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REPORT OF THE SECOND SURVEY ON AVAILABLE OMICS TOOLS

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No. 100

REPORT OF THE SECOND SURVEY ON AVAILABLE OMICS TOOLS

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INTER-ORGANIZATION PROGRAMME FOR THE SOUND MANAGEMENT OF CHEMICALS

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The Environment, Health and Safety Division publishes free-of-charge documents in ten different series: **Testing and Assessment**; **Good Laboratory Practice and Compliance Monitoring**; **Pesticides and Biocides**; **Risk Management**; **Harmonisation of Regulatory Oversight in Biotechnology**; **Safety of Novel Foods and Feeds; Chemical Accidents; Pollutant Release and Transfer Registers; Emission Scenario Documents; and the Safety of Manufactured Nanomaterials.** More information about the Environment, Health and Safety Programme and EHS publications is available on the OECD's World Wide Web site (http://www.oecd.org/ehs/).

This publication was developed in the IOMC context. The contents do not necessarily reflect the views or stated policies of individual IOMC Participating Organizations.

The Inter-Organisation Programme for the Sound Management of Chemicals (IOMC) was established in 1995 following recommendations made by the 1992 UN Conference on Environment and Development to strengthen co-operation and increase international co-ordination in the field of chemical safety. The participating organisations are FAO, ILO, OECD, UNEP, UNIDO, UNITAR and WHO. The World Bank and UNDP are observers. The purpose of the IOMC is to promote co-ordination of the policies and activities pursued by the Participating Organisations, jointly or separately, to achieve the sound management of chemicals in relation to human health and the environment.

FOREWORD

This document presents responses to a questionnaire survey on available tools of three major technologies in the field of genomics (i.e. transcriptomics, proteomics and metabolomics) conducted by Japan and reviewed by the OECD/IPCS Advisory Group on Toxicogenomics.

This document is published on the responsibility of the Joint Meeting of the Chemicals Committee and the Working Party on Chemicals, Pesticides and Biotechnology .

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REPORT OF THE SECOND SURVEY ON AVAILABLE OMICS TOOLS

1. Introduction

1. This paper is intended to provide information on the current approaches in toxicogenomics. Toxicogenomics is an integration of toxicology and genomics and it is defined as the study of the response of a genome to hazardous chemicals. Genomics uses three major technologies, transcriptomics, proteomics and metabolomics. Transcriptomics deals with genome wide scale mRNA expression using DNA microarray and other high through put technologies that can estimate quantity of mRNA. Proteomics deals with a large number of proteins encoded by a genome. Metabolomics deals with metabolite profiling using mass spectrometry or nuclear magnetic resonance spectrometry. These technologies are rapidly developing in life sciences and application of genomics to toxicology and ecotoxicology is one of promising methodologies for evaluation and estimation of chemical risks.

2. In order to evaluate chemical risks in the environment, test methods have been widely applied to elucidate effective concentrations of chemicals. Although these methods have been used in many countries, information obtained from the results is limited. On the other hand, omics study can provide genome-wide information and it is expected that, through systematic efforts to generate mechanistic information using omics technologies, diagnostic and predictive assessments of hazardous chemicals can be established for risk assessment.

3. In the preparation for the OECD/IPCS Workshop on Toxicogenomics in Kyoto on 13-15 November 2004, the OECD Secretariat conducted a survey of existing toxicogenomic tools in member countries (Kyoto Survey). This survey was mainly focused on ecotoxicogenomics and the result was circulated at the Workshop (see Annex 4). The information of the survey was useful as a snapshot of current activities applying toxicogenomic tools for chemical assessments. Since the survey, there has been accelerating development in the toxicogenomic field. During the time, genome information has been accumulated for various species and new technologies have been developed. In view of this situation, the OECD/IPCS Advisory Group on Toxicogenomics agreed to follow-up current approaches in toxicogenomics in OECD member countries.

4. In order to explore the opportunities for using toxicogenomic tools for risk assessment, a concise summary of available tools would be beneficial. Moreover, such summary will facilitate establishment of co-operative relationship among researchers to develop toxicogenomic tools in OECD member countries.

2. Survey

5. It was proposed by the Advisory Group to develop a Detailed Review Paper or other form of document compiling the currently available genomics tools, by means of a questionnaire survey to follow up on the one conducted in preparation for the Kyoto Workshop. This survey aimed at gathering information on available toxicogenomics methods covering both mammalian effects and ecological effects, and experiences in using omics tools for evaluation of chemicals including hazard identification, hazard characterization, analyses of functional mechanism and signal transduction, and risk assessment of chemicals.

6. The proposal was endorsed by the OECD Joint Meeting of the Chemicals Committee and Working Party on Chemicals, Pesticides and Biotechnology at its 39th meeting in February 2006. An outline of the survey had been developed by the lead country, Japan, and was reviewed and endorsed by the Advisory Group in July 2006 (see Annex 1). The information to be compiled includes;

- Type of miroarrays or other tools (commercially available arrays or self-prepared ones, number of genes in the microarray, criteria for their selection, etc),
- Precise name of the species,
- Chemicals that have been tested using the tools, and
- Reference to the publication (or planned publication).

7. The questionnaire was sent to the OECD Working Group of National Co-ordinators of the Test Guidelines Programme (WNT), as well as the contacts identified in the Kyoto survey, the participants in the Kyoto Workshop and other researchers. This questionnaire was distributed on 21 July 2006 and the answers were collected between August and November 2006.

3. Results

8. The summary of the questionnaire responses and each detailed response are shown in Annex 2 and 3 respectively. Answers to the survey were obtained from eight countries. Five countries (Japan, Korea, the Netherlands, Switzerland, and the United States) contributed to the 2004 survey as well. Three countries (France, Germany and the United Kingdom) answered for the first time.

9. From these countries, 62 omics applications were reported whereas 42 omics applications were reported in 2004. In contrast to the increase of the number of omics studies, however, the number of species studied was decreased. There was no information gathered on bacteria, yeast and amphibians in 2007. With regard to birds, only studies in the cormorant were reported. The number of target chemicals also changed. Endocrine disrupting chemicals and related chemicals had been the major interest in the 2004 survey, but a wider range of chemicals was the subject of

study in this updated survey.

10. During the three years since the 2004 survey, application of omics technologies to toxicology drastically changed. In 2004, nearly 80% of studies were transcriptome analysis and its ratio was decreased to 55% in 2007 (Table 1). Instead, newly developed omics technologies in metabolomics and proteomics have been largely introduced. Especially, the number of metabolomics has been increased (from 2 to 11). It is also notable that new technologies such as surface enhanced laser disruption ionized mass spectrometry (SELDI-MS) have been emerging as a tool for proteomics.

