



Classic Spotlight: the Awesome Power of Conjugation

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oday, antibiotic resistance is widely recognized as one of the great global threats confronting modern medicine. Following the discovery of sexuality in Escherichia coli by Lederberg and Tatum, reported in Nature and the Journal of Bacteriology (JB) in 1946 and 1947 (1, 2), studies began documenting the transmission of antibiotic resistance among the Enterobacteriaceae by a cell contact-dependent mechanism termed conjugation. Of particular concern were discoveries of large resistance transfer factors (RTFs), or R plasmids, encoding multiple-antibiotic resistance that were rapidly and efficiently transmitted among different species of Enterobacteriaceae. Many of these reports were published in JB throughout the 1960s. During this period, the emergence of antibiotic resistance among Gram-positive cocci, especially in clinical settings, was of increasing concern, but initial efforts failed to identify transmissible R plasmids. It was not until 1974, in their seminal paper published in JB, that Alan Jacob and Susan Hobbs presented the first definitive evidence for conjugative transfer of plasmid-borne antibiotic resistance by a Gram-positive species (3). They discovered that a "plasmid of 50 \times 10⁶ molecular weight" encoded resistance to multiple antibiotics and was highly transmissible by a conjugative mechanism between strains of Streptococcus faecalis (now Enterococcus faecalis). Jacob and Hobbs concluded, "The discovery of transferable plasmid-borne antibiotic resistance in S. faecalis may afford an explanation for the great increase in antibiotic resistance of group D streptococci." Indeed, in large part because of conjugative DNA transfer, today most clinical isolates of enterococci, streptococci, and staphylococci are susceptible to only a small and waning list of antimicrobials.

Not all antibiotic resistance genes are carried on conjugative R plasmids. However, studies in the 1970s and 1980s documented the contributions of chromosomal elements termed transposons to the epidemic spread of antibiotic resistance among bacterial populations. In the early days, this was attributed to the ability of transposons bearing antibiotic resistance genes to "hop" onto conjugative plasmids for dissemination to susceptible strains. But another seminal discovery reported in JB, by Arthur Franke and Don Clewell in 1981, introduced a new paradigm of genome plasticity vis-à-vis elements they termed conjugative transposons (cTns) (4). Now more broadly classified as integrative and conjugative elements (ICEs), these elements bear the signatures of

transposons but also carry cassettes of genes encoding type IV secretion systems (T4SSs) that mediate conjugative transfer. Franke and Clewell discovered the first conjugative transposon, designated Tn916, in Streptococcus faecalis (E. faecalis). They showed that chromosomally borne Tn916 codes for resistance to tetracycline and moves intercellularly not only by hopping onto conjugative plasmids but also, strikingly, independently of any plasmids. They rigorously excluded alternative mechanisms of Tn916 transfer such as transduction and transformation, cautiously concluding that Tn916 might "encode its own transfer functions." It is now recognized that ICEs can comprise a significant proportion of the variable DNA found in bacterial chromosomes and also that these elements can serve as vectors for transmission of linked chromosomal DNA. Franke and Clewell's discovery of an antibiotic resistance element with the dual attributes of a transposon and conjugation system fostered our present-day appreciation of the widespread importance of ICEs in genome evolution and antibiotic resistance gene transfer in an era of indiscriminate antibiotic use.

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