

DEVELOPING AND TESTING MOLECULAR MARKERS IN CANNABIS SATIVA (HEMP) FOR THEIR USE IN VARIETY AND DIOECY ASSESSMENTS

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C. sativa ($2n = 20$) is an extremely popular species belonging to the Cannabaceae family. Despite its use for medical, recreational and industrial purposes, boasting a long history, genetic and biotechnological research on this plant species is in its infancy, also as a result of the legal implications and the prohibition campaign linked to its use and cultivation. For many years, the development of new varieties was not the exclusive preserve of breeders since home growers have easily transitioned their activities from growing to breeding cannabis lineages. Recently, the use of genomics, led to a boost in approaches aimed at marker-assisted selection, germplasm management, genetic discrimination of varieties and forensic applications. Nonetheless, the use of molecular markers for varietal constitution through marker assisted breeding (MAB) is still in its infancy. This study represents therefore an attempt to fill this gap through the development of microsatellites (SSR) markers to be used for the genotyping of high breeding value varieties. Starting from 41 SSR developed *in silico*, we selected 20 highly polymorphic and informative loci that were tested over 104 individuals belonging to 11 different varieties. Selected markers proved to be successful in assessing homozygosity, genetic stability, and variation within and between varieties. Population structure analysis identified 8 genetic groups, clustering individuals based on sexual behaviors (dioecious and monoecious) and geographical origin. We believe this study can provide to the scientific community but also to producers and consumers, important tools for the purposes of genetic characterization, conservation of biodiversity, genetic improvement and traceability in this increasingly attentive plant species.