G713

Protein Expression Pattern in MCF-7 Human Breast Cancer Cells after Exposure to Gamma Radiation

Hyeon-kyung jung[P], Myeong-sok Lee[C]

Department of Biological Science, Sookmyung Women's University, Seoul 140-742

Breast cancer is highly treatable by surgery, radiation theraphy,chemotheraphy and hormonal theraphy. But tumor cells have resistancefor radiation when they exposure repeated radiation. In this research, we observed different protein expression pattern between normal tumor cells and radio-resistant tumor cells.We made radio-resistant cell(MCF-RC1) from human breast cancer cell(MCF-7) and then, they were exposured 3Gy gamma radiation. And each cell was harvested in time courses. Two-dimensional polyacrylamide gel electrophoresis(2-D PAGE) was performed to compare the proteinsynthesis pattern between MCF-7 and MCF-RC1. After SDS PAGE, the gels were stained with coomassie brilliant blue R-250 staining and silver staining. They were analysed using the PDQuest software.In this study, we found some different protein expression pattern between radio-sensitive cells and resistant cells. Each increasedprotein in resistant cells(MCF-RC1) is related with cell cycle arrest or resistant of stress like gamma-radiation. On the other side, down-regulated proteins in resistant cells are involved in apoptosis or sensitivity of stresss.

G714

Genetic Characterization and Population Data for the Tetranucleotide STR Polymorphism D11S488 in the Korean Population

Yong Teak Shim[P], Seung Tae Kang[1], Hyang A Jeon[1], Jong Gil Na[C]

[P]Department of Biology, Kunsan National University, Kunsan 573-701; [C1]Department of Biological Science, Kunsan National University, Kunsan 573-701

The high variability of the short tandem repeats(STRs) and their relative simplicity when used as polymorphic markers, makes them useful tools for population genetics and forensic identification purposes. Allele and genotype frequencies for the STR locus D11S488 was determined in a Korean sample(n=225) using Amp-FLP. This tetranucleotide STR provided easily interpretable results. A high degree of polymorphism, as determined by gross length measurement, is very often due to complex underlying sequence variation. Alleles at locus D11S488 possess a compound repeat region consisting of (AAAG)n and (GAAG)n repeats. A total of 11alleles were found in our population samples. Population data of loci D11S488 revealed a high polymorphism with hetrozygosity rates of 0.89. No deviations from Hardy-Weinberg expectations were observed. The mean exclusion chance(MEC) was 0.77, the polymorphic information content(PIC) was 0.85, the power of discrimination(PD) was 0.96 and the matching probability was 0.04. Our results suggest that this locus should be a very useful STR locus for forensic practice in Korea.

G715

Analysis of the New Multiplex STR Loci D7S820, D10S1426 and D18S535 in Population Study

Yong Teak Shim[P], Seung Tae Kang[1], Se Hui Lee[1], Jong Gil Na[C]

[P]Department of Biology, Kunsan National University, Kunsan 573-701; [C1]Department of Biological Science, Kunsan National University, Kunsan 573-701

The application of multiplex short tandem repeat(STR) loci reduces costs while gene mapping, paternity testing, and forensic analysis. A multiplex PCR composed of the three highly variable tetranucleotide tandem repeat loci D7S820, D10S1426 and D18S535 have been established. Tetra-nucleotide tandem repeat markers are interesting for forensic sciences, because they may present less stutter on the electrophoretic pattern. We analyzed variation at the multiplex STR system in a sample from 294 unrelated individuals in the Korean population. No deviations from Hardy-Weinberg equilibrium were observed. The heterozygosity rates were 0.78(D7S820), 0.90(D10S1426) and 0.78(D18S535), leading to a combined discrimination power (PD) of 0.9997. PIC values are also highly informative at each locus. The combined probability of identity (Pi) for the 3 STR loci was 2.97 10-4. The result demonstrates that these multiplex STR loci can be useful for human identification in forensic cases in Korea

G716

Characterization of Polymorphic Loci of the *mariner* in *Drosophila simulans*

Sang Hyun Jee[P], Go Eun Kim[1], Chi Hyun Ahn[1], Seung Hyun Hong[1], Jae In Lee[1], Jong Kil Choo[C]

Department of Life Science, College of Natural Science, Chung-Ang University, Seoul 156-756

The *mariner*-like transposable elements (MLEs) are extremely widespread from prokaryotes to eukaryotes including vertebrates. The *mariner* elements were isolated from three strains of *Drosophila simulans* in the natural population of Korea. The molecular characteristics of *mariner*elements were analyzed by PCR-based and DNA hybridization analysis. It was revealed that the natural population of *D. simulans* possessed nonautonomous elements of 1230 bps in length lacking inverted terminal repeats (ITRs). The mRNA accumulation of this element was examined by reverse transcriptase PCR and RNA dot hybridization analysis, and nucleotide polymorphisms of *mariner* elements by mutation were analyzed with single-strand conformational polymorphism (SSCP) and multiple sequence alignment. It appeared that the *mariner* elements would encode mutant as well as wild type transposases from multiple alleles in the variable loci of chromosome. Therefore, it is likely that various mutant and wild type transposases might induce heteroalleric effect. Suggesting that transposase activity of the *mariner* elements is downregulated by the mechanism of vertical inactivation.