

EVOLUTION, IDENTIFICATION AND EXPRESSION OF NONCODING RNAS IN ANIMALS

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We are exploring the hypothesis that most of the genome of humans and other complex organisms is devoted to an RNA-based regulatory system, whose major function is to direct the complex patterns of gene expression that underpin multicellular differentiation and development. Here we report our largely unpublished results that show (i) that a significant proportion of the mammalian genome is not evolving neutrally, and that the amount of noncoding sequences showing functional constraint is at least an order of magnitude greater than those encoding proteins; (ii) the use of noncoding RNA microarrays containing thousands of sequences to interrogate the dynamic expression of noncoding RNAs during embryonal stem cell and myoblast differentiation, T-cell and macrophage activation, and early gonadal development, among others; (iii) the identification of very large numbers of previously unidentified miRNAs and sno-like RNAs in insect and mammalian genomes using new algorithms; and (iv) network-level conservation of matches between intronic sequences and others elsewhere in the genome in functionally congruent clusters.