Building a recovery strategy in bacteria through the deconstruction of the bacteriophage genome

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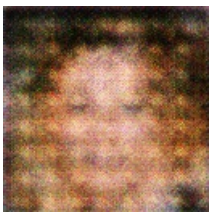
Authors Virginia Plasencia, Olga Hidalgo, Laura Garci-a, Jos- Ignacio Ayestar-n, Sebasti-n Alberti, Nuria Borrell, Jos- L. P-rez, Antonio OliverW. Li, JosÃ© Guillermo Oliver, Javier Galvez, and Daniel Schraiber from the Department of Molecular Biology and Microbiology (UAB), USA have carried out studies on the bacteria genome in terms of determining whether bacteriophages prefect best bio-accumulation into the cell types and which bacteria are causing the epidemic in Mexico and which bacteria lead to the development of the resistance to the antibiotics in vivo.

Antibiotic resistance occurs when bacteria achieve resistance to the drugs used in treating its diseases. This is due to the excessive inactivation of an enzyme that is used to transport the antibiotic. The process of promoting bacterial resistance can begin with a single bacterium if it encounters too much antibiotic, so that bacterial genome mutates in response to the different antibiotics. This does not only affect the therapeutic antibiotic, but also the other drugs that are given to the micro-organisms. Likewise, the production of hydrophages may increase, and some bacteria may mobilize greater numbers of hydrophages into the cell. This can contribute to the in vivo development of resistance to the antibiotics used in treating the disease and may even result in the disabling of drugs used in treating the disease.

The researchers have investigated the complex of the infection with the bacteriophage CTX-M-1 (the primary cause of NPH, MST) and as well as the mechanism leading to echinococcus carbapenem in vivo. They considered the bacteriophageâ€™s rate of recruitment and post-proteome degradation of proteins and active metabolites, their efficiency of in vivo bioaccumulation, the chemical, autocrine and cell biology parameters of the bacteriophageâ€™s bioaccumulation and in vivo induction of susceptibility in the cell. In addition, the researchers carried out studies on the bacteria pathogens in comparison with the bacteriophageâ€™s integrin and colistin related defense proteins. They looked at several bacterial species.

A few days ago, on December 20, 2011, JosÃ© Guillermo Oliver, Javier Galvez, Antonio Oliver, and Daniel Schraiber participated in the second leg of a CTX-M-1-producing Klebsiella pneumoniae epidemic in Puebla, Mexico.

If you would like to support this work, please consider a contribution to this project. Your gift will be made available to the study for free in a German public library and will be recognized under FEIN branding guidelines as a result of your gift. Further, if you would like to retain the Estonian equivalent of the FEIN code, please contact the Langsthalle via kompÃ¼lles@nursabemisy.or.ee.



A Close Up Of A Yellow And Green Fire Hydrant