S4 Aptamer Nanochips for Water Pollutant Detection and Medical Applications. Soyoun Kim. *Department of Chemistry, Dongguk University, Seoul 100-715 Korea Nanobiolab, National Research Laboratory(NRL), MOST.*

The development of reagents with high affinity and specificity to water pollutant small molecules is important for the high throughput detection of water pollution. Aptamers are short, single-stranded oligonucleotides with ability to specifically recognize target molecules with high affinity. Here we report the selection of ssDNA aptamers that bind to one of important water pollutant - Bisphenol A. High affinity aptamers were isolated from a 1015 random library of 60 mer ss DNAs using the SELEX procedure. Importantly, the selected aptamers specifically bound to the Bisphenol A, but not to another PCBs like DHP, on a protein chip-based assay. Using these aptamers, we developed an aptamer-based biosensor for water pollutants and detected Bisphenol A from tap water with specificity. This novel aptamer-based water pollutant detection sensor could be applied to the universal detection of water pollutant with high sensitivity.

S5 Use of Japanese Medaka (*Oryzias latipes*) cDNA Microarrays in Endocrine Disrupting Chemical Risk Assessment. Yoshi Kagami. *Chief Technology Officer/Chief Research Scientist, Ecogenomics, Inc., Fukuoka, Japan.*

Endocrine disrupting activity of environmental chemicals has been one of the major public concerns since it could cause reduction in reproductive success and affect human and wildlife populations. Up to this date, only biomarkers used to detect chemicals' potential endocrine disruption (estrogenicity) in experimental fish species are vitellogenin (a female-specific glucolipoprotein yolk precursor) and choriogenin (a precursor of egg envelope protein), and this fact motivated us to look for other useful biomarkers to assess endocrine disrupting effects of the environmental chemicals. Furthermore, several reports have shown that fish exposed to environmentally relevant concentrations (up to 100 ng/l) of 17β-estradiol (E_2) for the period prior to sex differentiation and the time of sex differentiation caused disruptions in the process of sexual differentiation (e.g. formation of a retrogonadal cavity and oocyte development in genotypic male, significant change of the sex ratio towards the female sex, etc.), and alteration in the egg production pattern in the subsequent adults. This clearly indicated that early life stages of fish development were sensitive to low concentrations of E_2, and such exposure is now known to lead to distinctive pathological endpoints. Therefore, we were interested in the endocrine disruption studies using both adult and embryo of medaka that were exposed by estrogen and estrogen-like chemicals. Naturally, development of a bioassay tool was important in order to reduce time, cost, and labor of single biomarker- and pathological observation-dependent test methods, thus, we developed adult and embryonic medaka cDNA microarrays which contain 833 and 2,222 cDNA probes, respectively. In this presentation, experiments using these microarrays and estradiol-exposed medaka will be introduced in details, and their analyzed results will be discussed as well.

S6 Application of Toxicogenomic Researches using Fish. Jeong-Ho Lee. *Genetics & Breeding Research Center, National Fisheries Research and Development Institute (NFRDI), Korea.*

With the recent progress made in large-scale genome sequencing projects a vast amount of novel data is becoming available. A comparative sequence analysis, exploiting sequence information from various resources, can be used to uncover hidden information, such as genetic variation. With DNA markers, it is theoretically possible to observe and exploit genetic variation in the entire genome. Popular genetic markers in the aquaculture community include allozymes, mitochondrial DNA, RFLP, RAPD, AFLP, microsatellite, SNP, and EST markers. The application of DNA markers has allowed rapid progress in aquaculture investigations of genetic variability and inbreeding, parentage assignments, species and strain identification, and the construction of high-resolution genetic linkage maps for aquaculture species. Microsatellites can provide a backbone for the linkage map and afford some transferability, while AFLPs would saturate the map and fill gaps with a large number of markers. Moreover, if SNPs can be added to maps, a high-density AFLP/microsatellite/SNPs map can facilitate rapid mapping of EST/Type I markers and eventually comparative mapping as well as genetic association studies. In this study, genetic divergence within and between farmed and wild olive flounder (*Paralichthys olivaceus*) was assessed by means of microsatellite DNA markers. All of the 8 microsatellite loci screened in this study showed marked polymerphisms. Marked reductions of genetic variability in the farmed olive flounder compared with the wild olive flounder were observed in terms of number of microsatellite alleles. We conclude that, based on the reduced genetic variability observed in the farmed olive flounder, bottleneck effects occurred when the farmed olive flounder was founded. In addition, we present a strategy that allows rapid identification of candidate SNPs using publicly available EST databases. Single-nucleotide polymorphisms (SNPs) represent a new form of functional marker, particularly when they are derived from expressed sequence tags (ESTs). These polymorphisms can provide a rich source of useful molecular markers in genetic analysis, and can be used as excellent markers for genetic mapping because of their representation of functional genes and potential for high throughput genotyping. In this study, a collection of 9,101 eastern oyster (*Crassostrea virginica*) ESTs was assembled into contiguous sequences (contigs), and then visually inspected to identify primer pairs capable of amplifying specific alleles. Using the advanced single-tube Tm-shift SNP genotyping method, we have been able to validate of 32 candidate SNPs in eastern oysters from several distant geographic sites in order to obtain polymorphisms as much as possible. These results suggest that at least 90.6% of them were true polymorphisms and the majority of predicted SNPs identified using this approach represent true genetic variation in eastern oyster.