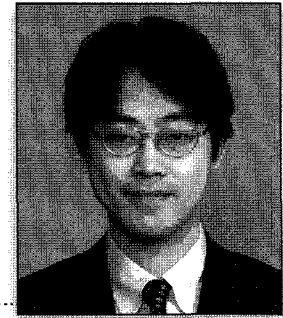


Finding Functional Elements in Non-Coding Region by Comparative Genome Study

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Recent expansion of genomic sequence data enables us to do comparative genomics searching for the functional elements that have not been identified by experiments yet. In this study, cis-regulatory elements are focused on. Gene expression could be controlled by multiple factors, not simply by 5' upstream region (including promoter) but also by remote enhancers in either 5' upstream or 3' downstream region in vertebrate genomes. To reveal this sort of complex structure of gene regulatory system, comparative genomics study is quite useful. Evolutionary conservation in intergenic region can be used as a landmark for site of unalterable function. Large scale comparison of genomic sequences among evolutionary closely related species can identify candidates of remote enhancers even if they are located far apart (like dozens of kilobases) from promoter. Together with transgenic animal system by using BAC/PAC transgene technique, candidates of enhancers can be functionally confirmed effectively. Furthermore, enhanced multiple species comparison can show emergence or deletion of lineage specific cis-elements. With enough number of species to be compared, individual transcription factor binding sites may be identified. Our research on the vertebrate Dlx gene system will be shown in this presentation as a successful example of an efficient combination of evolutionary genomics, bioinformatics and mouse developmental studies.