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**Long non-coding RNAs during embryogenesis of the sea urchin**

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Intriguing studies suggest that long non-coding RNAs (lncRNAs) tend to act in *cis* with neighboring protein-coding genes. Based on this notion, we assessed whether lncRNAs originate from adjacent genomic regions of selected protein-coding genes, such as early-*H2A* histone and *strim1*, that play important functions during development of the sea urchin *Paracentrotus lividus*.

Downregulation of *H2A* expression relies on the *sns5* chromatin insulator placed at the 3'-end of *H2A*. Northern blot hybridization show that a lncRNA (of ~600 nt), not overlapping with the *H2A* mRNA, is transcribed from *sns5*, following *H2A* expression.

The *strim1* locus encodes the first echinoderm TRIM-containing factor which functional role has been characterized. By RT-PCR and gene-transfer analysis we found that a lncRNA originates from the *strim1* gene promoter, and that its transcription positively correlates with that of *strim1*.

Our preliminary findings are consistent with the notion that lncRNAs might be important regulators for developmental processes.

Keywords: long non-coding RNA, protein-coding genes, embryogenesis, sea urchin