

Abstract: Finding Molecular Mechanisms behind IgA Nephropathy Utilizing Microarray and qPCR Technology

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Background: IgA Nephropathy (IgAN) is the most common glomerulonephritis around the world. The disease may lead to renal failure and unfortunately, after decades of research, the molecular mechanisms behind IgAN are still unknown. The diagnosis of the disease is depending on observing morphological changes and findings of IgA depositions in the glomeruli. However, it has been found out that even when a new kidney has been transplanted, the disease can reappear after some time. Furthermore, it is also been known that according to different races and regions, the situation is not the same. This phenomenon gives a clue that IgAN is a disease associated with gene regulations. **Method:** In order to find out the certain gene regulations triggering IgAN, large scale genomic analysis technologies have been utilized such as microarray (Affymetrix GeneChip) and qPCR (Taqman). Biopsies from patients and health controls (living donors) have been collected from the Sahlgrenska University Hospital in Gothenburg area, Sweden and extracted RNA have been used for microarray experiments. The total numbers of patients and controls are 15 and 26 respectively. Taqman qPCR has also been chosen to evaluate the results obtained from microarray for some selected potential genes. Above all, statistical analysis for large scale genomic data is playing the most important role in finding out relevant gene regulations. **Results:** Depending on statistical microarray analysis, many extracellular matrix (ECM) genes are shown significant increased expression in the patients comparing to health controls as well as the corresponding pathway, ECM-receptor interaction pathway, which has come up as the top one up regulated pathway. More than that, some other genes such as MECOM, JUN, FOS that have been found to have significant up or down regulation may also have strong influence to IgAN. A gene list has been selected from the global microarray analysis to further evaluate using Taqman qPCR and the results are consistent. The result is solid and it indicates the interaction among those particular genes may lead us a solution for the disease. **Conclusion:** With the help of statistical analysis, the significantly regulated genes can ultimately narrow down the number of targets and reduce the labor devoted to the experiments. In this project, based on the significantly regulated genes in IgAN, associated pathways and gene ontology categories are also identified. It indicates that extracellular matrix genes as well as the relevant pathway may be important in triggering the disease.

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