

Clonal plant as experimental organisms - DNA mutation rate evaluation in the radiation contaminated area of Fukushima Daiichi NPP accident

Shingo KANEKO (Fukushima University)

The Fukushima Daiichi Nuclear Power Plant accident in March 2011 caused severe radioactive contamination in the surrounding environment. Since the accident, much attention has been paid to the biological and genetic consequences of organism inhabiting the contaminated area. The effect of radiation exposure on genetic mutation rates is little known, especially for low doses and *in situ* conditions. Evaluating DNA mutation by low levels of radiation dose is difficult due to the rare mutation event and lack of sequence information before the accident. In this study, correlations with air dose levels and somatic DNA mutation rates were evaluated using Next Generation Sequencer for the clonal plant, *Phyllostachys edulis*. This bamboo is known to spread an identical clone throughout Japan, and it has the advantage that we can compare genetic mutation rate among identical clone growing different air dose levels. We collected 94 samples of *P. edulis* from 14 sites with air dose rates from 0.04 ~ 7.80 $\mu\text{Gy/h}$. Their clonal identity was confirmed by analysis using 24 microsatellite markers, and then, sequences among samples were compared by MIG sequence. The sequence data were obtained from 2,718 loci. About ~200,000 bp sequence (80 bp X 2,718 loci) were obtained for each sample, and this corresponds to about 0.01% of the genome sequence of *P. edulis*. In these sequences, 442 loci showed polymorphism patterns including recent origin mutation, old mutation, and sequence errors. The number of mutations per sample ranged from 0 to 13, and did not correlate with air dose levels. This result indicated that DNA mutations have not accumulated in *P. edulis* living in the air doses levels less than 10 $\mu\text{Gy/h}$. Our study also suggests that mutation rates can be assessed by selecting an appropriate experimental approach and analyzing with next generation sequencer.