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## Analysis of RNA interference (RNAi) intermediates during Tf1 integration in the fission yeast *Schizosaccharomycespombe*

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Integration of retroviral elements into the host genome is a phenomena observed among many classes of retroviruses. Much information concerning integration of retroviral elements has been documented based on *in vitro* analysis or expression of selectable markers. To identify possible integration events of the LTR retrotransposon, Tf1, within silent regions of the S. pombegenome, we focused on performing an *in vivo* genome-wide analysis of Tf1 integration events from the nonselective phase of the retrotransposition assay. After analyzing 1000 individual colonies streaked from four independent Tf1 transposed patches under nonselection conditions we detected a population of G418S/neo+ Tf1 integration events that would have been overlooked during the selective phase of the assay. Interestingly, further RNA analysis from the G418S/neo+ cells revealed 50% of clones expressing the neo selectable marker. S. pombecells have in place mechanisms such as DNA methylation, histone modification, and RNA interference (RNAi), to control retroviral activity. There are increasing reports suggesting that RNAi may play a role in silencing virally infected eukaryotic cells. RNAi was also shown to be involved in the inhibition of viruses and silencing of viruses in plants, insects, fungi, and nematodes. We utilized denaturing Polyacrylamide gel electrophoresis (PAGE) and Northern Blot hybridization using a DIG-labeled neo probe to detect the presence of microRNAs in G418S/neo+ clones.

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