Table 1. Comparison of the survey results obtained in 2004 and 2007

	2004	2007
Countries	5	8
Total studies	42	62
Transcriptomics	33	32
Proteomics	7	19
Metabolomics	2	11
Publications	10	32

11. As a consequence of increase in the number of omics applications, number of publications was also increased. In 2004, ten publications had been cited in the report and nine of them were from Korea, whereas 30 papers were published from various countries in 2007. Although peer review of the papers is not the purpose of this survey, this increase seems to reflect substantial increase of related studies.

4. Discussion and perspectives

12. From this survey, it is clear that omics technology is largely adopted as a tool in toxicology. More countries are engaged in a toxicogenomic approach to evaluate hazardous effects of chemicals than three years ago. The number of applied technologies, target chemicals and publications of related papers has increased in these three years. In addition, several data become available in the public domain. But it is notable that there is a drastic change of groups and subjects in transcriptomics between the two surveys. Only nine omics applications were identified as projects that continued during three years. Thirty three applications reported in 2004 were not reported in 2007. There may be two reasons for this; one is related to the circulation of the questionnaire, e.g. the questionnaire was not passed to the same group as the previous survey. Thus, it may be important to communicate with all groups which are listed in both surveys. In order to follow-up the work of these groups, it may be desirable to list key persons who can communicate almost of all researchers who are engaged in toxicogenomics in their own countries. A comprehensive survey of published literature is also recommended.

13. The other reason is that many groups that reported in 2004 may have already stopped their study. Although this is speculation, should they have stopped their study because of technical

reasons such as reproducibility and difficulty of normalization of samples, this information would be helpful to other researchers. Alternatively, if studies terminated due to lack of funding, it could be an indicator of policy of each country. In this survey, source of funding and amount of budget were not included in the questionnaire but this information may be useful in order to evaluate the interest on toxicogenomics of each country.

14. International harmonization is very important to further develop toxicogenomics. It is essential to examine if different laboratories can obtain conclusive results regardless of countries and/or platforms. In this context, omics studies are encouraged to be open, thus it is recommended to submit transcriptome data to the Gene Expression Omnibus of the National Center for Biotechnology Information (http://www.ncbi.nlm.nih.gov/geo/) or ArrayExpress in the European Bioinformatics Institute (http://www.ebi.ac.uk/arrayexpress/), as is recommended for DNA microarray studies. In addition, it would be also helpful to make a list of studies that are submitted to public databases.

15. It is also important to continue to survey the omics status in order to evaluate substantial progress in this field. Based on this survey, it may be useful to make a single database that can give up-to-date information to facilitate establishment of co-operative relationships among researchers to develop toxicogenomic tools. When establishing this database, ongoing activities regarding toxicogenomics database development in other countries, i.e. the US, should be considered in order to harmonize and merge the available information. In addition, an annual meeting of academic societies such as Society of Toxicology and Society of Environmental Toxicology and Chemistry may be useful to harmonize these technologies.

ANNEX 1: OUTLINE OF THE SURVEY ON AVAILABLE TOXICOGENOMICS METHODS FOR HAZARD/RISK ASSESSMENT OF CHEMICALS (EXTRACT, JULY 2006)

Background and objective

In 2004, in preparation for the OECD/IPCS Workshop on Toxicogenomics in Kyoto on 13-15 October 2004, the OECD Secretariat collected information on the existing and forthcoming toxicogenomics methods from member countries and other organisations. Information on the genomic-based methods (transcriptomics, proteomics, metabolomics, etc.) which was developed for studying toxic effects of chemicals was accumulated, focusing on environmental effects of chemicals on ecosystem. The result from this exercise is provided for information. The Workshop appreciated this information, but noted that some important information is missing while the compilation included some irrelevant information. It was also pointed out that the linkage between ecotoxicogenomics and mammalian toxicogenomics is essential.

During the last 2 years, the progress in this area of science has been remarkable, and several toxicogenomics meetings and symposia in various research communities have been held. Taking into account the progress, the OECD and IPCS agreed to prepare a new summary document of recent development of toxicogenomics methods covering both mammalian effects and ecological effects, and experiences in using omics tools for evaluation of chemicals including hazard identification, hazard characterization, analyses of functional mechanism and signal transduction, and risk assessment of chemicals. This survey project is led by Japan and supervised by the OECD/IPCS Advisory Group on Toxicogenomics.

The result of the survey will facilitate collaborative works between laboratories of different countries and reduce the cost of development of new methods and establish data bases of each animal species.

Survey

This paper and attachments should be forwarded by the receivers to relevant researchers. Researchers are invited to complete the response form with information on their experience in using genomic-based methods (transcriptomics, proteomics, metabolomics, etc.) in toxicological, ecotoxicological, or phermaceutical studies. Specific information required is listed in the following:

Species:
(1) Common name of the species
(2) Scientific name of the species
Genome Sequence:

(3) Genome sequence of the species been obtained? (Finished/In progress/No)
(4) Number of expression sequence tags (or genes sequenced)

Microarray:

(5) Does the method include a microarray? (Yes/No)
(6) If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)

Proteomics:

(7) Does the method include proteomics? (Yes/No)
(8) If yes, please provide information on the technology. (2D-PAGE or other methods)

Metabolomics:

(9) Does the method include metabolomics? (Yes/No)
(10) If yes, please provide information on the technology (MNR,LC-MS or other methods)

Other technologies:

(11) Does the method include other technologies? (Yes/No)
(12) If yes, please provide information on the technology.

Scale and Chemicals:

(13) Scale (Number of genes, proteins or chemicals that can be analyzed)
(14) Names and CAS numbers of the chemicals studied using the method

References:

(15) Publication
(16) Supplemental websites or database accession numbers

Others:

(17) Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)
(18) Comments (as appropriate)

Contact Information:

(19) Main researchers
(20) Affiliation
(21) Country
(22) Email address
(23) Phone number
(24) Fax number

Examples of information to be filled in the response form are attached. In addition to the response form, please provide MIAME (Minimum Information about a Microarray Experiment) format information if available.

The responses should be sent back by e-mail to the OECD Secretariat by **Friday, 15 September 2006**.

The researchers named in the responses may be contacted by Taisen Iguchi (Okazaki Institute for Integrative Bioscience, National Institutes of Natural Sciences, Japan) for further information. The information collected will be included in a draft prepared by Japan and reviewed by the OECD/IPCS Advisory Group on Toxicogenomics in order to produce a report including information of genomic-based methods that have been applied in scientific studies. The report will be submitted to the OECD Joint Meeting with a view to declassification.

