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Introduction to the multi-author review on conjugative transposons

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Until the late 1970s it was thought that almost all gene transfer events in bacteria were mediated by plasmids. Then Don Clewell and co-workers identified an *Enterococcus faecalis* strain which could transfer tetracycline resistance in the absence of plasmid DNA [1]. Further analysis of this strain revealed that transfer was mediated by an 18-kb genetic element, Tn*916,* which was integrated into the chromosome of both donor and recipient. As well as transfer to other bacteria, this element was also capable of intracellular transposition, so the term 'conjugative' transposon was coined [2]. In subsequent years it has become apparent that conjugative transposons are ubiquitous in bacteria and form a very heterogeneous group of genetic elements. This heterogeneity has led to some controversy and confusion about naming these elements and deciding exactly what a conjugative transposon is. Therefore, as suggested by Whittle et al. (this review), it is best to define conjugative transposons in the broadest possible terms. Thus, they are discrete DNA elements, usually integrated into the bacterial genome, which can transfer from a donor to a recipient by conjugation.

The fact that conjugative transposons have such a broad host range makes them exceedingly important in bacterial evolution, i.e. in disseminating genes between distantly related organisms [3, 4]. Furthermore, these elements can sometimes mediate deletion events, rearrangements and can provide a substrate for homologous recombination. They are also very important from a clinical point of view, as they have been shown to transfer antibiotic resistance to pathogenic organisms [4, 5]. The broad host range of these elements has also been exploited extensively by researchers investigating the molecular genetics of bacteria; as these elements have been used as mutagens and as cloning vectors, some examples can be found in references [6–9].

The aim of this multi-author review is to provide an overview of our current understanding of conjugative transposons and to provide an appreciation of the diversity of these genetic elements.

The initial step in the transposition process of all conjugative transposons investigated to date is excision from the donor genome to produce a circular intermediate, which can then transfer by conjugation to a recipient where it inserts into the genome. The first review (Mullany et al.) gives an overview of the insertion and excision mechanisms that are used by different conjugative transposons.

The review by Rice shows how different conjugative transposons, and other genetic elements, can associate to form new mobile elements in Gram-positive bacteria, which have different properties from the parental elements. The review by Adams et al. explores a group of genetic elements which are not in themselves conjugative but which encode mobilisation functions and can be mobilised by conjugative elements. These elements have been termed the mobiliseable transposons. The Adams review investigates the properties of the clostridial mobiliseable transposons. Whittle et al. also review elements termed mobiliseable transposons, which have been discovered in the *Bacteroides* group. The mobiliseable transposons from the *Bacteroides* seem to use different genetic mechanisms for their movement than do those from the *Clostridia*. Whittle et al. also review the properties of the *Bacteroides* conjugative transposons and how they interact with other genetic elements to promote the spread of antibiotic resistance in this group of organisms.

Perhaps surprisingly, conjugative transposons have only recently been identified in the well-studied *Enterobacteriaceae*. However, the reviews by Pembroke et al. and Beaber et al. illustrate that these elements are very important in the *Enterobacteriaceae*. Interestingly, the conjugative transposons from the *Enterobacteriaceae* are the first to have been discovered which seem to demonstrate incompatibility.

Most of our understanding of conjugative transposons comes from their study in human pathogens. However, since these organisms represent the minority of bacteria, the review by Scott is timely in examining what is known about conjugative transposons in commensal bacteria and in bacteria that inhabit the gastrointestinal tract of farm animals.

In the last 20 years our understanding of how genes are transferred among organisms has increased dramatically, and the central role of conjugative transposons in this process is beginning to be appreciated. If we are to prevent the rapid spread of antibiotic resistance, we need to understand the mechanisms of conjugative transposition and how these genetic elements interact with others to promote gene transfer. This multi-author review presents the state of the art in some aspects of conjugative transposition.

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