



Functional Genomics of Kidney Glomerulus

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Project description: As the genome projects are near completion, an important step in the functional analysis of the genome data is the determination of a transcriptome corresponding to the specific cellular function and states of differentiation. Such analyses require methods allowing for the isolation of highly homogenous populations of the cells and/or microorgans from *in vivo* situations. We have developed a new isolation technique of mice glomeruli retaining *in vivo* transcribed mRNA at 97% purity (Am J Pathol 2002;161:799-805). This new technique allowed us to make a series of oligo -dT-primed cDNA libraries. Then 10,000 cDNA clones were picked from the three adult libraries and 5,000 cDNA clones were picked from the standard new-born library and sequenced from 5' prime end in a single read of 500-800 bp length. Blast search against the EMBL/Sanger institute (ENSEMBL) database and the CELERA gene database resulted in 13253 high quality hits ($e\text{-value} < e^{-20}$), representing 6478 different genes, and left 93 putative novel genes without any matches either in the ENSEMBL or the CELERA gene databas. All annotation data are entered into a glomerulus transcript database (GLOMBASE) and are to be continuously updated. We have also generated a cDNA chip containing these clones (GLOMCHIP) and a large amount of preliminary data, which demonstrates that novel glomerulus-specific genes can rapidly be discovered with the use of these developed tools. Our global approach towards the glomerulus transcriptome will provide an improved platform for the discovery of fundamental biological functions, the pathology of the glomerulus, and potential drug targets for the future.

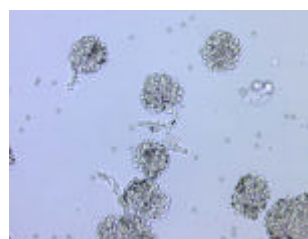


Fig.1 Isolated mouse glomeruli by Dynabeads perfusion technique

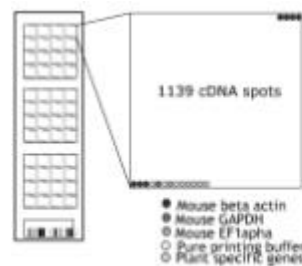


Fig.2 The pictures of GLOMCHIP

