LIFE SCIENCES SAMPLE--Original Abstract

Bacillus·anthracis·(B. anthracis)· is·a·gram-positive·bacteria·that·induces·anthrax; and·it·has·two-pathogenic mega-plasmids-that·are-pX0l and-pX02.·Between these-two; although·its·size·is·about·l 98Kb,·genetic-function·of X01·has·not·been·known·except·for·a·part·called·pat hogenic·island,·which·includes·three-toxin·component·genes·that·are-*pag*, *lef* ·and·*cya*.·Proteomic·system·was·used·to·verify·if there·was·a·protein·that was·controlled·by-pX01-plasmid.·By using·thermo-sensitive·character·of-pX01-plasmid,·strain·that·pX0l was·artificially·removed· from·*B.·anthracis*·H9401 (pX0!+/pX02+)·1 was·obtained.· Protein-regulation·data·was·obtained by·using·2D-DIGE·system·and·Decyder· software.·The·1,728·of proteins·had·appeared·in· wild type·strain·and·1,684 appeared in·strain that pX0l plasmid was cured. Among·these,·27· proteins·had disappeared·and 8 proteins· appeared by·removing· pX0l plasmid.·In addition,·52· proteins ·were·down·regulated·and·15·proteins were·up-regulated by·removing·pX0 1plasmid. Total·102·proteins ·had·been·identified·by ·MALDI-TOF/TOF,·and·among·them ·were·49·proteins·with unknown·functions. ·There·were·31·proteins·identified·as they participated·in metabolism,·2· in·cellular· process, 18 in·genetic·information·processing,·and·5·in· environmental information·processing.·Among· these, 7 proteins were·identified·as·they were· anticipated·to·participate·in·virulence·and pathogenesis. Functions·of those·in·other·bacteria· based·on documents·about·identified·proteins·was investigate,·and·characteristic·changes in·*B.·anthracis*·H9041 derivative as pX0l plasmid·curing·was·made·researches. Germination·rate·of pX01+/pX02+ B.·*anthracis* and pX0 l-/pX02+B.·anthracis derivative were·different·and was·ctytotoxic percentage for macrophage. Also,·revelation of S100 B protein·in·host was·increased when·the·host was·infected·with pX01+/pX02+·*B. anthracis* and pX0l-/pX02+ *B.* anthracis derivative."

LIFE SCIENCES SAMPLE--Edited Version

Bacillus anthracis is a gram-positive bacterial organism that is responsible for anthrax. This organism has two pathogenic plasmids: pX0l and pX02. The genetic function of pX0l, which consists of approxiniately 198 kb, is not known, except for a region called the "pathogenic island," which includes three genes—pag, lef, and cya—that code for three toxic proteins. A proteomic system of analysis was used to verify the existence of proteins that are controlled by this plasmid. Taking advantage of the thermosensitive character of the pX0l plasmid, reserarchers have been able to remove it from *B anthracis* H9401 (pX0l+/pX02+). Protein regulation data were obtained using two-dimensional difference gel electrophoresis and Decyder software. A total of 1728 proteins were identified in the wild type strain of this organism and 1684 in the pX0l plasmid. Of these, 27 disappeared and eight appeared when the pX0l plasmid was removed. An additional 52 proteins were down-regulated and 15 were up-regulated when this plasmid was removed. A total of 102 proteins have been identified using the matrix-assisted laser desorption ionization/time of flight method of analysis, including 49 whose functions are unknown. Among these, 31 participate in metabolic processes, two in cellular processes, 18 in the processing of genetic information, and five in the processing of extracellular information. another seven proteins participate in bacterial virulence and pathogenesis. We investigated the functions of these proteins in other bacteria, particularly in the *B anthracis* derivative H9041. Germiination rates for pX0 1+/pX02+ *B anthracis* and its pX0 l-/pX02+ derivative were different, but both organisms were cytotoxic in macrophages. It was also revealed that S100B protein levels increased in the host that was infected with pX0I+/pX02+ *B anthracis* or its pX0I-/pX02+ derivative. **(AU: Please add a sentence summarizing your conclusions about these findings.**

LIFE SCIENCES SAMPLE--Published Version

Bacillus anthracis is a gram-positive bacterial organism responsible for anthrax. This organism has two pathogenic plasmids: pX01 and pX02. The genetic function of pX01, which comprises about 198 kb, is not known, except for a region called the pathogenic island, which contains three genes-pag, lef, and cya-that code for three toxic proteins. A 2-D difference gel electrophoresis (2-D DIGE) system was used to verify the existence of proteins controlled by the pX01 plasmid, and protein regulation data were obtained using DeCyder software. A total of 1728 proteins were identified in the wild-type strain of this organism and 1684 in the pX01 plasmid. Twenty-seven of these proteins disappeared and eight appeared when the pX01 plasmid was removed. An additional 52 proteins were downregulated and 15 were upregulated when this plasmid was removed. A total of 102 proteins have been identified using the MALDI-TOF method of analysis, including 49 whose functions are unknown. Among these, 31 participate in metabolic processes, two in cellular processes, 15 in the processing of genetic information, and five in the processing of extracellular information. Another seven proteins participate in bacterial virulence and pathogenesis. We investigated the functions of these proteins in other bacteria, particularly the B. anthracis derivative H9041. Bacterial growth differed between pX01+/pX02+ B. anthracis and its pX01-/pX02+ derivative as did the cytotoxicity of macrophages infected by pX01+/pX02+ B. anthracis and the pX01-pX02+ derivative. We also found that S100B protein levels increased in the host infected with pX01+/pX02+ B. anthracis or its pX01-/pX02+ derivative. These data suggest that the pX01 plasmid plays a key role in the regulation of protein functions in B. anthracis.