Contact person

Question about contents of the questionnaire:

Hajime Watanabe (Okazaki Institute for Integrative Bioscience, National Institute of Natural Sciences, Japan)

Question about practical issues and submission of the questionnaire:

Take Fukushima (Environmental Health and Safety Division, Environment Directorate, OECD)

ANNEX 2: SUMMARY OF THE 2006 SURVEY RESPONSES *

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
1	Mouse (C57BL/6Crslc)	Finished		Yes (Affymetrix GeneChip: Mouse Genome 430A, Mouse Genome 430-2)	No	No	Yes ("Percellome method" to normalize transcriptome data to cell number of the sample (mRNA copy number per cell))	Ca. 45,000 probe set data, finished up to 90 chemicals (See Annex 4 for more detail.)	1,2-dichloro-3-nitrobenzene, 1H-1-2-3-triazol, etc. (See Annex 4 for more detail.)	Yes	National Institute of Health Sciences, Japan
2	Medaka	No		Yes (Custome cDNAarry for brain of medaka, Medaka embryo array (Ecogenomics Co, LTD)	No				tributyltin, PCBs, mixture of TBT and PCBs	in prepareing	Faculty of Agriculture, Kyushu Univerity, Japan
3	Rat (White Norway)	in progress	More than 90% of the estimated 2.8 Gb genome is available (state August 2006)	Yes (GeneChip Rat Genome 230 2.0 Array, (Affymetrix))	Yes (2D-PAGE, Proteinchip (SELDI-MS))	No	No	genomics: 31.000 probe sets, 28.000 rat genes; proteomics: approx. 1000 annotated protein spots (work in progress)	N-nitrosodiethylamine (NDEA), Aflatoxin B1 etc. (See Annex 4 for more detail.)		BfR, Germany

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
4	Rat (White Norway)	in progress	more than 90% of the estimated 2.8 Gb genome is available (state August 2006)	Yes (GeneChip Rat Genome U34A Array (Affymetrix))	Yes (2D-PAGE, Proteinchip (SELDI-MS))	No	No	approx. 8.800 genes, 710 annotated protein spots (395 unique genes)	N-nitrosomorpholine (NNM)	Yes	BfR, Germany
5	Gulf Killifish	No		No	Yes (Surface Inhanced Laser Desorption and Ionization -Time of Flight Mass Spectrometry (SELDI-TOF MS); Matrix Assisted Laser)	No	No	Infinite number of proteins	Estradiol; Methoxychlor; Trenbolone	No	EPA, the U.S.
6	Sheepshead MinNow	No		No	Yes (Surface Inhanced Laser Desorption and Ionization -Time of Flight Mass Spectrometry (SELDI-TOF MS); Matrix Assisted Laser)	No	No	Infinite number of proteins	Estradiol, Methoxychlor, Bisphenol-A etc. (See Annex 4 for more detail.)	Yes	EPA, the U.S.
7	Zebrafish	Finished	1,091,927	Yes (Custom cDNA Array)	No	No	No	5,000	Retinoic Acid, Ibuprofen	Yes	Osiris Therapeutics, Inc., the U.S.

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
8	Zebrafish	Finished		No	Yes (2D-LC/LC-MS/MS (mudPIT) with accurate mass full scan spectra)	No	No	depending on sample cleanup: ~1000	EDCs (estradiol, ethinylestradiol, cadmium)	Yes	Eawag, Switzerland
9	Chlamydomonas reinhardtii			No	Yes (2D-LC/LC-MS/MS (mudPIT) with accurate mass full scan spectra)	No	No	depending on sample cleanup: ~1000	various herbicides nanoparticles (TiO2)	Yes	Eawag, Switzerland
10	Chlamydomonas reinhardtii			Yes (Custom)	No	No	Yes (mutant analysis, reportergene constructs, real time PCR)	screening of gene expression profiles on whole genome array, variaty of pollutants and stress conditions causing photo-oxidative stress		Yes	Eawag, Switzerland
11	Zebrafish			Yes (Custom and Commercial (Affymetrix))	No	No	Yes (functional approach (mutants, knock-down), real time PCR)	screening of gene expression profiles on whole genome array, variety of chemicals covering a broad range of modes of toxic action			Eawag, Switzerland
12	Red Worm/ Marsh Red Worm	No	17225	Yes (Custom)	Yes (2D-PAGE)	Yes (1H-NMR, GC-MS)		8000 genes, 50 metobolites (NMR) 100-200 metabolites (GC-MS)	Copper chloride, cadmium chloride etc. (See Annex 4 for more detail.)	Yes	Cardiff Univerity, UK

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
13	Nematode	Yes	~20,000	Yes (Custom Oligonucleotide)	Yes (2D-PAGE)	Yes (1H-NMR)	Yes (RNAi, knock-out mutants)	20,000 transcripts, 50 metabolites by 1H-NMR	Copper chloride, cadmium chloride etc. (See Annex 4 for more detail.)	Yes	Cardiff Univerity, UK
14	Mouse	Finished	See Annex 4 for detailed information	Yes (Custom: Mouse Sigma Compugen oligolibrary)	No	No	No	selection of 11K genes with a bias towards immunological and toxicological relevance	bis(tri-n-butyltin)oxide (TBTO), benzo[a]pyrene, cyclosporin A, acetaminophen		RIVM, The Netherlands
15	Rat	Finished	See Annex 4 for detailed information	Yes (Custom: rat array ready oligo set v1.0 Operon Biotechnologies GmbH)	No	No	Yes (Real time RT-PCR)	5705 C6-amino-linked oligos	bis(tri-n-butyltin)oxide (TBTO)	Yes	RIVM, the Netherlands
16	Rat	Finished	See Annex 4 for detailed information	Yes (Commercial: Affymetrix RG U34A)	No	No	No	8799 probe sets	Hexachlorobenzene	Yes	RIVM and University of Utrecht, The Netherland
17	Rat	Finished	See Annex 4 for detailed information	Yes (Custom: rat array ready oligo set v1.0 Operon Biotechnologies GmbH)	No	No	No	5705 C6-amino-linked oligos	Lactobacillus casei Shirota	Yes	RIVM, The Netherlands

