Retrovirology



Invited speaker presentation

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Host support of Ty3 retrotransposition in *Saccharomyces cerevisiae* Suzanne Sandmeyer*, Virginia Bilanchone, Nadia Beliakova-Bethell, Kristina Christiansen and Kim Nguyen

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Ty3 is a Saccharomyces cereviae LTR retrotransposon. The structure of Ty3 is similar to that of a simple retrovirus. It is 5.4 kb in length and encodes overlapping GAG3 and POL3 reading frames flanked by 340 bp long terminal repeats. Expression of Ty3 results in production of Gag3 and Gag3-Pol3 polyproteins which assemble together with genomic RNA into in association with P-body proteins. VLPs are also associated with these clusters. The nucleo-capsid domain of Ty3 Gag3 is required in trans for recruitment of Ty3 RNA into P bodies. The untranslated regions of Ty3 RNA are sufficient in cis for recruitment of RNA to P bodies, but the GAG3-POL3 coding domain of the RNA can also confer association with P body proteins. In contrast, only the untranslated sequences confer packaging of a mini-Ty3 transcript. Upon assembly, Gag3 is processed into capsid, spacer, and nucleocapsid. Gag3-Pol3 is processed into those proteins and protease, junction, reverse transcriptase, and integrase. We propose that P-body proteins promote Ty3 VLP assembly and a mass spectrometry approach is being taken to further define the components of these dynamic complexes. However, in spite of genetic evidence that P-body proteins play a positive role in Ty3 production, these intracellular foci may also act as host traps to down-regulate transposition. Ty3-P body clusters become perinuclear over time and are physically associated with nuclear pores. A specific class of FG nucleoporins are required for Ty3 nuclear entry.