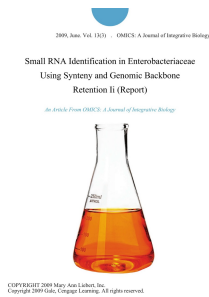


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SMALL RNA IDENTIFICATION IN ENTEROBACTERIACEAE USING SYNTENY AND GENOMIC BACKBONE RETENTION II REPORT EBOOKS 2019



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Introduction Noncoding RNAs (ncRNAs) are identified in all life forms (Eddy, 2002), and recently they have been identified to play a significant role in the survival of the organisms (Masse et al., 2003; Toledo-Arana et al., 2007). Small RNAs (sRNAs) are bacterial counterparts of ncRNAs ranging from ~50 to ~400 nucleotides (nt) in size (Argaman et al., 2001; Hershberg et al., 2003). The sRNAs are identified in diverse prokaryotes like Archaea (Dennis and omer, 2005; Klein et al., 2002), Actinobacteria (Panek et al., 2008), Cyanobacteria (Axman et al., 2005), Gammaproteobacteria (Sridhar and Rafi, 2007a) and in Firmicutes (Silvaggi et al., 2006). However, majority (~70%) of the sRNAs identified are from Enterobacteriaceae (gammaproteobacteria) genomes. These sRNAs are experimentally identified mostly in model organisms such as Escherichia coli K12-MG1655 (Blattner et al., 1997), Vibrio cholerae o1 El-Tor (Heidelberg et al., 2000) and Pseudomonas aeruginosa PAo1 (Stover et al., 2000). A variety of comparative approaches are being employed to identify the corresponding sRNA candidates in other related genomes.

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