The complexity of mammalian transcription

Piero Carninci

RIKEN Omics Science Center, RIKEN Yokohama Institute

The next generation sequencing technologies are profoundly influencing our way to study biology. We have previously developed cap-analysis gene expression (CAGE) to simultaneously mRNA/noncoding RNA starting sites and simultaneously detect their expression and adapted CAGE to few nanogram of RNA (nanoCAGE technology). CAGE technology was coupled to deep sequencing (DeepCAGE) to achieve comprehensive coverage of transcription starting site, and more recently also miniaturized for use with small amount of material (nanoCAGE) and to assign newly discovered promoters/5' ends to the rest of the RNA sequence (CAGEscan).

We have adapted these technologies for the all the next-generation sequencing platforms available. DeepCAGE is being used on a broad range of biological phenomena application. We have correlated promoter activity to the transcriptional network of the differentiation of THP-1, a myeloid leukemia cell and have provided the first description of the dynamics and architecture of a transcriptional network ongoing transition from proliferating to differentiated state.

DeepCAGE allows also detecting dynamic expression of repeat elements, which show peculiar expression patterns and provide alternative promoters and functional genome elements. We have also used deepCAGE on subcellular fractions as a part of the ENCODE project. We have detected clear patterns of expression of retrotransposon elements (RE) in a panel of human and mouse tissues, which have a regulatory role. Now, we have clearly identified specific patterns of RE-derived RNA in different cell compartments, with a particular interesting role of Line bound to the chromatin. Altogether, these data are pointing at a potential function of the retrotransposon elements.