

KE1 Repetitive Element = CIR2 Sequence of Chen & Shapiro: Further Analysis of the Methylation Site Hypothesis & the Evolution of Nontraditional Repetitive Elements in *Agrobacterium*

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Abstract:

As an independent project associated with a bioinformatics course, Ryosuke Kadoi (Hiram '04 grad) searched for conserved intragenic sequences within the *A. tumefaciens* C58 genome and found several nontraditional repetitive elements (2). In helping Ryosuke draft a manuscript on one of these elements, called KE1, I ran across a recent paper by Chen and Shapiro in which they describe long, conserved repetitive elements in the genomes of *Caulobacter crescentus* and other α -Proteobacteria that are associated with a methylation site for CcrM methylase. One of these elements in *A. tumefaciens*, called CIR2, turned out to be the same as KE1 (3). However, upon further inspection, CIR2/KE1 did not seem to fit the methylation site hypothesis very well. In this poster, I will present further analysis on the distribution of KE1 and other nontraditional repetitive elements, their relationship to the methylation site hypothesis, and their evolutionary history compared to that of the *Agrobacterium* genus and its sister taxa.

References:

1. K84/S4 Genome Consortium: Frank Arnold, Tom Burr, Sigrid Carle, Zijin Du, Adam Ewing, Stephen Farrand, Brad Goodner, Barry Goldman, Guixia Hao, Sara Heisel, Jinal Jhaveri, Subha Krishnan, Jing Lu, Nancy Miller, Eugene Nester, Gary Olsen, Dan Ondrusek, Nicole Pride, Joao Setubal, Steve Slater, Mark Vaudin, Lindsey Wilson, & Derek Wood.
2. Ewing et al., 2004, 25th Crown Gall Conference.
3. Chen & Shapiro, 2003, J. Bact. 185:4997-5002.