

Creation of a collection of variants of the *Bacillus anthracis* 1 CO strain with different biological properties to study the adaptation of the anthrax microbe to different living conditions

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The causative agent of anthrax is characterized by a complex cycle of existence in various morphological and functional forms (spores, vegetative capsular and acapsular), adapted to certain conditions. The short-term phase of existence in the body of sensitive animals is accompanied by active expression of pathogenicity factors and is replaced by spore formation, which ensures the preservation of the microbe in adverse environmental conditions. The study of the adaptation of anthrax microbe strains with different properties to different conditions of existence (macroorganism, soil) will make it possible to identify and characterize, including quantitatively, the key features of strains that affect the manifestation of pathogenic properties. The purpose of the research is the selection of variants of the *B. anthracis* strain, which differ in individual phenotypic properties and genetic characteristics, and their comprehensive study with an assessment of the possibility of using them in experimental work. Materials and methods: we used the original strain *B. anthracis* 1(CO) isolated from an animal with anthrax. The criteria for selecting cultures were their phenotypic properties: cultural and morphological, capsular and toxin formation, enzymatic activity, sensitivity to anthrax bacteriophages, nutritional requirements, *in vitro* virulence. Results: variants were isolated that differ from the original typical strain in capsular formation, which do not show toxin formation on the SOPEK medium, are incapable of spore germination on a minimal nutrient medium, are characterized by weak proteolytic activity, are not able to lyse washed sheep erythrocytes, have lecithinase activity, are resistant to the lytic action of specific bacteriophages, unable to hydrolyze starch and glycogen. Cultures with all variants of the plasmid composition were obtained. Among the studied isogenic variants, four MLVA genotypes and two SNP genotypes were identified. According to the degree of virulence *in vitro*, they belonged to four different groups.