Infection biology: The elusive third factor

June 22 2012

Researchers from Ludwig-Maximilians-Universität (LMU) in Munich have identified an enzyme that is involved in a modification pathway that is essential for bacterial pathogenicity. Because it shows no similarity to other known proteins, it may be an ideal target for development of novel antimicrobial drugs.

Studies on a number of pathogenic bacteria have shown that these strains become pathogenic only when an enzyme called elongation factor P (EF-P) is chemically modified on a conserved lysine residue. EF-P is a universally conserved translation factor, which is involved in protein synthesis. Two enzymes are known to be involved in modifying the conserved lysine of EF-P, however these enzymes cannot fully account for the pattern of modification seen on EF-P in living cells.

The mystery molecule

Thus, at least one other protein must be involved in the modification process – however to date it has proved to be particularly elusive. Now a research team led by LMU biochemist Daniel Wilson, who is also affiliated with the Center for Integrated Protein Science Munich (CIPSM), a Cluster of Excellence at LMU, has succeeded in identifying the mystery protein as the enzyme YfcM and showing that it displays hydroxylase activity. Strikingly, YfcM shows no sequence similarity to any other known protein and therefore may have a unique structure.

This is not the only reason why discovery of YfcM will arouse great interest. "YfcM may turn out to be an ideal target for the development of

new - and urgently needed – antibiotics, however more insight will be needed to ascertain the role of the YfcM mediated hydroxylation of EF-P," says Wilson.

Provided by Ludwig Maximilian University of Munich