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Molecular characterization of the activity and requirements of a novel and promiscuous bacteriophage integrase

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Stx bacteriophages are responsible for the dissemination to and production of Shiga toxin genes (stx) in the Enterohaemorrhagic *E. coli* (EHEC). These toxigenic bacteriophage hosts can cause severe, life-threatening illness and Shiga toxin (Stx) is responsible for the severe nature of EHEC infection. At the point of infection, the injected phage DNA can direct its integration into the bacterial chromosome becoming a prophage; the host cell is then known as a lysogen. Unusually, our model Stx phage, Φ24B, can integrate into at least four distinct sites within the *E. coli* genome that shared no easily identifiable recognition sequence pattern. The identification of what are actually required for phage and bacterial DNAs recombination has been tested using both an in vitro and in situ recombination assays. These assays enable easy manipulation of bacterial attachment site (attB) and phage attachment site (attP) sequences. The aim of our study is to fully characterize the requirements of this promiscuous integrase, carried by the Stx phage Φ24B (IntΦ24B), to drive integration. So far, a number of successful assays have enabled us to identify the minimal necessary flanking sequences for all of four attB sites (50 bp each side) and attP site (150 bp each side). The later one is very similar in size to the lambda attP (117 bp each side of the crossover site). Moreover, within these four attB sites, we have identified the primary site.

Biography

Mohammed R Mohaisen has completed his BSc degree in General Biological Sciences and MSc degree in Medical Microbiology, Anbar University, Iraq. He is currently a PhD student at the Institute of Integrative Biology, University of Liverpool, United Kingdom.

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