G. 유전

G101

Genetic Variation and Polymorphism in Rainbow Trout (*Oncorhynchus mykiss*) Analysed by Amplified Fragment Length Polymorphism

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The objective of the present study was to analyze genetic distances, variation and characteristics of individuals in rainbow trout (*Oncorhynchus mykiss*) using AFLP method as molecular genetic technique, to detect AFLP band patterns as genetic markers, and to compare the efficiency of agarose gel electrophoresis (AGE) and polyacrylamide gel electrophoresis (PAGE), respectively. In PAGE, a total of 288 bands were generated, and 220 bands (76.4%) were polymorphic. As calculated by bandsharing analysis, an average of genetic difference of individuals was approximately 0.590 0.125 in this population. In AGE, the single linkage dendrogram resulted from two primers (M11 + H11 and M13 + H11), indicating six genetic groupings. In AGE, the genetic distances among individuals of within-population, ranged from 0.108 to 0.392. By comparison with the individuals in PAGE, genetic distance between No. 10 and No. 7 showed the shortest value (0.071), also between No. 16 and No. 14 showed the highest value (0.242). As with the PAGE analysis, genetic differences was certainly apparent with 13 of 16 individuals showing greater than 80% AFLP-based similarity to their closest neighbour. The three individuals (No. 14, No. 15 and No. 16) in Kangwon-do formed distinct genetic distancesas. Consequently, AFLP markers of this fish could be used as genetic information such as species identification, genetic relationship or analysis of genome structure, and selection aids for genetic improvement of economically important traits in fish species.

G102

Bithorax Complex Genes Control the Expression of *ming* and *eagle* Genes Expressed in the *Drosophila* Nervous System

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The homeotic genes encode transcription factors that are implicated in the regulation of axial patterning in *Drosophila*. Eight homeotic genes are located in two chromosomal complex, the Antennapedia complex (*lab: labial, pb: proboscipedia, Dfd: deformed, Scr: sex combs reduced, Antp: antennapedia*) and Bithorax complex (*Ubx: ultrabithorax, abd-A: abdominal-A, Abd-B: Abdominal-B*). Molecular Genetic studies carried out in Drosophila demonstrate that these homeotic genes are expressed in ectoderm, visceral mesoderm and nervous system, establishing segmental identity along the anteroposterior axis. The homeotic genes are expressed at the highest levels in the developing nervous system. However, virtually few is known about the roles of these genes in embryonic nervous development in *Drosophila*. In this study we tried to show that the Bithorax complex genes are involved in development of the nervous system. *ming*was used as a marker gene, which is required to establish the normal CNS axomal pattern and controls cell fate within neuroblast cell lineages. The homeotic mutations affected the expression of the neurogenic gene. We will also present the mutant effect of the homeotic gene on the expression of *eagle*, which is another marker gene of the nervous system.

G103

Functional Analysis of RAD4 Homologous Gene in Yeast

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The RAD4 gene of Saccharomyces cerevisiae is essential for the incision step of UV-induced excision repair. A yeast RAD4 gene has been previously isolated by functional complementation. In order to identify the RAD4 homolog gene from fungus Coprinus cinereus, we have constructed cosmid libraries from electrophoretically separated chromosomes of the C. cinereus. The 13 C. cinereus chromosomes were resolved by pulse-field gel electrophoresis, hybridized with S. cerevisiae RAD4 DNA, and then isolated homologous C. cinereus chromosome. The insert DNA of the RAD4 homolog was contained 3.2 kb. Here, we report the characterization of fungus C. cinereus homolog of yeast RAD4 gene. Southern blot analysis confirmed that C. cinereus contains the RAD4 homolog gene and this gene exists as a single copy in C. cinereus genome. When total RNA isolated from C. cinereus cells was hybridized with the 1.2 kb PvuII DNA fragment of the S. cerevisiae RAD4 gene, a 2.5 kb of transcript was detected. In order to investigation whether the increase of transcripts by DNA damaging agent, transcripts levels were examined after treating the cells. The level of transcript did not increase by untraviolet (UV). This result indicated tnat the RAD4 homolog gene is not UV inducible gene. Gene deletion experiments indicate that the RAD4 homolog gene is essential for cell viability.

G104

Expression of HRD3 Gene, a Gene Involved in DNA Repair and Cell Viabibity

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The RAD3 gene of Saccharomyces cerevisiae is required for excision repair and is essential for cell viability. RAD3 encoded protein possesses a single stranded DNA-dependent ATPase and DNA and DNA-RNA helicase activities. To examine the extent of conservation of structure and function of RAD3 during eukaryoticevolution, the RAD3 homolog gene was isolated by screening of genomic DNA library. The isolated gene was designated as HRD3 (Homologue of RAD3 gene). Southern blot analysis confirmed that S. pombe chromosome contains the same DNA as HRD3 gene and this gene exists as a single copy in S. pombe. The transcript of 2. 8 kb was detected by northern blot analysis. The level of transcripts increased by ultraviolet (UV) irradiation, indicating that HRD3 is one of the UV-inducible gens in S. pombe. Furthermore, the predicted partial sequence of HRD3 protein has 60% identity to S. cerevisiae RAD3 gene. This homology is particularly striking in the regions identified as being conserved in a group of DNA helicases. Gene deletion experiments indicate that the HRD3 gene is essential for viability and DNA repair function. These observations suggest a evolutionary conservation of other protein components with which HRD3 interacts in mediating its DNA repair and viability functions.