Temporal regulation describes how the gene expression in cell is programmed to change in time manner. It is a fundamental process for each living cell, but studied the most at eukaryotic cell related to cell cycle and development. However, temporal regulation is reported also to be of a highest importance for such processes at *Prokaryotes* as: bacteria sporulation; capsule formation associated with virulence of pathogenic *Staphylococcus aureus*; cell cycle maintenance of *Caulobacter crescentus*; circadian programming of gene expression at cyanobacteria. Bacteria need to adapt to the rapidly changing environment in a decision-making process to increase their survival. The decision is usually made *via* sensing the external and internal signals in a timely manner. In order to respond adequately, bacteria process the information and generate the output, which may be released as a change in gene expression. In general, the cell gene expression profile remains constant as long as the conditions stay undisturbed. Sometimes change in the environment may trigger the specific time-sequenced program of gene expression to facilitate bacteria adaptation, fitness or survival. Although, the regulation of gene expression is being relatively well explored in many bacterial processes, the mechanisms underlying the temporal control as well as the principles of the gene circuitry orchestration in time manner are not well understood. There are some special circumstances, where the gene expression dynamics in time may play particularly important role. It is related to the key process affected the diversity at Prokaryotes, which is the horizontal gene transfer. Mobile DNA modules while transferring between the hosts are challenged to successfully install their genes. The timing properties and molecular basis of these processes are still enigmatic and understood only to some extent. We will use a Type II restriction-modification system (RMs) as our model to study the temporal control of their gene expression at the step of entry to a new host. RM systems are extremely successful in dissemination of their genes in the bacteria and archaea via horizontal gene transfer. It seems a key factor to their success is a built-in regulatory design, which enable them to acquire the new hosts and challenge the interspecies barriers as the half of *Prokaryotes* contains at least one of RMs out of 4 different Types of RMs. In addition, their "regulatory equipment" packed in a simple genetic structure must be independent on host factors background to facilitate RMs installation. RM systems are classified into four main types, with Type II being the simplest in the genetic structure. It is typically composed of two independent enzymes: a restriction endonuclease (REase) that cleaves DNA at a specific sequence, and a modification methyltransferase (MTase) that acts on the same sequence to protect it from cleavage by the cognate REase. The REase can degrade DNA entering the cell, while resident host DNA remains safe due to methylation by the MTase. Relatively simple mechanisms must exist to provide the coordinated, temporal control of REase expression. It is especially crucial during the transfer of R-M system to a new host cell, the genome of which is unprotected by methylation. Their unregulated expression may lead to fail the host entry or host death. One of a strategy employed by RMs is to delay REase expression, to allow the MTase first to complete genome methylation. The time-dependent control of toxic nuclease was never characterized in detail. In addition, our hypothesis will be tested using powerful technique of the single-cell technology and time-lapse imaging to monitor the dynamics of gene expression at individual cells. We expect to show the principles of the gene circuitry orchestration in time manner and to establish the key players in this process. We predict our results to provide insight into, and lay groundwork for further studies of regulatory design, transcription activation/repression and molecular ecology of type II RM system. This work will help to understand the basic mechanisms responsible for adaptation of bacteria to the changing environment and development of protection barrier to maintain themselves in hostile phage-abundant conditions.