SnoRNAs homology search

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Motivation

- one of most abundant group of ncRNA in eucaryotic cells
- surprisingly diverse regulating functions
CD-box guide 2'-O-methylation(s)
HACA-box guide pseudouridylation(s)
SnoRNPs - Proteins

- HACA-snoRNP -> direct binding of enzym catalytic component
  - Cbf5|diskerin -> pseudouridyl-synthase
- kink-turn formed by L7Ae|NHP2
- binding of target
  - Gar1 -> binding/release of target RNA
- coordinative function
  - Nop10 -> associated with other proteins
**snoRNPs - Proteins**

- CD-snoRNP -> protein bridge to secure enzyme
- Catalytic component
  - Fibrillarin
    - 2'-O-methyltransferase
- Nop56/58 binds enzyme
- Kink-turn formed by L7Ae|NHPX
- mostly intron encoded in vertebrata
- mostly independent with promotors in yeast
snoRNAs - different genomic organisation

- snoRNAs often clustered in host genes
- hotspot in vertebrata: gas-5 like host gene
snoRNAs located in nucleolus
most function in rRNA processing
  - known methylated nucleotides and pseudouridines located in key regions of rRNA
  - are essential for fine-tuning of ribosome-function
endonucleotie cleavage of pre-rRNA
box-motifs responsible for targeting snoRNA to nucleolus
**snoRNAs & splicing**

- scaRNAs
- share structure, box-motifs and guiding-function with 'normal' snoRNAs
- hybrids with HACA and CD domain or 'twins'
- RNPs have same core proteins
- targets on snRNAs
- located at Cajal bodies
- HACA domains share CAB-box-motif in apical loop
BRAIN SPECIFIC snoRNAs

- tissue-specific expression
- mostly CD-box snoRNAs
- target mRNA of serotonin receptor
- subject to genomic imprinting
  - maternal or paternal expressed
  - exception HBI-36 but this is encoded in serotonin receptor coding region on X-chromosome
- organized in tandem repeats
- conserved 5’-GGACC...GGTCC-3’ terminal stem
snoRNAs & RNA silencing pathway

- sdRNAs
- microRNA precursors
- high abundand sdRNAs are derived from weakly expressed snoRNAs
- ’orphan’ snoRNAs
SNO RNAs & …

- tRNA modification in archae
- telomerase RNA
- ribonuclease MRP RNA
SnoRNPs - Maturation & Trafficking

- Maturation takes place at Cajal Bodies
- Exact steps and involved proteins are not exactly known yet
- Known assembly factors
  - Naf1 <-> Gar1 (HACA)
  - Bcd1 <-> Nop56 (CD)
  - IBP160 in most cases about 40nts upstream of snoRNA
- Forwarding of mature snoRNPs to modification sites needed
  - Probably these diverse regulating RNAs are regulated themselves through various mechanisms at several levels
present in archae and eucaryotes -> emerged 2-3 billion years ago
high vertical, very low horizontal conservation
extensive variations in nucleotide but conserved box-motifs, antisense-elements and structure
but also high similarity in nucleotides but different or no guiding function
HOMOLOGY - APPROACHES

1. sequence & structure homology
   - conservation of sequence and structure
   - recognisable by BLAST, INFERNAL, GotohScan, ...

2. functional homology
   - same guiding function
   - target prediction with RNAsnoop for H/ACAs
     and RNAduplex for CDs

3. snoRNA clusters in orthologue hostgenes to find homologue snoRNAs
1. recombination of guiding function
   - two modifications guided by different snoRNAs in one organism have a single guide snoRNA in another organism
2. separation of guiding function

- two modifications guides by one snoRNA in one organism are guided by two different guide snoRNAs in another organism


A common sequence motif determines the cajal body-specific localization of box h/aca scarnas.  

Genome-wide analysis of chicken snornas provides unique implications for the evolution of vertebrate snornas.  

Small rnas derived from snornas.  
THANK YOU

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