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Functional genomics analysis for single cells and small quantities of cells

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Functional genomics analysis in single cells and low quantity of cells has tremendous applications, but the sensitivity and fidelity of current protocols remain a challenge. We previously established a procedure called whole DNA pool amplification (WPA) for highly sensitive and specific amplification of a complex DNA mixture [Pan, PNAS 2008]. Basing on WPA, PCR and deep sequencing, we developed a series of methods for transcriptome and epigenomics analysis. One method is whole mRNA transcriptome (WMA), with which we lysed single cells and process all steps toward amplicon dscDNA in a single tube. We analyzed a panel of single neurons, detected expected expression profiles, and revealed new differentially expressed transcripts. The second method is for globally analyzing the CpG methylation patterns (CpGMaps). With 100 or less melanoma cells, it detected the differentiated DMRs (differentially methylation regions) comparing to normal melanocytes. The third method is for profiling DNase I hyper-resistant sites (DHRS) in genome-wide, which identified the DNase I hyper-resistant sequences for as low as single cells with cell line K562, and revealed its relationship with DNA methylatyion and DNase I hyper-sensitive sites (DHS). The forth method is for single cell telomere length analysis. With this, we demonstrated the different heterogeneity in telomere length for the cell lines derived from different ages of donors and variants passages of a fibroblast cell line. Currently we are finalizing the protocols, and applying these technologies in stem cell differentiation, iPS reprogramming, carcinogenesis and the molecular mechanism underline neural function definition

Biography

Xinghua Pan obtained his Ph.D from Fudan University and postdoctoral studies from the Chinese Academy of Medical Sciences and Yale University School of Medicine. He is a research faculty at the Yale Department of Genetics, leading a team for single cell functional genomics studies on stem cells, cancers and neurons, supported by NIH grants and a Connecticut stem cell grant. He has published more than 60 academic papers and book chapters, with 6 biotech patents issued, and serving as an editorial board member and reviewer for multiple reputed journals, also with adjunct professorship and honors from several institutes

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