A bacterial conjugation machinery recruited for pathogenesis

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Type IV secretion systems (T4SS) are multicomponent transporters of Gram-negative bacteria adapted to functions as diverse as DNA transfer in bacterial conjugation or the delivery of effector proteins into eukaryotic target cells in pathogenesis. The generally modest sequence conservation between T4SS may reflect their evolutionary distance and/or functional divergence. Here, we show that the establishment of intraerythrocytic parasitism by Bartonella tribocorum requires a putative T4SS, which shares an unprecedented level of sequence identity with the Trw conjugation machinery of the broad-host-range antibiotic resistance plasmid R388 (up to 80% amino acid identity for individual T4SS components). The highly conserved T4SS loci are collinear except for the presence of numerous tandem gene duplications in B. tribocorum, which mostly encode variant forms of presumed surface-exposed pilus subunits. Conservation is not only structural, but also functional: R388 mutated in either trwD or trwH encoding essential T4SS components could be trans-complemented for conjugation by the homologues of the B. tribocorum system. Conservation also includes the transcription regulatory circuit: both T4SS loci encode a highly homologous and interchangeable KorA/KorB repressor system that negatively regulates the expression of all T4SS components. This striking example of adaptive evolution reveals the capacity of T4SS to assume dedicated functions in either DNA transfer or pathogenesis over rather short evolutionary distance and implies a novel role for the conjugation systems of widespread broad-host-range plasmids in the evolution of bacterial pathogens.
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