P034 Reverse splicing of a mobile twin-ribozyme group I intron into the natural SSU rRNA insertion site

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Reversal of the group I intron self-splicing reaction, termed reverse splicing, coupled with RT and genomic integration potentially mediate an RNA-based intron mobility pathway. Compared to intron homing, reverse splicing is less specific and represents a likely explanation for many intron transposition events. However, the frequency and general role of an RNA-based mobility pathway in the spread of natural group I introns is still unclear. We have used the twin-ribozyme intron (Dir.S956-1) from the myxomycete *Didymium* to test how a group I intron selects between potential insertion sites in the SSU rRNA *in vitro*, in *E. coli* and in yeast. Dir.S956-1 is the most complex group I intron known to date. It is mobile in sexual crosses, harbours a functional homing endonuclease gene (the I-*Dir*I HEG), and encodes two distinct ribozymes (DiGIR1 and DiGIR2). Whereas DiGIR1 represents an unusual ribozyme class directly involved in I-*Dir*I mRNA processing, DiGIR2 is a canonical group I ribozyme responsible for intron splicing and intron circularisation. Surprisingly, the results from reverse splicing experiments show a highly site-specific RNA-based targeting of Dir.S956-1 into its natural SSU rRNA site. Intron transposition into novel SSU rRNA sites was not detected in *E. coli* or yeast. We suggest that reverse splicing, in concert with the endonuclease-mediated homing mechanism, accounts for group I intron spread into the homologous sites of different strains and species.