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
18	Rainbow trout	No	(>250,000 in total available at Genbank)	Yes (GRASP salmonid cDNA array and from sept 2006 "Geniom" (flexible oligo array))	Yes (2D-PAGE, Maldi-TOF, Q-TOF, FT-ICR)	Yes (NMR (up to 900 MHz available))	Yes (Analytical chemistry, various molecular biomarkers (RT-PCR, ELISA, Western blot, enzyme activity assays), histology, field work)	16,000 spots on GRASP array, up to 150,000 spots on Geniom array	Selected pharmaceuticals and complex sewage effluents	Yes	Göteborg University, Sweden
19	Mouse	Finished	See Annex 4 for detailed information	Yes (Affymetrix: mouse430A)	No	No	No	22600 genes	β -Estradiol, Bisphenol A, Di-n-butyl phthalate	Yes	National Institute of Natural Sciences, Japan
20	Mouse	No		No	Yes (2D-PAGE)	No	No	200 spots	β -Estradiol	NA	National Institute of Natural Sciences, Japan
21	Rat	Finished	Full genome	Yes (Agilent full genome gene chip)	Yes (2DE)	No	Yes (Quantitative PCR)	41 000 trancripts and variants	flutamide, finasteride, clofibrate, phenobarbital	Yes	Bayer Cropscience, France
22	Medaka	Finished	See Annex 4 for detailed information	No	No	Yes (NMR)	No	NMR estimated to detect ca. 100 metabolites	Low molecular weight endogenous metabolites	Yes	University of Birmingham, UK
23	ChiNook salmon	?	?	No	No	Yes (NMR)	No	NMR estimated to detect ca. 100 metabolites	Low molecular weight endogenous metabolites	Yes	University of Birmingham, UK

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
24	Roach	?	?	No	No	Yes (MS (specifically FT-ICR MS))	No	MS estimated to detect ca. 1000 metabolites	Low molecular weight endogenous metabolites	None to date	University of Birmingham, UK
25	European flounder	No	14000 clones	Yes (Custom, University of Birmingham)	Yes (2D PAGE University of Stirling)	Yes (NMR)	Yes (Q-PCR)	NMR estimated to detect ca. 100 metabolites cDNA array 14,000 clones	Metabolomics: Low molecular weight endogenous metabolites; cDNA array: Estradiol etc. (See Annex 4 for more detail)	Yes	University of Birmingham, UK
26	3-spined stickleback	Yes	Full genome	Yes (Custom, University of Birmingham)	No	Yes (NMR)	No	NMR estimated to detect ca. 100 metabolites, cDNA aray 15,000 clones	Metabolomics: Low molecular weight endogenous metabolites; cDNA array: Estradiol etc. (See Annex 4 for more detail)	None to date	University of Birmingham, UK
27	Water flea	in progress	See Annex 4 for detailed information	No	No	Yes (MS (specifically FT-ICR MS))	No	MS estimated to detect ca. 1000 metabolites	Low molecular weight endogenous metabolites	None to date	University of Birmingham, UK
28	Common mussel	?	?	No	No	Yes (NMR)	No	NMR estimated to detect ca. 100 metabolites	Low molecular weight endogenous metabolites	In preparation	University of Birmingham, UK
29	Mediterranean mussel	No	?	No	No	Yes (NMR)	No	NMR estimated to detect ca. 100 metabolites	Low molecular weight endogenous metabolites	In preparation	University of Birmingham, UK

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
30	Mouse	No		Yes (Affymetrix system)	Yes (2D-PAGE)	No	Yes (Blood biochemical analysis, histopathology)	>22,000 know genes	CCl4, ENU, Bromobenzene etc. (See Annex.4 for more detail.)	Yes	Korea Institute of Toxicology, Korea
31	Mouse (Balb/c)	No		Yes (Commercial: Applied Biosystem)	No	No	No	32,381 genes	hexachlorobenzene, cyclosporine A, tacrolimus	No	NITR, KFDA, Korea
32	Mouse (C57BL/6J)	No		Yes (Commercial: Affymetrix)	No	No	No	>22,000 know genes	Cadmium, 2-bromopropane	No	NITR, KFDA, Korea
33	Rat (F344/N)	No		Yes (Commercial: Applied Biosystem)	No	No	Yes (Blood biochemical and urine analysis, histopathology)		HgCl2		NITR, KFDA, Korea
34	Human	No		Yes (Commercial: Affymetrix)	Yes (2D-PAGE & MALDI/TOF)	No	Yes	>22,000 know genes	Mitomycin C, Methyl methanesulfonate etc. (See Annex 4 for more detail.)		NITR, KFDA, Korea
35	Human (TK6)	No		Yes (Commercial: Applied Biosystem)	Yes (2D-PAGE & MALDI/TOF)	No	Yes	>22,000 know genes	MNNG, H2O2		NITR, KFDA, Korea
36	Mouse	No		Yes (Commercial: Affymetrix)	Yes (2D-PAGE & MALDI/TOF)	No	Yes	>22,000 know genes	MMNG, TPA, H2O2, EGCG(food ingredient)		NITR, KFDA, Korea

No.	Common name of the species	Genome sequence been obtained?	Number of expression sequence tags or genes sequenced	the method include a microarray? (If yes, platform of the microarray (Custom /Commercial))	proteomics? (If yes, information on the technology)	metabolomics? (If yes, information on the technology)	other technologies? (If yes, information on the technology)	Scale (Number of genes, proteins or chemicals that can be analyzed)	Chemicals studied	Publications	Organisation and Country
37	Mouse	No		Yes (Commercial: Applied Biosystem)	Yes (2D-PAGE & MALDI/TOF)	No	Yes (Blood biochemical analysis, histopathology)	>22,000 know genes	CCl4, Acetaminophen, ANIT, Thioacetamide		NITR, KFDA, Korea
38	Human (K562)	No		Yes (Commercial: Affymetrix)	Yes (2D-PAGE & MALDI/TOF)	No	Yes	>22,000 know genes	1,2-dibromoethane Glycidol 8-OH-hydroxyquinoline Emodin Methylcarbamate o-nitrotoluene(D-mannitol 1,2-dichlorobenzene)		NITR, KFDA, Korea
39	Nematode	Finished		Yes (Custom)	No	No	No	9000	cadmium, Mercury, lead, diethylstilbestrol,methyltestosterone,cortisol	Yes	
40	Commom cormorant	No	6930	Yes (Custom)	Yes (2D-PAGE)	No	No	1061	PCDDs, PCDFs etc. (See Annex 4 for more detail.)	Yes	
41	ascidian (or tunicate)	Finished	690,000	Yes (Custom: Agilent Technologies)	No	No	Yes (Chemical analyses of organotin compounds)	10,000 genes		Yes	
42	Water flea	in progress	55,000	Yes (Custom)	No	No		300genes	CuSO4, H2O2, PCP, NF	Yes	University Reading, UK
43	Water flea	No	13000 clones	Yes (Custom)	No	No	No	13000clones	Ibuprofen, Cadmium	Yes	

*More detailed information for each response is available in Annex 4.

