

## Genomic analysis of the sex chromosomes in *Cannabis sativa*

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*Cannabis sativa*-derived tetrahydrocannabinol (THC) production is increasing very fast worldwide. *C. sativa* is a dioecious plant with XY chromosomes, and only females (XX) are useful for THC production. The *C. sativa* sex chromosomes sequence would improve early sexing and better management of this crop; however, the *C. sativa* genome projects failed to identify the sex chromosomes so far. Moreover, dioecy in the Cannabaceae family is ancestral, *C. sativa* sex chromosomes are potentially old and thus very interesting to study as little is known about the last steps of sex chromosome evolution in plants. Here we RNA-sequenced a *C. sativa* family and performed a segregation analysis for all *C. sativa* genes using the probabilistic method SEX-DETECTOR. We identified >500 sex-linked genes. Mapping of these sex-linked genes to a *C. sativa* genome assembly identified a single chromosome pair with a large non-recombining region. Further analysis of the >500 sex-linked genes revealed that *C. sativa* has a strongly degenerated Y chromosome and represents the oldest plant sex chromosome system documented so far. Our study revealed that old plant sex chromosomes can have large non-recombining regions and be very differentiated and still be of similar size (homomorphic).