S1 MAQC: The MicroArray Quality Control Project.
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DNA microarrays have been identified by the U.S. Food and Drug Administration's (FDA's) Critical Path Initiative (www.fda.gov /oc/initiatives/criticalpath/) as a key opportunity for advancing medical product development and personalized medicine through the identification and qualification of biomarkers of efficacy and safety. The FDA launched the MicroArray Quality Control (MAQC) project in February 2005 in order to address reliability concerns raised in publications (*e.g.*, Marshall E, *Science* 306: 630-631, 2004) about microarrays as well as other performance, standards, quality, and data analysis issues. It is anticipated that the MAQC effort will facilitate the appropriate application of microarray data in the discovery, development, and review of FDA-regulated products. The MAQC-I (MAQC Phase I) evaluated technical performance of microarray platforms in identifying differentially expressed genes (DEGs) or potential biomarkers. Gene expression data on four titration pools from two distinct, commercially available reference RNA samples were generated at multiple test sites using a variety of microarray platforms. The resulting rich reference data set consists of over 1,300 microarrays and additional measurements for over 1,000 genes with quantitative technologies such as qPCR. The MAQC-I involved 137 scientists from 51 organizations including the six FDA centers (CBER, CDER, CDRH, CFSAN, CVM, and NCTR), government agencies (EPA, NIH, and NIST), microarray and RNA manufacturers, microarray service providers, academic laboratories, and other stakeholders. The MAQC-I observed high intra-platform reproducibility across test sites, as well as inter-platform concordance in terms of DEG lists. Similar results were obtained from a rat toxicogenomics validation study. The apparent lack of reproduceebility previously reported is likely caused, at least in part, by the common practice of ranking genes solely by a statistical significance measure (*P*) and selecting DEGs with a stringent significance threshold without considering the fold change. MAQC-I results were published in the September 2006 issue of *Nature Biotechnology* as a series of six research papers (http://www.nature.com/nbt/focus/maqc/) and reprinted in October 2006 as a supplement by Nature Publishing Group. The MAQC-I was featured by *Cell* (127:657-659, 2006), *Nature* (442:1067-1070, 2006), *Science* (313:1559, 2006), *Nature Methods* (3:772, 2006), and *Analytical Chemistry* (78:7358-7360, 2006). The MAQC-II (MAQC Phase II) is progressively working toward consensus on the "best practices" of developing and validating predictive models (classifiers) for clinical and preclinical applications. Multiple data sets have been distributed to dozens of organizations for independent analysis, and predictive models will be evaluated by confirmatory data sets being generated by MAQC participants. We welcome and appreciate the community's participation in the MAQC project.

S2 Development of Ecotoxicogenomics Using *Caenorhabditis Elegans*.
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Recently huge number of chemicals flooded around our environment. These chemicals affect to several physiological systems, maturation, growth, reproduction and behavior of human and wildlife. From the view of ecotoxicology, we always concern about total impact against ecological system. That is difficult since the hazard potency of all chemical for all life in ecosystem can not be evaluated. So we think that introducing toxicogenomical tool and analysis is a potent to solve this problem. We subjected to *Caenorhabditis elegans* (*C. elegans*) as a model organism and DNA microarray for genome wide analysis tool to develop ecotoxicogenomics. *C. elegans* is one of the most popular research model animals. Its genome analysis was completed. Then its genomic, neurological and aging mechanisms are well characterized. First, we attempted to establish a novel *C. elegans* bioassay system for sensing chemicals using gene expression patterns. The effects of chemicals on gene expression were estimated by cDNA microarray. The hierarchical clustering method was applied to analyze their response patterns. The biological impacts by chemicals are classified according to the similarity of their responses in cluster analysis. We found that each cluster, which is a group of similar response patterns, corresponds to kind of stimuli. The threshold value for chemicals is shown to be less than 1 nM. The accumulated of gene expression patterns and responded gene information by this assay system enable to provide not only the quantities and/or qualities of known chemicals but also these of unknown chemicals in environment samples. It is possible that this system can evaluate total biological effect level in pollution, since gene expressions reflect composite effects of sources in pollution. From the genomic study, *C. elegans* conserves many common genes between from bacteria to human. This is indicated that we can estimate the effects of specific chemicals which present in environment on many ecological animals from independent gene expression data obtained by *C. elegans in vivo* bioassay. This study is supported by a grant in aid for scientific research from the Japan Society for the Promotion of Science (JSPS).

S3 On-Chip Electrophoresis - a Versatile Technology for Improving Toxicogenomic Workflows.
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During the last decade, multiple genomic approaches in the area of gene expression analysis or detection of genetic variations have been implemented in the field of experimental toxicology. On-chip electrophoresis on a microfluidic platform like the 2100 bioanalyzer, became an important analysis tool. Lab-on a-chip technology enables multiple quality control approaches in the workflow of RNA, DNA and protein analysis. Especially in the area of RNA quality control prior to microarray or qPCR experiments, the platform and it's associated RNA integrity number (RIN) has been considered as the gold standard for RNA integrity assessment. In addition, the ability to separate, size and quantify multiplex PCR or RFLP products allows improving important steps of the toxicogenomic workflow. Examples are optimization of PCR conditions, screening through high number of analytes and identification of targets out of a heterogeneous sample pool.