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**“Studies of *Bacillus subtilis* competence-induced protein A
(CoiA), a proposed transformation-specific resolvase”**

by

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11:00 AM

International Center for Public Health, Auditorium C109

Join Zoom Presentation:

<https://rutgers.zoom.us/my/irc18?pwd=UGJrQjF6Z3o1b1FFR244bWRFZkJKdz09&omn=94960231304>

Meeting ID: 640 451 9436

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ABSTRACT

Natural transformation is the ability of some bacterial species to internalize environmental DNA and utilize it to alter their genetic code. The state allowing intake and recombination of environmental DNA is called competence. Homologous recombination (HR) is an event in which two DNA molecules exchange strands with identical or nearly identical sequences. In the context of competence for transformation, the exchange occurs between the incoming transformation DNA (tDNA) strand for a homologous strand within the recipient's genome. HR results in the formation of triple-stranded heteroduplex DNA structures called displacement loops (D-loops) consisting of a displaced strand of genomic DNA (gDNA) that are formed during HR and must be cleaved to complete the recombination process. The protein responsible for this cleavage, a D-loop resolvase, remains unknown. Previous work implicated Competence inducible protein A (CoiA), encoded by a late competence gene of unknown function, that is widely distributed in Firmicutes as a likely candidate for the missing D-loop resolvase. To study the function of CoiA in *B. subtilis*, a series of bioinformatic and genetic studies were undertaken to identify CoiA active-site residues. Utilizing protein structure prediction and alignment as well as protein sequence alignment approaches, we identified a PD-(D/E)XK endonuclease motif in CoiA. The functional importance of this CoiA PD-(D/E)XK motif was confirmed through site-directed mutagenesis of conserved residues. Uncovering the functional role of *B. subtilis* CoiA identifies a dedicated transformation D-loop resolvase and furthers our understanding of the biochemistry of homologous recombination in bacteria.