

## Genomic tools for medicinal plant breeding

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Genetic diversity within medicinal plants may be connected with qualitative and quantitative differences in metabolic profiles. Genetic markers linked with these differences may be applied to select more productive genotypes with improved level of target active compounds. Such enriched plant material influence economy of further extraction and purification steps. Preliminary, random marker systems were used in the process of development of genetic markers linked to useful traits. These systems include Amplified Fragment Length Polymorphism (AFLP) markers and various modification of this universal method, especially the methods for detection of dynamic, epigenetic changes of genomes. Nowadays, the availability of Next Generation Sequencing (NGS) technologies is leading to a revolution of plant breeding. This technology allows the mass sequencing of genomes and transcriptomes. Huge amounts of co-dominant markers can be statistically analyzed on structured populations leading to development of genetic maps and identification of quantitative trait loci QTL. In association based approach significant, phenotypic effects are connected with changes on genomic level. Both approaches lead to development of markers linked to valuable trait (i.e. higher level of active compound) in narrow or wide genetic background.

Along with growing number of sequenced plant genomes and our better understanding of biochemical processes leading to production of valuable plant natural products (PNPs) it become possible to search for direct relations between level of compound and genetic variation in enzymes involved in the pathway. Analysis of gene families connected with comparison of enzymatic efficiency may lead to selecting of effective combination of genes for subsequent introduction as multigene construct into host for biotechnological production of target valuable compounds.