

Comparative Genomics of Diabetes-What Are We Looking For?

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Abstract:

Worldwide, the prevalence of type 2 diabetes mellitus is on the rise. There are many studies indicating that there are major genetic components in the pathogenesis of human diabetes. To date, however, there are virtually no genes identified with specific alleles that are clearly involved in the inheritance of diabetes. I will discuss a genomic approach to pursue these genes using the mouse as a lead example for understanding the genomic pathogenesis, as well as devising the most effective strategies to pursue this genomic quest. I want to explore questions such as how do we define the end-points used for linkage or QTL studies, how many genes might be required to trigger development of diabetes, and is the same genomic combination of alleles required to develop the disease in one group of animals or humans in comparison to other groups of the same species or across species. Furthermore, how will we analyze *in vivo* the validity of these “diabetes” genes in a genomic context required for their phenotypic expression? Finally, how will we use this information once we obtain it? A comparative genomics approach will be required and should be instructive.