Expression Analysis of Glycosyltransferase Genes in Human, Mouse, and Rat

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1 Introduction

Glycans are complex carbohydrate sugar chains found on the outside of the cell in most organisms and play key roles in embryogenesis, cell recognition, and disease. The structure of the glycan is known to have a large variety among organisms, tissues, and even the same type of cell. Some tissues express glycans that are not found on other tissues, while on the other hand, the same type of glycan may contain subtle differences, mostly at the non-reducing end of the glycan. The varieties of the glycan might be generated by the coordinated action of glycosyltransferases, which are the enzymes that synthesize glycans by attaching a nucleotide sugar one by one to a particular site on a glycan. The cloning of hundreds of glycosyltransferase genes and the advancement of microarray technology makes it possible to analyze the expression of glycan related genes on a large scale. In this study, we analyzed the transcriptome of the glycosyltransferases to extract the expression patterns of these enzymes across organisms. So far, we were able to confirm that in several organisms including human, mouse, and rat, the co-expression patterns of those glycosyltransferases that attach internal sugars were clearly evident compared to those that attach donor sugars to the non-reducing end of the glycan.

2 Methods and Results

The microarray data used was published by Andrew et al. for human and mouse [1], and for rat [2]. Three filters, absolute fold change of at least 2, maximum expression value at least 100, and t-test P-value of < 0.05 are used to remove genes whose expression values were considered to be of low reliability. After filtering, the glycosyltransferase genes were selected using the KEGG/PATHWAY database [3]. 52, 35, and 20 glycosyltransferase genes of human, mouse, and rat, respectively, were thus selected. Then, the Pearson correlation coefficient of each gene was calculated. For each glycosyltransferase, the number of genes whose Pearson correlation coefficient > 0.8 was counted. The glycosyltransferases were categorized according to their donor sugar. Finally, the number of co-expressed pairs of genes was averaged over each category.

Figure 1 illustrates the amount of co-expression in each category. The percentage of co-expression of each category was not well conserved across organisms, especially among the glycosyltransferases of higher co-expression. However, in all three organisms, there is a tendency for sialyltransferases, fucosyltransferases and sulfonyltransferases to co-expresses weakly in comparison to the other transferases.

3 Discussion

The microarray datasets used in this study contains samples from many tissues. It is known that there is a wide variety of glycans across various tissues, so we expect that the expression of the glycosyltransferases would change in this dataset. In this work, we categorize the glycosyltransferases in a simple way; that is, we ignored the acceptor site and the type of glycan that is attached. Despite this simplification, we were able to

find a general pattern in the co-expression of glycosyltransferase genes across human, mouse, and rat. In all three organisms, sialyltransferase, fucosyltransferase, and sulfonyltransferase co-expressed weakly compared to all the other transferases. These transferases attach monosaccharides to the non-reducing end of the glycan. That is, there is no further attachment of monosaccharides after these are attached. The non-reducing end of the glycan is where a large variety is observed among tissues and organisms. Our results correspond well with this fact, where the non-reducing end of the glycan structure has more variety, and the transcription of the glycan which catalyzes the non-reducing end also has more variety. This indicates that the expression patterns of glycosyltransferases can be a key factor in the understanding of glycan structure.

In reality, the synthesis of the glycan is much more complex. There are many enzymes other than glycosyltransferases that may affect glycan synthesis, such as glycosidases, nucleotide sugar transporters, and enzymes that synthesize the nucleotide sugars. Therefore, it might be interesting to take these enzymes into account for more in-detailed analysis.

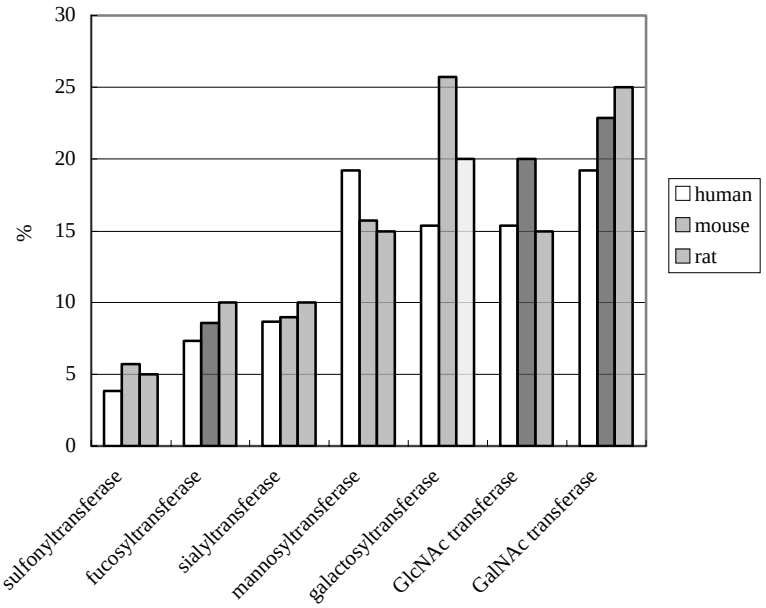

Figure1. Percentage of genes with correlation coefficient > 0.8.

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References

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