CAGE application for avian embryogenesis

R.M. Deviatiiarov

Institute of Fundamental Medicine and Biology, Kazan Federal University, Kazan, ruselusalbus@gmail.com

O.A. Gusev

Division of Genomic Technologies, Center for Life Science Technologies (CLST), RIKEN, Yokohama, Japan, oleg.gusev@riken.jp

Next generation sequencing (NGS) technologies drastically increase available genomic data. For example, Genomes OnLine Database lists more than 13.5K sequenced eukaryotic genomes (https://gold.jgi.doe.gov), or the 10K Genome Project which already sequenced about 280 vertebrate genomes. Furthermore, researchers develop new approaches for functional annotation of these genomes as microarrays, ChipSeq, RNAseq, which should provide information about tissues- or processes-specific genes and pathways. Similar to RNA-seq, CAGE is applicable for comparison of RNA expression in different samples, including tissues, primary cell cultures under normal conditions, or under an external stimulation, or within a time course. Among the transcriptomic methods, CAGE is a powerful technique that allows identification of transcription start sites (TSS) with 1 bp resolution, and it is therefore useful for gene regulation studies as it allows identification of specific transcription factor (TF) binding sites. CAGE was applied in model organisms like mouse, human, fruit fly, and zebrafish to improve its gene annotations. In our study, we performed a genome-wide promoterome annotation for chicken's embryos during embryogenesis. Totally for CAGE libraries preparation we used 26 samples from 1.5 h to 20 day of development. These samples were sequenced on HeliScope single molecule sequencer platform and mapped to Gallus_gallus-5.0 genome assembly. This approach provides comprehension of gene regulation features within amniotic vertebrates and therefore should be useful in avian and reptilian studies as well. For example, in our future analysis of the response to temperature changes during chicken development.

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1. A. Forrest, H. Kawaji, M. Rehli et al (2014) A promoter-level mammalian expression atlas, *Nature* **507**:462-470.

2. M. Lizio, J. Harshbarger, H. Shimoji et al (2015) Gateways to the FANTOM5 promoter level mammalian expression atlas, *Genome Biol* **16**:22.