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Insights: Publications

lncRNA-Induced Spread of Polycomb Controlled by Genome Architecture, RNA Abundance, and CpG Island DNA

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Long noncoding RNAs (lncRNAs) cause Polycomb repressive complexes (PRCs) to spread over broad regions of the mammalian genome. We report that in mouse trophoblast stem cells, the Airn and Kcnq1ot1 lncRNAs induce PRC-dependent chromatin modifications over multi-megabase domains. Throughout the Airn-targeted domain, the extent of PRC-dependent modification correlated with intra-nuclear distance to the Airn locus, preexisting genome architecture, and the abundance of Airn itself. Specific CpG islands (CGIs) displayed characteristics indicating that they nucleate the spread of PRCs upon exposure to Airn. Chromatin environments surrounding Xist, Airn, and Kcnq1ot1 suggest common mechanisms of PRC engagement and spreading. Our data indicate that lncRNA potency can be tightly linked to lncRNA abundance and that within lncRNA-targeted domains, PRCs are recruited to CGIs via lncRNA-independent mechanisms. We propose that CGIs that autonomously recruit PRCs interact with lncRNAs and their associated proteins through three-dimensional space to nucleate the spread of PRCs in lncRNA-targeted domains.
