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A Moving Landscape for Comparative Genomics in Mammals

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posed to sequences that accumulate as stable mRNA in the cytoplasm? Where precisely are the promoter regions of the genes? Is there read-through transcription, especially on loops that contain two or more TUs? Although splicing is clearly co-transcriptional, are the introns shed from the loops before the end of the TU? What holds the bases of the loops together? What is the relationship, if any, of LBC loops to the TADs defined by Hi-C experiments?

In this lecture I will outline recent studies on LBCs and discuss new experimental approaches that can be applied to answer some of these outstanding questions.

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Today we count some 62,000 species of vertebrates (half are fishes) including some 550 species of mammals on earth. The genome sequencing of non-laboratory species in recent years is expanding our breadth and understanding of genetic bases of adaptation and evolution in varied and amazing ways.

Recent completion and inspection of whole genome sequence and assembly for over 200 species of mammals, from platypus to panda to human, offer the prospect of a better view of the patterns of changes within genome organization across the mammalian radiations. In 2009 my colleagues and I have created Genome-10K, an international consortium of scientist who have set a goal of gathering, sequencing, assembling, and annotating to high quality some 10,000 vertebrate genomes with 2nd and 3rd generation sequencing technology within the coming five years. These activities and advances provide an enormous Bioinformatics challenge whose solution will provide future zoologists of every persuasion a genome sequence resource for their favorite study animal. The applications and potential for the genome sequence in several research questions will be discussed.

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