

Survey & evolutionary analysis of snoRNAs in annelid introns.

Stefan Dietrich¹, Natasha Hill¹, Christoph Bleidorn² and Stefanie Hartmann¹

¹ *Institute for Biology & Biochemistry, University of Potsdam,*

² *Institute for Biology, University of Leipzig*
s.dietric@uni-potsdam.de

Non protein coding RNAs (npcRNA) are prevalent in intronic regions of eukaryotic organisms. Because npcRNAs are involved in many cellular processes a better understanding of the distribution and the function of npcRNA in these regions could help to determine their impact to regulation processes and to understand the evolution and the development of higher organism. One type of npcRNAs are small nucleolar RNAs (snoRNA), which are known to predominantly modify rRNA. SnoRNAs can be divided into (i) the C/D box snoRNAs, which guide the methylation of target RNAs and (ii) the H/ACA box snoRNAs, which guide pseudouridulation [Bac02].

We surveyed the presence and distribution of snoRNAs in intronic regions in the two annelid species *Capitella teleta* and *Helobdella robusta*. SnoRNAs in intronic regions were identified by using the software Infernal and snoRNA covariance models from the RNA database Rfam [Na09, Gri05]. The Infernal package allows to use snoRNA covariance models to search nucleic acid sequences for homologous snoRNA structures. We will discuss the type and distribution of snoRNAs identified in *Capitella teleta* and *Helobdella robusta* intron sequences.

To evaluate how evolutionary conserved the identified snoRNAs are, we then analysed the occurrence of snoRNAs in orthologous intronic regions in the two annelids. For this, gene families of orthologs were available for nine taxa, including *Capitella teleta* and *Helobdella robusta*; these were based on orthologs from the OMA database [Sch07]. Using CIWOG, which is based on detecting introns due to position and sequence similarities between closely related genes, we identified the positions of introns in the orthologous gene sequences (“orthologous introns”) [Wil09]. We will discuss our analysis of snoRNAs that are evolutionary conserved between the two annelids.

References

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