Site-specific Recombination and Transposition Mediated by the Novel Piv/MooV DNA Recombinases

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The Piv/MooV family of DNA recombinases includes DNA transposases and site-specific invertases from a rapidly increasing number of prokaryotic systems. We have previously demonstrated that the completely conserved amino acid motifs from the Piv/MooV recombinases are required for catalytic activity of the site-specific DNA invertase, Piv. Piv controls phase variation of type IV pili in *Moraxella lacunata*, mediating inversion of a 2.1 kb chromosomal segment that encodes the pilin subunit. Although Piv apparently utilizes a conservative recombination mechanism for DNA inversion, molecular modeling of Piv revealed a RNaseH-fold in the amino-terminal third of the protein with conserved acidic residues positioned to coordinate at least one divalent metal cation. This structural motif is found in nucleases, Holliday junction resolvases (RuvC family), and the DDE-motif retroviral integrases/transposases. We have pursued the roles of each of the conserved acidic residues D9, E59, D101 and D104, which the predicted Piv tertiary structure places in the catalytic pocket. In addition, the function of a predicted RuvA-like helix-hairpin-helix motif in the central region of Piv is currently under investigation. A model based on these structure/function studies and characterization of recombination intermediates and products will be presented.