

This bachelor thesis summarizes available information about currently used next-generation sequencing (NGS) methods where a big progress was achieved during last few years. Great advantage of NGS is the ability to gain huge amount of data at much lower cost per base compared to the Sanger sequencing. However, there are various pitfalls in data analysis.

Nowadays it is possible to sequence the entire genomes of individuals. Nevertheless, this approach remains challenging when studying many individuals, e.g. in phylogenetics. Recently, several approaches for effective reduction of genome complexity arose: transcriptome sequencing (RNA-Seq), target enrichment, restriction digest-based methods (RAD-Seq, RLL, GBS), genome skimming (shallow sequencing), etc. Each method has both advantages and disadvantages that affect its utility in phylogenetics.

Furthermore, the thesis deals with polyploid speciation and particularity of phylogenetics in polyploid plants – selection of suitable markers followed by data processing and phylogenetic analyzes. The last part of the thesis is devoted to my future research of polyploid genus *Curcuma* L.