ANNEX 3: DETAILED RESPONSES TO THE QUESTIONNAIRE

1

Date:	16 August, 2006
Name of the method/project:	Chemical Safety Toxicogenomics (Percellome Toxicogenomics Project (Single oral exposure series: TTG1))
Name of the contact person	Jun Kanno
Organisation:	National Institute of Health Sciences
Country:	Japan

No	Question	Answer
Species		
1	Common name of the species	Mouse (C57BL/6Cr slc)
2	Scientific name of the species	mus musculus
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	finished
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affymetrix GeneChip: Mouse Genome 430A, Mouse Genome 430 2.0
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	"Percellome method" to normalize transcriptome data to cell number of the sample (mRNA copy number per cell)
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	Ca. 45,000 probe set data, finished up to 90 chemicals and on going project. Project subcode TTG1 (single oral exposure series): standard data for one chemical consist of 4 dose levels (C, L, M, H) and 4 time points (2, 4, 8, 24 hr), triplicate, total 48 GeneChip data per one organ (Liver is always monitored, plus extra organ in some cases).
14	Names and CAS numbers of the chemicals studied using the method	1,2-dichloro-3-nitrobenzene,3209-22-1 1H-1-2-3-triazol,288-36-8 1H-1-2-4-triazol,288-88-0 2-4-dinitrophenol,51-28-5 2-Aminomethylpyridine,3731-51-9 2-chloro-4-6-dimethylaniline,63133-82-4 2-Vinylpyridine,100-69-6 3-amino-1H-1-2-4-triazole,61-82-5 3-methylcholanthrene,56-49-5 4-amino-2,6-dichlorophenol,5930-28-9 4-Ethylnitrobenzene,100-12-9 9-cis retinoic acid,5300-03-8 Acephate,30560-19-1 Acetaldehyde,75-07-0 Acetaminophen,103-90-2 Agaritine,2757-90-6 All-trans retinoic acid,302-79-4 AraC,147-94-4 Aspirin,50-78-2 Azacytidine,320-67-2 Benzene ,71-43-2 Bisphenol A,80-05-7 Bromobenzene,108-86-1 Caffeine,58-08-2 Carbaryl,63-25-2 Carbon tetrachloride,56-23-5 Cisplatin,15663-27-1 Citric acid-calcium salt,813-94-5 Clofibrate,637-07-0 Coenzyme Q10,303-98-0 Dexamethasone,50-02-2 Diethylnitrosamine,55-18-5 Diethylstilbestrol,56-53-1 DMSO,67-68-5 Domoic acid,14277-97-5 Ethanol,64-17-5 Ethynyl estradiol,57-63-6 Formalin,50-00-0

		Forskolin,66575-29-9 Fullerene,99685-96-8 Genistein,446-72-0 Glycyrrhizin2K,1405-86-3 Hydroxycitric Acid-Calcium salt,27750-10-3 Ibuprofen (dl-p-isobutylhydratropic acid),15687-27-1 Indigo,482-89-3 Isoniazid,54-85-3 Levothryoxine (T4),51-48-9 MEHP,4376-20-9 Methanol,67-56-1 Methoprene,40596-69-8 Methoprene acid,53092-52-7 Monocrotaline,315-22-0 N-ethyl-N-nitrosourea,759-73-9 N-methylaniline,100-61-8 Omeprazole,73590-58-6 Paclitaxel (Taxol),33069-62-4 Paraquat dichloride,1910-42-5 Pentachlorophenol,87-86-5 Permethrin,52645-53-1 Phenobarbital sodium,57-30-7 Phenytoin,57-41-0 Pregnenolone Carbonitrile,1434-54-4 Pyriproxyfen,95737-68-1 Rifampicin,13292-46-1 Sodium Arsenite,7784-46-5 Tamoxifen,10540-29-1 TCDD(2,3,7,8-Tetrachlorodibenzo-p-Dioxin),1746-01-6 TCDF(2,3,7,8-Tetrachlorodibenzofuran),51207-31-9 Tebufenozide,112410-23-8 Testosterone propionate,57-85-2 Thalidomide,50-35-1 Toluene,108-88-3 Transplatin,14913-33-8 Tributyltin chloride,1461-22-9 Troglitazone,97322-87-7 Trybutyltin,56573-85-4 Valproic acid sodium salt,1069-66-5 Warfarin,81-81-2
References		

15	Publications	"Per cell" normalization method for mRNA measurement by quantitative PCR and microarrays. Kanno J, Aisaki K, Igarashi K, Nakatsu N, Ono A, Kodama Y, Nagao T. BMC Genomics. 2006 Mar 29;7:64.
16	Supplemental websites or database accession numbers	http://toxicomics.nihs.go.jp/db/, http://www.nihs.go.jp/tox/TTG_Archive.htm
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	The aim of this Chemical Safety Toxicogenimics (Percellome Toxicogenomics Project) is to develop the predictive toxicology for faster, cheaper and more accurate risk assessment through the development of the gene cascade data based on the high-precision transcriptome database/informatics. We believe that this approach should lead to our ultimate goal of generating "virtual mouse" in silico in the future.
18	Comments (as appropriate)	For this purpose, a systematic approach is proposed to normalise the mRNA expression values from DNA microarrays and quantitative-PCR in a "per one cell" basis, designated as "Percellome". This Percellome system will enable us to plot all data on to one common linear scale. Transcriptome data between experimental groups, between studies, and even between different organs can be directly compared without further normalisation. This system, developed primarily for Affymetrix Gene Chips, can be expanded to other platforms and quantitative-PCR as long as they meat a few requirements. Direct data comparison between different laboratories would be possible in this respect.
		Our Percellome toxicogenomics projects monitors, for example, the time- and dose-dependent alteration of gene expression induced by various chemicals in mouse (4 time points and 4 dose levels, total of 16 groups, 3 mice each). The percellome data can be visualised as a three-dimensional graph (X=time, Y=dose, Z=expression per one cell) containing 45,000 layers of surface corresponding to each of the probe sets in the Affymetrix MOE430v2 Gene Chip ("MilleFeuille" data). X and Y axes can be any experimental parameters. This MF data is biologist-friendly that it is helpful to extract biologically plausible alterations and to develop further methods for drawing the gene cascades.
Contact Information		
19	Main researchers	Jun Kanno, Ken-ichi Aisaki, Katsuhide Igarashi, Noriyuki Nakatsu, Satoshi Kitajima, Atsushi Ono, Yukio Kodama

20	Affiliation	Division of Cellular and Molecular Toxicology, Biological Safety Research Center, National Institute of Health Sciences
21	Country	Japan
22	Email address	kanno@nihs.go.jp
23	Phone number	+81-3-3700-9619
24	Fax number	+81-3-3700-9647

2

Date: 17 November, 2006
Name of the method/project:
Name of the contact person Yuji Oshima, PhD.
Organisation: Faculty of Agriculture, Kyushu Univerity
Country: Japan

