

DEVELOPING AND MAPPING MOLECULAR MARKERS IN *HYPERICUM PERFORATUM* L. FOR INVESTIGATING APOMIXIS

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St. John's wort (*Hypericum perforatum* L.) is a medicinal plant that produces pharmaceutically important metabolites with antidepressant and anticancer activities. It is additionally regarded as a serious weed in many countries. Recently gained information has shown that *H. perforatum* is also an attractive model system for the study of apomixis. This species is characterized by a relatively small genome size, being $1C=0.650$ pg which corresponds to about 630 Mbp, and a versatile mode of reproduction, ranging from complete sexuality to nearly obligate apomixis. It has a basic chromosome number equal to 8, and its wild populations are composed mainly of tetraploids ($2n=4x=32$), although diploid ($2n=2x=16$) and hexaploid ($2n=6x=48$) chromosome numbers have also been reported. It is known that diploid genotypes are sexual whereas polyploids reproduce by pseudogamous facultative apomixis. Embryo sacs may be either reduced (meiotic) or unreduced (aposporic) and both types of egg cells may be either fertilized (gamic) or develop parthenogenetically (agamic), resulting in six possible categories of progenies. A better understanding of its reproductive and inheritance patterns is required to facilitate the identification of genetic factors associated with apomixis. Molecular markers and linkage maps are basic investigative tools which have not been extensively used to analyze the genetic control of apospory, parthenogenesis and apomixis within this system. The recovery of molecular markers linked to the mode of reproduction and related to the expression of apomictic determinants is a preliminary step towards the understanding of the genetic control and molecular regulation of apomixis in *H. perforatum*. Fine mapping of the chromosomal regions that control the expression of apomixis is also a major requirement for the isolation or validation of candidate genes for apomixis. To gain an insight into the genome organization and inheritance pattern of *H. perforatum*, a molecular analysis at the diploid level has been attempted using random and sequence-specific DNA markers for either anonymous or coding regions. Amplified fragment length polymorphism (AFLP) along with simple sequence repeat (SSR) and target region amplification polymorphism (TRAP) markers were developed and analyzed in a hybrid population which was created by crossing diploid sexual plants from two unrelated ecotypes, each chosen for antagonist morphological traits. The construction of a first genetic linkage map for sexual *H. perforatum* using a two-way pseudo-testcross strategy is presented. The development of informative molecular marker systems (microsatellites and

arbitrarily chosen multigene family domains) for *H. perforatum* and their application to genetically characterize apomictically reproducing polyploid *H. perforatum* is also reported and discussed.

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