“Novel functions for small nucleolar RNAs”

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Small nucleolar RNAs (snoRNAs) function as guides to target the post-transcriptional modification of specific sites in ribosomal RNAs and other nuclear RNAs.
In recentyears, RNA deep sequencing datasets have revealed a wealth of small fragments derived from snoRNAs (termed sdRNA for snoRNA-derived small RNAs) that stably accumulate in the cell. A small number of studies suggest that some sdRNAs may play a role in the regulation of either splicing or translation. In parallel to this, using computational and experimental approaches, we and others have identified human miRNA precursors displaying extensive similarity to snoRNAs, on the level of genome context, characteristic sequence features, predicted secondary structure and binding partners, suggesting an evolutionary relationship between a subset of snoRNAs and miRNAs. We recently examined human sdRNA accumulation patterns, to investigate the extent of conservation and variability in the processing of snoRNAs. sdRNA profiles of many snoRNAs are specific, conserved across various cell types and resemble the cleavage profiles of miRNAs. Many do not show characteristics of general RNA degradation, as seen for the accumulation of small fragments derived from some snRNA or rRNA. One box C/D snoRNA, HBII-180C, was analyzed in greater detail, revealing the presence of sdRNAs that are complementary to several pre-messenger RNAs including FGFR3. Functional analyses demonstrated that this region of HBII-180C can influence the alternative splicing of FGFR3 pre-mRNA, supporting a role for some snoRNAs in the regulation of splicing.