No	Question	Answer
Species		
1	Common name of the species	Medaka,
2	Scientific name of the species	Oryzias latipes
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custome cDNAarry for brain of medaka, Medaka embryo array (Ecogenomics Co, LTD, http://www.ecogenomics.co.jp/english/index.htm)
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	
14	Names and CAS numbers of the chemicals studied using the method	tributyltin, PCBs, mixture of TBT and PCBs
References		
15	Publications	in prepareing

16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	To access a mixture toxicity of TBT and PCB in behavior and reproduction.
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Yuji Oshima PhD.
20	Affiliation	Faculty of Agriculture, Kyushu Univerity
21	Country	Japan
22	Email address	yoshima@agr.kyushu-u.ac.jp
23	Phone number	81-92-642-2905
24	Fax number	81-92-642-2908

3

Date:	09/15/2006
Name of the method/project:	Detection and analysis of hepatotoxic modes of action for the prediction of carcinogenic effects of chemicals in the subacute toxicity test (repeated dose 28-day oral toxicity study/ OECD TG 407)
Name of the contact person	Hans-Bernhard Richter-Reichhelm
Organisation:	Federal Institute for Risk Assessment (BfR)
Country:	Germany

No	Question	Answer
Species		
1	Common name of the species	White Norway rat
2	Scientific name of the species	Rattus norvegicus
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	in progress
4	Number of expression sequence tags (or genes sequenced)	more than 90% of the estimated 2.8 Gb genome is available (state August 2006)
Microarray		
5	Does the method include a microarray? (Yes/No)	yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	GeneChip Rat Genome 230 2.0 Array, (Affymetrix)
Proteomics		
7	Does the method include proteomics? (Yes/No)	yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE, Proteinchip (SELDI-MS)
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	no
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	no
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	genomics: 31.000 probe sets, 28.000 rat genes; proteomics: approx. 1000 annotated protein spots (work in progress)
14	Names and CAS numbers of the chemicals studied using the method	N-nitrosodiethylamine (NDEA; CAS 55-18-5), Aflatoxin B1 (CAS 1162-65-8), Cupferron (N-nitrosophenylhydroxylamin; CAS 135-20-6), Carbontetrachloride (CAS 56-23-5), Diethylhexyl phthalate (DEHP; CAS 117-81-7), Clofibrate (CAS 637-07-0), Diallyl phthalate (CAS 131-17-9), Benzaldehyde (CAS 100-52-7), Ketoconazole (CAS 65277-42-1)
References		
15	Publications	
16	Supplemental websites or database accession numbers	data will be made publicly available upon publication
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	toxicology
18	Comments (as appropriate)	cooperation between academic institution and industry, funded by Federal Ministry of Education and Research (Alternatives to animal testing), project will be finished September 2007
Contact Information		
19	Main researchers	Krisztina Paal, Axel Oberemm
20	Affiliation	BfR
21	Country	Germany
22	Email address	Krisztina.Paal@bfr.bund.de, Axel.Oberemm@bfr.bund.de
23	Phone number	++49(0)30 8412-3296
24	Fax number	++49(0)30 8412-3851

4

Date:	09/15/2006
Name of the method/project:	Identification and prevalidation of hepatocellular biomarkers for detection and prediction of carcinogenic effects of chemicals
Name of the contact person	Hans-Bernhard Richter-Reichhelm
Organisation:	Federal Institute for Risk Assessment (BfR)
Country:	Germany

No	Question	Answer
Species		
1	Common name of the species	White Norway rat
2	Scientific name of the species	Rattus norvegicus
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	in progress
4	Number of expression sequence tags (or genes sequenced)	more than 90% of the estimated 2.8 Gb genome is available (state August 2006, http://www.hgsc.bcm.tmc.edu/projects/rat/)
Microarray		
5	Does the method include a microarray? (Yes/No)	yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	GeneChip Rat Genome U34A Array (Affymetrix)
Proteomics		
7	Does the method include proteomics? (Yes/No)	yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE, Proteinchip (SELDI-MS)
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	no
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	no
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	approx. 8.800 genes, 710 annotated protein spots (395 unique genes)
14	Names and CAS numbers of the chemicals studied using the method	N-nitrosomorpholine (NNM, CAS 59-89-2)
References		
15	Publications	Proteomics 5 (7):1914-1927, 2005; Toxicol.Lett. 158 (Suppl. 1):S70-P3-16, 2005 (more comprehensive paper in preparation)
16	Supplemental websites or database accession numbers	data will be made publicly available upon publication
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology
18	Comments (as appropriate)	cooperation between academic institution and industry, funded by Federal Ministry of Education and Research (Alternatives to animal testing)
Contact Information		
19	Main researchers	Axel Oberemm
20	Affiliation	BfR
21	Country	Germany
22	Email address	Axel.Oberemm@bfr.bund.de
23	Phone number	++49(0)30 8412-3238
24	Fax number	++49(0)30 8412-3851

5

Date:	05 September, 2006
Name of the method/project:	Proteomic Approach to Classify Chemicals by Mode of Action
Name of the contact person	Michael J. Hemmer, Calvin C. Walker
Organisation:	Environmental Protection Agency
Country:	United States of America

No	Question	Answer
Species		
1	Common name of the species	Gulf Killifish
2	Scientific name of the species	Fundulus grandis; plasma; hepatocytes
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	NA
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	Surface Inhanced Laser Desorption and Ionization - Time of Flight Mass Spectrometry (SELDI-TOF MS); Matrix Assisted Laser Desorption and Ionization - Time of Flight Mass Spectrometry (MALDI- TOF MS)
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	Infinite number of proteins
14	Names and CAS numbers of the chemicals studied using the method	Estradiol (50-28-2); Methoxychlor (72-43-5); Trenbolone (10161-33-8);
References		
15	Publications	No
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology; Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Michael J. Hemmer and Calvin C. Walker
20	Affiliation	U.S. Environmental Protection Agency
21	Country	United States of America
22	Email address	hemmer.michael@epa.gov; walker.calvin@epa.gov
23	Phone number	850-934-9243; 850-934-9245
24	Fax number	850-934-9201

6

Date:	05 September, 2006
Name of the method/project:	Proteomic Approach to Classify Chemicals by Mode of Action
Name of the contact person	Michael J. Hemmer, Calvin C. Walker
Organisation:	Environmental Protection Agency
Country:	United States of America

No	Question	Answer
Species		
1	Common name of the species	Sheepshead Minnow
2	Scientific name of the species	Cyprinodon variegatus; plasma; hepatocytes
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	Surface Inhanced Laser Desorption and Ionization - Time of Flight Mass Spectrometry (SELDI-TOF MS); Matrix Assisted Laser Desorption and Ionization - Time of Flight Mass Spectrometry (MALDI- TOF MS)
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	Infinite number of proteins

