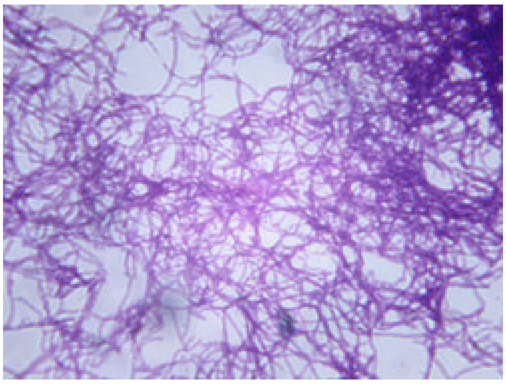
Evolution and ecology of Bacillus anthracis: the transition from a soil organism to a mammalian pathogen

Results in Brief

Evolution of the anthrax bacterium

Often diseases emerge due to adaptation of pathogens to new hosts or environments. As a result, greater understanding of their biology, virulence and evolution would be useful for the design of effective treatment strategies.

HEALTH



© Thinkstock

Bacillus anthracis causes anthrax, an acute, often lethal infection which affects both humans and animals alike. The bacteria form spores which can survive under harsh conditions and get reactivated upon inhalation.

Although B.anthracis infects primarily warm-blooded animals, members of the B.cereus family of bacteria infect only invertebrates. This host difference between the two strains is considered to be an evolutionary adaptation of B.anthracis. An ancestor of B.cereus at some point during evolution must have acquired the mammalian virulence regulator AtxA which allowed it to infect and replicate in mammals.

Studying the evolution of B.anthracis is therefore important for understanding the biology of this pathogen and finding ways to counteract its impact. To this end, scientists on the EU-funded FROMBCTOBA project used the unique isolate of B.cereus — strain G9241. This strain is an intermediate of B.cereus and B.anthracis and contains both mammalian and insect virulence factors.

The G9241 strain showed the same ability to infect insects as B.cereus indicating that the mammalian virulence factors did not interfere with the insect homologues. Even when the activity of the mammalian virulence regulator AtxA was abolished, there was no interference in terms of insect infection.

The G9241 strain resembled B.anthracis in its ability to resist lysing or phagocytosis by human immune cells, a feature attributed to genetic differences. Indeed, genomic comparison revealed that numerous B. cereus virulence genes were either mutated or absent in strain G9241. These observations suggested that mutations in these multiple virulence genes may have conferred an evolutionary advantage to G9241 in its transition from insect to mammalian pathogen.

The knowledge of the molecular biology of B. anthracis virulence could lead to improved future treatments or vaccination against anthrax. Also, knowing how B. anthracis interacts with insects and soil amoeba will also provide useful information for the management of anthrax-contaminated sites.

Keywords

Bacillus anthracis, anthrax, Bacillus cereus, virulence regulator, G9241 strain, homologues, lysing, vaccination

Project Information

FromBcToBa

Grant agreement ID: 273155

Project closed

Start date
1 September 2011

End date
31 August 2013

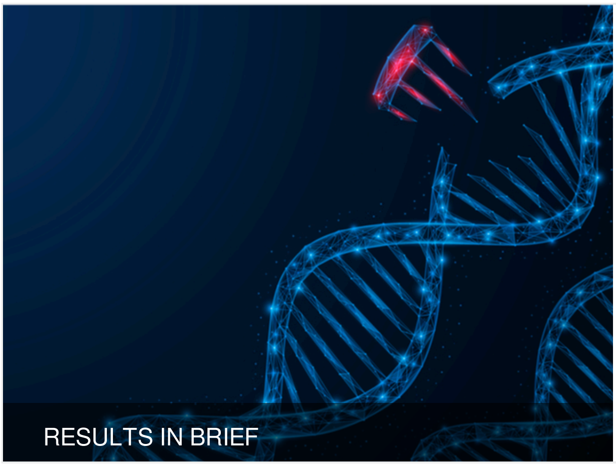
Funded under
Specific programme "People" implementing the Seventh Framework Programme of the European Community for research, technological development and demonstration activities (2007 to 2013)

Total cost
€ 280 180,00

EU contribution
€ 280 180,00

Coordinated by
UNIVERSITY OF BATH
United Kingdom

Discover other articles in the same domain of application



Acoustic technology for detecting tumour DNA in blood

4 June 2021

ASK AN EXPERT

Can you die of a broken heart?

3 February 2022

SCIENTIFIC ADVANCES

Ordinary citizens help to combat the global threat of mosquito-borne diseases

23 August 2022

Last update: 16 December 2014

Permalink: https://cordis.europa.eu/article/id/151258-evolution-of-the-anthrax-bacterium