

Conference abstract PO-65

Karyogeography and Hybrid Origin of European *Potentilla* species (Rosaceae)

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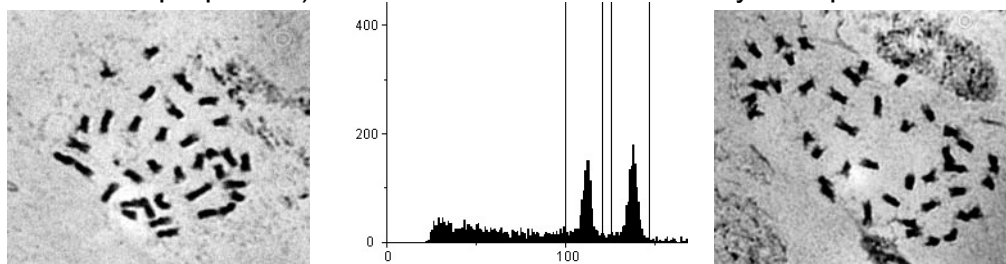
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Hybridisation is a widespread evolutionary process, potentially initiating the origin of novel species. The merging of genomes into a single individual, thereby, may be accompanied or followed by a change in ploidy. Hybridisation and polyploidisation challenge taxonomic research, as these processes may result in a plethora of genetically recombined and cytologically altered hybrids such as in the genus *Potentilla* or further pharmaceutically highly useful genera. *Potentilla* shows extensive and wide cytological variations and has been chosen as an established evolutionary model to study hybrid speciation based on the geographic distribution of parental and hybrid forms as well as karyological, morphological and molecular genetic variation at the population level. Here we present the karyological aspect. The study focuses on 11 European *Potentilla* species including three selected species of assumed hybrid origin and their putative parents. The cytology of 185 populations of known geographic origin was studied by means of light microscopic analysis of mitotic chromosomes and flow cytometry. Parental species were found to be cytologically completely or almost uniform, while the putative hybrids exhibited an extensive variation in ploidy both within and among populations. Comparison of the cytology of parental and hybrid populations at a local scale were suggestive of multiple independent polyploidisation events associated with the origin of some of the hybrid forms at least. Aneuploid cytotypes were found in populations showing evidence for recent hybridisation only. This observation suggests selection for genetically and cytologically balanced genomes following hybridisation. Our evolutionary studies are intended to finally provide a theoretical and practical basis to attain more consistent and predictive (e. g. with respect to phytochemical properties) taxonomic classifications of hybrid species.



Flow cytometric measurement of the somatic DNA-content of a *Potentilla* sample relative to a standard (left); Mitotic divisions of *P. alpicola* cytotypes: $2n = 35$ (middle), $2n = 42$ (right)