14	Names and CAS numbers of the chemicals studied using the method	Estradiol (50-28-2); Methoxychlor (72-43-5); Bisphenol-A (08-05-7); 4-tert-Pentylphenol (80-46-6); Endosulfan (115-29-7); Chloropyrifos (2921-88-2); Tamoxifen (100540-29-1); Trenbolone (10161-33-8); Raloxifen (82640-04-8); Formestane (566-48-3); 1,4,3-Androstatriene-3,17-dione (633-35-2); Testosterone (58-22-0); 5 alpha-Dihydrotestosterone (521-18-6); 11-Ketotestosterone (564-35-2); Flutamide (13311-84-7); Cyproterone acetate (427-51-0)
References		
15	Publications	Toxicological Sciences 2006; doi: 10.1093/toxsci/kfl079
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Michael J. Hemmer and Calvin C. Walker
20	Affiliation	U.S. Environmental Protection Agency
21	Country	United States of America
22	Email address	hemmer.michael@epa.gov; walker.calvin@epa.gov
23	Phone number	850-934-9243; 850-934-9245
24	Fax number	850-934-9201

7

Date:	Saturday, September 2, 2006
Name of the method/project:	Zebrafish Microarray
Name of the contact person	Christopher Ton
Organisation:	Osiris Therapeutics, Inc.
Country:	USA

No	Question	Answer
Species		
1	Common name of the species	Zebrafish
2	Scientific name of the species	Danio rerio
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished
4	Number of expression sequence tags (or genes sequenced)	1,091,927
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom cDNA Array
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	5,000

14	Names and CAS numbers of the chemicals studied using the method	Retinoic Acid; Ibuprofen
References		
15	Publications	Physiological Genomics (2003) 13:97-106
16	Supplemental websites or database accession numbers	http://www.ncbi.nlm.nih.gov/
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Christopher Ton
20	Affiliation	Osiris Therapeutics, Inc.
21	Country	USA
22	Email address	christopher.ton@gmail.com
23	Phone number	617-699-4286
24	Fax number	410-522-6999

8

Date: August 14, 2006
Name of the method/project: Toxicoproteomics on zebrafish
Name of the contact person Marc J-F Suter
Organisation: Eawag
Country: Switzerland

No	Question	Answer
Species		
1	Common name of the species	zebrafish
2	Scientific name of the species	Danio rerio
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	NO
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	YES
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-LC/LC-MS/MS (mudPIT) with accurate mass full scan spectra
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	NO
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	NO
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	depending on sample cleanup: ~1000
14	Names and CAS numbers of the chemicals studied using the method	EDCs (estradiol, ethinylestradiol, cadmium) dimethylnaphthalene, crude oil
References		

15	Publications	Proteomic analysis of protein profiles during early development of the zebrafish, Danio rerio. TL Tay, Q Lin, TK Seow, KH Tan, CL Hew, Z Gong, Proteomics 2006, 6(10): 3176-3188 Proteomics of early zebrafish embryos. V Link, A Shevchenko, C-P Heisenberg, BMC Developmental Biology, 2006, 6:1 (http://www.pubmedcentral.net/picrender.fcgi?artid=1363346&blobtype=pdf)
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Marc J-F Suter and collaborators
20	Affiliation	Eawag
21	Country	Switzerland
22	Email address	suter@eawag.ch
23	Phone number	0041 (0)44 823 5479
24	Fax number	0041 (0)44 823 5311

9

Date:	August 14, 2006
Name of the method/project:	Functional proteomics on Chlamydomonas reinhardtii
Name of the contact person	Marc J-F Suter
Organisation:	Eawag
Country:	Switzerland

No	Question	Answer
Species		
1	Common name of the species	Chlamydomonas reinhardtii
2	Scientific name of the species	Chlamydomonas reinhardtii
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	NO
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	YES
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-LC/LC-MS/MS (mudPIT) with accurate mass full scan spectra
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	NO
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	NO
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	depending on sample cleanup: ~1000
14	Names and CAS numbers of the chemicals studied using the method	various herbicides nanoparticles (TiO2)
References		

15	Publications	Chlamydomonas reinhardtii proteomics. EJ Stauber, M Hippler Plant Bhysiol Biochem 2004, 42(12):989-1001
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Marc J-F Suter and collaborators
20	Affiliation	Eawag
21	Country	Switzerland
22	Email address	suter@eawag.ch
23	Phone number	0041 (0)44 823 5579
24	Fax number	0041 (0)44 823 5311

10

Date:	August 14, 2006
Name of the method/project:	Functional genomics on Chlamydomonas reinhardtii
Name of the contact person	Rik I.L. Eggen
Organisation:	Eawag
Country:	Switzerland

No	Question	Answer
Species		
1	Common name of the species	Chlamydomonas reinhardtii
2	Scientific name of the species	Chlamydomonas reinhardtii
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	YES
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	custom
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	mutant analysis, reportergene constructs, real time PCR
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	screening of gene expression profiles on whole genome array, variaty of pollutants and stress conditions causing photo-oxidative stress

14	Names and CAS numbers of the chemicals studied using the method	
References		
15	Publications	various publications from Fischer B.B. and Eggen, R.I.L.
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Rik I.L. Eggen and collaborators
20	Affiliation	Eawag
21	Country	Switzerland
22	Email address	eggen@eawag.ch
23	Phone number	0041 (0)44 823 5320
24	Fax number	0041 (0)44 823 5311

11

Date:	August 14, 2006
Name of the method/project:	Toxicogenomics on zebrafish
Name of the contact person	Rik I.L. Eggen
Organisation:	Eawag
Country:	Switzerland

No	Question	Answer
Species		
1	Common name of the species	zebrafish
2	Scientific name of the species	Danio rerio
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	
4	Number of expression sequence tags (or genes sequenced)	
Microarray		
5	Does the method include a microarray? (Yes/No)	YES
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	custom and commercial (Affymetrix)
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	functional approach (mutants, knock-down), real time PCR
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	screening of gene expression profiles on whole genome array, variety of chemicals covering a broad range of modes of toxic action
14	Names and CAS numbers of the chemicals studied using the method	
References		

15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Rik I.L. Eggen and collaborators
20	Affiliation	Eawag
21	Country	Switzerland
22	Email address	eggen@eawag.ch
23	Phone number	0041 (0)44 823 5320
24	Fax number	0041 (0)44 823 5311

