Topology of Pseudomonas aeruginosa chromosome. The role of partitioning protein ParB.

The research conducted in the last decade demonstrated that bacterial chromosomes are precisely organized spatiotemporal structures. They are folded into 3-4 strictly determined macrodomains of up to 1.5 Mb, *e.g*. ori and ter domains with replication initiation and termination sites, respectively, that during cell-cycle are relocated into the defined places in the cell. Besides macrodomains, chromosomes contain smaller (30 to 400 kb) chromosome interaction domains (CIDs), representing frequently interacting parts of the nucleoid and multiple, small, transcriptional microdomains. Topology of nucleoid is species-specific, since it results from the primary DNA sequence, species-specific nucleotide content, negative supercoiling regulated by action of topoisomerases, transcription machinery and most importantly from to the impact of various species-specific nucleoid associated proteins (NAPs), which bend, wrap, loop and bridge distant DNA fragments. In many bacterial species the main role in organization of ori macrodomain (with replication start site *oriC*), is fulfilled by partition protein ParB that binds to high affinity binding sites, *parS*s, spreads, bridges, loops various DNA loci, helps to condense newly replicated DNA by loading SMC proteins (Structural maintenance of chromosomes) and participates in transfer of compacted ori domains into dedicated locations in the cells. We have recently discovered that in *Pseudomonas aeruginosa*, an important opportunistic pathogen, ParB protein binds not only to nine palindromic *parS* sequences but also to heptanucleotide (*parS* half-site) occurring in more than 1000 copies in the genome. ParB discriminates between the binding sites depending on its availability, that in turn may be regulated by the cell-cycle. The putative role of ParB-half-*parS* interactions in genome topology and gene expression under different growth conditions will be analyzed by use of the state-of-art genome-wide techniques. The concept of partitioning ParB protein being the master regulator linking vital cell processes with metabolic state through changes in DNA topology is a new and exciting concept.