7 Summary

The dissertation aimed to analyze the role of DNA-methylation in the model cyanobacterium *Synechocystis* sp. PCC6803. With the help of new omics techniques like SMRT-sequencing and bisulfite-sequencing we identified five methylation motifs, namely: ^{m5}CGATCG, G^{m6}ATC, GG^{m4}CC, GA^{m6}AGGC and GG^{m6}AN7TTGG/CCA^{m6}AN7TCC. *In silico* analyses identified putative DNA-methyltransferases that are likely responsible for the methylation of these motifs. The DNA-methyltransferases M.Ssp6803I (*slr0214*) and M.Ssp6803III (*slr1803*) methylate the motifs ^{m5}CGATCG and G^{m6}ATC (Scharnagl *et. al.*, 1998). Bisulfite-sequencing revealed that the first cytosine of the motif ^{m5}CGATCG became C^{5} methylated. Further analysis showed a functional role of M.Ssp6803I for DNA repair. The DNA-methyltransferase M.Ssp6803II (*sll0729*) methylates the first cytosine of the core sequence GG^{m4}CC. Initial analyses of the Δ*sll0729* mutant showed a growth and pigmentation phenotype. However, these changes in mutant Δ*sll0729* were unstable due to the appearance of suppressor mutants. The suppressor clones Δ*sll0729::supp*_1 and Δ*sll0729::supp*_15 were isolated and analyzed using microarray analysis. The results showed changed gene expression of only two genes. For example the *sll0470* transcrip, bearing a GGCC methylation motif in the promotor region, was found in higher abundances in the initial mutant Δ*sll0729* as well as in suppressor clones compared to wild type. These analysis reveald that the expression of few selected genes might be regulated via the activity of M.Ssp6803II. Interestingly, the suppressor clones showed decreased cell size, lower DNA content and reduced UV-tolerance compared to wild type. Therefore a role of DNA-methylation via M.Ssp6803II on chromosome stability, DNA-replication and DNA-repair mechanisms is assumed. These changes could be correlated with the function of the topoisomerase IV subunit A (*sll1941*), which was found in lowered abundance in transcriptome and proteome analyses of the suppressor clone. The DNA-methyltransferase M.Ssp6803IV and M.Ssp6803V are modifying the methylation motifs GA^{m6}AGGC and GG^{m6}AN7TTGG/CCA^{m6}AN7TCC. M.Ssp6803IV is essential for the viability of *Synechocystis* 6803. Proteome analysis of the Δ*slr6095* mutant reveal changes in the abundance of NrdR and NrdA, which indicates a role of M.Ssp6803V in processing genetic information. Here, a first comprehensive functional analysis of DNA methylation among cyanobacteria was performed, which showed that this mechanism fulfills divers roles in the

cyanobacterial cell such as gene expression regulation, DNA-replication and DNA-structure maintenance.