## Lsm-bound antisense RNAs play role in *Halobacterium salinarum* NRC-1 transposition regulation

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Insertion sequences (IS) are widely spread in bacteria and archaea and are well known for their impact in host genomes. IS transposition events may inflict gene disruptions, massive deletions and even the creation of new features by rearranging stretches of DNA. Therefore, transposition are usually kept at low rates by several mechanisms, such as the translational repression of transposase-encoding mRNAs. Hfq binding proteins associated to antisense RNAs (asRNAs) were reported to inhibit the translation of transposase-encoding transcripts from IS200 family in Salmonella. The repression occurs by Hfq-bound asRNA base pairing on the 5' UTR and transposase (tnpA) first codons, preventing the 30S ribosomal subunit from attaching to Shine-Dalgarno sequence. Lsm, the Hfq homologue in archaea, is an important agent in posttranscriptional regulation of protein-coding mRNAs in Halobacterium salinarum NRC-1. Nevertheless, interaction between Lsm-bound asRNAs and transposase-encoding transcripts is still unexplored in this haloarchaeon. Starting from RNA immunoprecipitation sequencing (RIP-seq) data, we aligned reads to reference genome and generated read counts per position for pulled-down Lsm and control libraries. We also computed fold change per position based on read counts, in order to avoid overestimation of interaction regions. This allowed us to identify Lsm-bound RNAs interacting within IS transcripts in *H. salinarum* NRC-1 grown at reference condition. We found antisense interaction regions at the 5' end of IS200/IS605 family transcripts, frequently spanning the beginning of transposase-encoding sequences, suggesting a regulation mechanism similar to that described in bacteria. These preliminary results encourage a genome-wide analysis to evaluate whether Lsm-bound asRNAs are bona-fide IS transposition regulators in archaea, by the means of comparing the expression levels of transposase genes in Lsm knockout mutants and different growth conditions.

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