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Short Communication

Molecular Microbiology and Latest Studies on Genetic Transformation in Bacteria

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ABSTRACT

The studies of proteolytic enzymes and the mechanisms of macromolecule turnover in bacteria continued effectively in this period. The mechanisms of regulation of protease synthesis in Bacillus megaterium were disclosed. The studies on mechanisms of turnover of cell wall mucopeptide in B. megaterium were expanded to the analogous analyses in E. coli. The systematic analysis of effects of several factors on the process of sporulation in B. cereus finally led to the discovery of the wholly new phenomenon of "micro cycle sporogenesis".

Keywords: Protease enzyme.

INTRODUCTION

The systematic analysis of effects of several factors on the process of sporulation in B. cereus finally led to the discovery of the wholly new phenomenon of "microcycle sporogenesis". The microcycle sporogenesis was defined as direct transition of outperform bacterial spores to new sporangia without halfway cell division. The processes of subcellular (biochemical) differentiation of a bacterial cell were also studied competently at the Department of General Microbiology using majorly Bacillus megaterium as a model bacterium.

The study of mechanisms of genetic transformation in pneumococci was the main scientific interest of the newly entrenched Department of Microbial Genetics and flexibility of the Institute of Microbiology CAS. The effects of various factors on organization of pneumococcal transformation as well as the kinetics of penetration of modifying DNA into pneumococcal cells have been exclusively studied since that time. The studies of proteolytic enzymes and the mechanisms of macromolecule turnover in bacteria continued effectively in this period. The mechanisms of regulation of protease synthesis in Bacillus megaterium were disclosed. The studies on mechanisms of turnover of cell wall mucopeptide in B. megaterium were expanded to the analogous analyses in E. coli. The enhancement of conditions of Mycobacterium phlei mutagenesis provided a large collection of mutants. The comprehensive analysis of bacterial plasmids became the main scientific attentiveness of the Department of Bacterial Genetics of the Institute of Microbiology. The interrelation of plasmid DNA with cytoplasmic membrane was analyzed and the mutants of plasmid R6K with enlarged number of plasmid copies in a cell were isolated and distinguished. The new method for estimation of the number of plasmid copies in a bacterial cell was evovled. The studies of type I restriction-modification systems of E. coli, proceeding in collaboration with Portsmouth University (UK), continued by isolation and detailed distinguished of novel mutants in the individual subunits of these complexes Neisseria meningitidis is the other model bacterium that has been calculated at the Laboratory of Molecular Biology of Bacterial Pathogens. Detailed analyses of N. meningitidis genes controlled by iron level and of structure and function of the FrpC protein found in all tested clinical segregates were performed.

A hallmark of bacterial genetics is the ability to analyze very large populations of cells to discover rare genetic events. A hallmark of bacterial genetics is the ability to analyze very large populations of cells to discover rare genetic events. Although a wide diversity of genetic tricks has been developed for specific purposes in particular bacteria, bacterial genetics depends on a relatively small core of tools for dissection of the structure and function of genes. The essential tools involve the isolation of mutations, the ability to transport genes between bacterial strains, the ability to isolate recombinants, and the capacity to do complementation tests.

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