Gene expression analysis in Scots pine in response to red and far-red light
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Light is vital for plant growth, morphogenesis and metabolism. Genome expression pattern under red light and far-red light is extensively studied in angiosperms but little is known about the gene regulation in this aspect with reference to Scots Pine. We studied gene regulation in *P. sylvestris* from northern Sweden grown under red and far-red light using *P. taeda* cDNA microarrays. Seeds from northern Sweden were grown under continuous red and far-red light under two separate experiments. Microarray was performed with *P. taeda* cDNA microarrays. Microarray data was normalised by LOWESS normalisation method and by computing the log ratios of the intensity measurements. Statistical analysis was carried out by calculating the t-test statistic and the corresponding p-values from the M-values for each gene in the dye swap experiment. The p-values were adjusted by FDR method using the R-statistical package. The microarray data analysis revealed expression of 405 genes which was enhanced under cR light treatment; while the expression of 239 genes was enhanced under the cFR light treatment. These results indicated that cR light acts as promoting factor whereas cFR antagonises the effect in most of the processes like C/N metabolism, photosynthesis and cell wall metabolism which is in accordance with former findings in *Arabidopsis*. Differentially expressed genes were annotated using Blast2GO tool.