBP (CREB-bindind protein) histone acetyltransferases, or with α-N-acetylglocosaminidases. The implication of the isolated retrotransposons and genes in both the origin and the evolution of sex chromosomes or in the control of sex determination of *R. acetosa* is discussed.