Summary:

Study presented in this PhD thesis focused on the molecular basis of flowering induction in a short-day plant *Chenopodium rubrum*. We looked for respective homologs of *CONSTANS* (*CO*), *FLOWERING LOCUS T* (*FT*) and *LEAFY* (*LFY*) genes, which act as crucial regulators in the photoperiod-dependent signal pathway in *Arabidopsis thaliana*.

We identified two *FT-like* (*FTL*) genes *CrFTL1* a *CrFTL2* differing in their expression patterns in tetraploid *C. rubrum*. *CrFTL1* showed rhythmic expression peaking in midday. Elevated expression of *CrFTL1* was correlated with flowering under permissive photoperiodic treatments, whereas it was not expressed at all under non inductive photoperiodic regimes. *CrFTL2* showed constitutive expression. *CrFTL1* very likely plays a role as a floral inducer, but the function of *CrFTL2* remains unknown.

Two *CO-like* (*COL*) genes *CrCOL1* a *CrCOL2* identified in *C. rubrum* are alternatively spliced and produce two variants of transcripts. One of them was standard with one intron located in conservative site, the other one had an additional intron corresponding to the 90 bp region of the first exon. This type of alternative splicing has not been described in other known *COL* genes. All forms of transcripts show allmost identical rhythmic transcriptional patterns peaking at the end of the night and differ only in the level of individual mRNA. Light strongly inhibited transcription of both *CrCOL* genes.

We have also identified a complete coding sequence of previously known *LFY* ortholog *CrFL*. Our results suggest absence of the second intron in genomic sequence of this gene in *C. rubrum* and also in *LFY* homolog *CbhLFY1* in *C. bonus henricus*. The second intron has been found in all other known *LFY* homologs.

We have also revealed that a part of *FTL* genomic sequence could serve for phylogenetical relationship determination in polyploid species related to *C. album*. This group is taxonomically complex and mutual relationships among species are not clear. The third intron of *FTL* genes showed to be a usefull molecular marker to elucidate the problem and was also suitable for tracing parental species of tetraploid *C. quinoa*, important crop of South America.

The complementation of *ft* and *co* mutants of *A. thaliana* by the *CrFTL* and *CrCOL* genes under the control of *35S* promoter is in progress in our lab at the moment. Our preliminary results strongly suggest that *CrFTL1* is orthologous to *FT* and alternatively spliced form of *CrCOL2* (*CrCOL2s*) complements *co* mutation in *A. thaliana*.