

## **Anthrax targets**

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A trawl of the genome of the deadly bacterium *Bacillus anthracis* has revealed a clutch of targets for new drugs to combat an epidemic of anthrax or a biological weapons attack. The targets are all proteins that are found in the bacteria but not in humans and are involved in diverse bacterial processes such as metabolism, cell wall synthesis and bacterial persistence. The discovery of a range of targets might bode well for creating a drug cocktail that could preclude the emergence of drug resistance.

Ravi Gutlapalli of the Department of Biotechnology, at Acharya Nagarjuna University in Guntur, Andhra Pradesh, India, and colleagues there and at Osmanaia University College for Women in Hyderabad, suggest that the search for drugs to fight <u>Bacillus anthracis</u> is of increasing importance as we face an ongoing threat of its use as a biological weapon. The team has now carried out a search of the <u>bacterial genome</u> and identified 270 non-redundant, non-human homologous genes and 103 essential genes of the bacteria as possible <u>drug targets</u>.

The team explains that they have fished out sixteen membrane-bound proteins, seven proteases and three <u>adhesion molecules</u> that are all novel from their trawl any one of which might now be used in the rational design of new drugs with previously unused modes of action. This latter point is most important in reducing the chances of the bacteria quickly evolving resistance.

Early diagnosis and treatment with potent antibiotics is essential in any



of the three clinical forms of anthrax: cutaneous, gastrointestinal and pulmonary. Unfortunately, the bacteria have evolved resistance to common antibiotics including ciprofloxacin, doxycycline and betalactam type drugs. The team now hopes that its identification of a range of novel targets for antibiotics will allow medicinal chemists to quickly screen for activity among diverse molecules as putative antibiotics.

With several possible targets in hand, researchers now need to create homology models of each against which potential drugs might be screened on the computer and thence synthesize in the laboratory and tested against the bacteria under secure conditions.

**More information:** "Genome wide search for identification of potential drug targets in Bacillus anthracis" in *Int. J. Computational Biology and Drug Design*, 2012, 5, 164-179

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