

Dissertation Abstract

Report no.	(Course-based) No.978	Name	Deepti Diwan
Dissertation title	Study on the demonstration of the systematic genome mutation within a single body based on genome distance method(ゲノム距離法によって単一個体内での系統的ゲノム変異の存在を立証する研究)		
<p>Individuals within a species have different genome sequences although the difference is very small. Studying this difference may be a key to understanding the initiating processes of mutation accumulation, in which a single cell will acquire a mutation, or series of mutations that may give it a competitive advantage over surrounding cells. However, even in the age of next-generation sequencing (NGS) it is experimentally undetermined whether cells within an organism have the same genome sequence in general or not, mainly because such an attempt has not been made due to the huge cost required for performing a large number of NGS experiments. On the other hand, there has been an interest in this problem since it is a biologically very basic problem in connection with the mutation rate of DNA. In this study, we first report that there are considerable differences in genome sequence between cells from a single organism, i.e., tree leaves of Japanese beech (<i>Fagus crenata</i>) or Yoshino cherry (<i>Prunus × yedoensis</i>) that could be detected by Genome Profiling (GP), a genome sequence analysis mainly utilizing the information obtained from the melting transition phenomenon of DNA fragments collected by random PCR. An intriguing phenomenon is also reported, namely, the degree of genome sequence difference (d_G) varied <i>systematically</i> from the bottom to the top of the plant, such that the greatest divergence was observed between leaf genomes from uppermost branches and the remainder of the tree. In our another study on a leaf from <i>Arabidopsis thaliana</i>, we observed spatiotemporal patterns of genome distance between neighboring sections of a leaf, thus, it was further revealed that the genome sequence varies systematically along the growth direction.</p> <p>As measured by GP, the genomic distance between two cells within an individual organism was non-negligible, and was correlated with physical distance (i.e., branch-to-branch or leaf petiole to tip distance). This phenomenon was assumed to be the result of accumulation of mutations occurring in each cell division, implying that the degree of divergence is proportional to the number of generations separating two cells.</p> <p>The genome distance method was further found to be capable of discriminating between two families and clustering of siblings born from the same parent. The results of this study have re-confirmed the universal nature of the genome distance-based approach and paved a path for future genome researches.</p>			