Summary

Pasque flower (*Pulsatilla patens* (L.) Mill) is currently a rare and endangered species of European flora, however in the beginning of the last century it was rather common across middle east Europe, including Poland. In the last fifty years *P. patens* dramatically decreased its population size in this area and became an endangered or critically endangered species, protected under Annex I of the Bern Convention, and listed in Annex II and Annex IV of the Habitats Directive of the European Union. Recently, *P. patens* has also been included in the list of rare and endangered species of the International Union for Conservation of Nature (IUCN). Rapidly declining populations of pasque flower became a major concern of scientists, which arouse new research topics involving, in particular, evolutionary processes in small, geographically isolated populations as well as factors limiting the size of *P. patens* populations.

Presented doctoral thesis is another stage of genetic research on *P. patens*, aimed to increase the knowledge on its genome resources based on the analyses of organellar genomes. To date, organellar genomes were mostly used to determine differences between species, regarding nucleotide sequences of particular genes as well as their presence and organization in the genome. On the other hand, intra-species diversity and genetic structure of populations based on the combined data from both organellar genomes were not extensively studied. Therefore, the main aim of the presented thesis was **the analysis of organellar genomes effectiveness in studies on variability and genetic structure of populations of the rare and endangered *Pulsatilla patens* (L.) Mill species.** This goal was achieved through comparative analyses of chloroplast and mitochondrial genomes, which included both newly sequenced genomes and those available in databases. The study was conducted on 16 individuals from 5 populations that were previously included in genetic analyses, using SSR and ISJ markers.

One of the research tasks carried out as part of this doctoral dissertation was the sequencing and characterization of the *P. patens* mitochondrial genome. The obtained results contradicted the hypothesis of the existence of one master circle chromosome. *P. patents* mitogenome revealed a multichromosomal structure, consisting of three linear chromosomes flanked by inverted repeated sequences, with a total length of 986,613 bp. Due to the size of mitogenome, for comparative analyses describing intra-species variability, specific mitogenome sequences of great potential in phylogenetic and phylogeographic studies were

selected. These 14 mitochondrial sequences with a length of more than 10 kb, which do not contain plastid-derived regions and long repeats, may be an alternative source of genetic information to the plastid genome. Eight such sequences were identified on the first chromosome (chMt1), four on the second (chMt2) and two on the third chromosome (chMt3).

The aim of comparative analyses, an another research task, was to describe the variability both at the intra- and inter-population level. The obtained results showed that the 14 selected mitogenome sequences demonstrated distinctively lower level of variability compared to the plastid genome. Moreover, chloroplast genomes, although more variable, identified the same number of haplotypes (11) as regions of the mitochondrial genome. It should be emphasized that combining the data from both the mitochondrial and chloroplast genomes enabled the molecular identification of individuals, which would be unrecognizable on the basis of either genome independently.

The conducted research has shown that the utility of organellar genomes data in comparative genomics studies has a great potential and sheds new light on the field of genetic variability of species. It certainly consist a valuable supplement to the knowledge about the genomic resources of species.