The molecular mechanisms that determine the expression of one or another set of genes resulting in different development pathways have been studied intensively in bacteriophages. Temperate phages, as opposed to virulent viruses, may choose to enter either a lytic or a lysogenic lifestyle following infection of a sensitive host. In the lytic infection cycle, new phages are produced, followed by lysis of the host cell and liberation of phage progeny into the surroundings. Whereas in the lysogenic infection cycle, the phages genome typically integrates into the bacterial chromosomal DNA, resulting in a dormant prophage, containing proteins in vivo.

Various truncations of CI were cloned, expressed in E. coli and purified. Subsequently, crystals were obtained for two of the constructs namely the C-Terminal Domain of CI (CTD-CI; residues 91-180) and the N-Terminal Domain (NTD-CI: residues 1-73). The crystals grown from CTD-CI belonged to space group P2_1_2_1 with unit cell parameters a=30.2 Å, b=30.2 Å and c=177.7 Å. CTD-CI is responsible for the oligomerization of the presumed CI hexamer [3]. Because of low sequence homology with known structures SAD/MAD techniques have been applied to overcome the phase-problem. The crystals were initially soaked in NaBr and CsI solutions and data were recorded. However, because of the unspecific binding of the HA we were not able to solve the phase problem, and we ended up producing a selenomethionine derivative.

We have furthermore succeeded in crystallizing the NTD-CI, which contains the DNA-binding domain of CI. The NTD-CI fold up in a putative Helix Turn Helix (HTH) domain. The crystal diffracted to 1.6 Å and belongs to the space group P2_1_2_1, with cell parameters a=23.68 Å b=43.84 Å and c=72.58 Å. Also here only low sequence identity is found with known HTH structures which complicates structure determination by molecular replacement technique, thus experimental phases will also be sought for this domain.

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\Delta S 8 C I, \text{ a truncated variant of the CI wild type protein, } [3] \text{ was also expressed and purified. The } \Delta S 8 C I \text{ in contrast to the CI protein only forms dimers and therefore only binds to only one operator site consisting of inverted repeated sequences. Parallel with crystallization studies } \Delta S 8 C I \text{ was used to perform small angle scattering studies with or without DNA. DLS and SAXS results showed a change in particle size when decreasing salt concentration in a solution of DNA and deltaS8. This preliminary indicates DNA-protein complex formation, and will be investigated further by SAXS (small angle neutron scattering).}
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