12		
	Date:	24-07-2006
	Name of the method/project:	Lumbricus rubellus ecotoxicology
	Name of the contact person	Dr Peter Kille/Dr David Spurgeon/Dr Jake Bundy
	Organisation:	Cardiff Univerity/Centre for Ecology and Hydrology/Imperial College of Science, Technology and Medicine
	Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Red Worm/Marsh Red Worm
2	Scientific name of the species	Lumbricus rubellus
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	17225
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	1H-NMR, GC-MS
Other technologies		
11	Does the method include other technologies? (Yes/No)	
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	8000 genes, 50 metobolites (NMR) 100-200 metabolites (GC-MS)
14	Names and CAS numbers of the chemicals studied using the method	Copper chloride (CAS 7447-39-4), cadmium chloride (CAS 7790-78-5), nickel chloride (CAS 7718-54-9), fluoranthene (CAS 206-44-0), chlorpyrifos (2921-88-2), atrazine (CAS 1912-24-9) (array and metabolomics) zinc, fluorinated anilines, pyrene (metabolomics only)
References		
15	Publications	Bundy, J.G., et al (2002) Metabonomic assessment of toxicity of 4-fluoroaniline, 3,5-difluoroaniline and 2-fluoro-4-methylaniline to the earthworm Eisenia veneta (Rosa): identification of new endogenous biomarkers. Environmental Toxicology and Chemistry 21, 1966-1972. Galay-Burgos M., et al (2003). Developing a new method for soil pollution monitoring using molecular-genetic biomarkers. Biomarkers, 8, 229-239. Spurgeon, D.J., et al. (2004) Molecular and cellular biomarkers of metal toxicity in Lumbricus rubellus; Validation by integration with a demographic parameter. Comparative Biochemistry and Physiology Part C: Toxicology and Pharmacology, 138, 11-21. Bundy, J.G. et al. (2004) Environmental metabonomics: applying combination biomarker analysis in earthworms at the field scale. Ecotoxicology 13, 797-806.
16	Supplemental websites or database accession numbers	www.earthworms.org
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr Peter Kille/Dr David Spurgeon/Dr Jake Bundy
20	Affiliation	Cardiff Univerity/Centre for Ecology and Hydrology/Imperial College of Science, Technology and Medicine
21	Country	UK
22	Email address	kille@cardiff.ac.uk / dasp@ceh.ac.uk / j.bundy@imperial.ac.uk
23	Phone number	+44 29 20 874 507 / + 44 1487 772 563 / +44 20 7594 3039
24	Fax number	

13

Date:	24 July, 2006
Name of the method/project:	C. elegans
Name of the contact person	Dr Peter Kille/Dr David Spurgeon/Dr Stephen Sturzenbaum
Organisation:	Cardiff Univerity/Centre for Ecology and Hydrology/Kings College London
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	
2	Scientific name of the species	Caenorhabditis elegans
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Yes
4	Number of expression sequence tags (or genes sequenced)	~20,000
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom Oligonucleotide
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	1H-NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	RNAi, knock-out mutants
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	20,000 transcripts, 50 metabolites by 1H-NMR
14	Names and CAS numbers of the chemicals studied using the method	Copper chloride (CAS 7447-39-4), cadmium chloride (CAS 7790-78-5), fluoranthene (CAS 206-44-0), atrazine (CAS 1912-24-9)
References		
15	Publications	Swain, S.et al 2004. C-elegans metallothioneins: New insights into the phenotypic effects of cadmium toxicosis. J. Mol. Biol. 341, 951-959; Spanier, Bet al 2005. Caenorhabditis elegans Neprilysin nep-1: An effector of locomotion and pharyngeal pumping. J. Mol. Biol. 352, 429-437; Menzel, Ret al 2004. Humic material induces behavioral and global transcriptional responses in the nematode Caenorhabditis elegans. Environ. Sci. Technol. 2005, 39, 8324-8332.
16	Supplemental websites or database accession numbers	www.earthworms.org
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr Peter Kille/Dr David Spurgeon/Dr Stephen Sturzenbaum
20	Affiliation	Cardiff Univerity/Centre for Ecology and Hydrology/Kings College London
21	Country	UK
22	Email address	kille@cardiff.ac.uk / dasp@ceh.ac.uk / stephen.sturzenbaum@kcl.ac.uk
23	Phone number	+44 29 20 874 507 / + 44 1487 772 563 / +44 20 7848 4406
24	Fax number	

14

Date:

Name of the method/project:	Immunotoxicogenomics in mouse
Name of the contact person	Henk van Loveren
Organisation:	National Institute for Public Health and the Environment (RIVM)
Country:	The Netherlands

No	Question	Answer
Species		
1	Common name of the species	mouse
2	Scientific name of the species	Mus musculus (spleen, thymus)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished http://www.ncbi.nlm.nih.gov/genome/seq/MmHome.html (NCBI)
4	Number of expression sequence tags (or genes sequenced)	availble in public http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?dbFrom=nucleotide&db=nucest&cmd=Search&cmd_current=Limits&orig_db=nucest&term=(txid10090%5Borgn%5D+AND+gbdiv_est%5Bprop%5D) (NCBI)
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom: Mouse Sigma Compugen oligolibrary
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No

12	If yes, please provide information on the technology.	NA
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	selection of 11K genes with a bias towards immunological and toxicological relevance
14	Names and CAS numbers of the chemicals studied using the method	bis(tri-n-butyltin)oxide (TBTO) (56-35-9); benzo[a]pyrene (50-32-8); cyclosporin A (59865-13-3); acetaminophen (103-90-2)
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Comparison of immunotoxic compounds with different mechanisms of action
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Kirsten Baken, Jeroen Pennings, Annemieke de Vries, Harry van Steeg, Henk van Loveren
20	Affiliation	National Institute for Public Health and the Environment
21	Country	The Netherlands
22	Email address	kirsten.baken@rivm.nl
23	Phone number	+31302743105
24	Fax number	+31302744446

15

Date:

Name of the method/project:

Name of the contact person	Janine Ezendam
Organisation:	National Institute for Public Health and the Environment (RIVM)
Country:	The Netherlands

No	Question	Answer
Species		
1	Common name of the species	rat
2	Scientific name of the species	Rattus norvegicus (liver, spleen, thymus, mesenteric lymph node)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished http://www.ncbi.nlm.nih.gov/genome/guide/rat/
4	Number of expression sequence tags (or genes sequenced)	Available at http://www.ncbi.nlm.nih.gov/genome/guide/rat/
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom: rat array ready oligo set v1.0 Operon Biotechnologies GmbH
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	5705 C6-amino-linked oligos
14	Names and CAS numbers of the chemicals studied using the method	*Lactobacillus casei* Shirota
References		
15	Publications	International Journal of Food Microbiology (2006) doi:10.1016/j.ijfoodmicro.2006.06.009
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Study on immune effects of probiotics
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Janine Ezendam, Kirsten Baken, Jeroen Pennings, Henk van Loveren
20	Affiliation	National Institute for Public Health and the Environment
21	Country	The Netherlands
22	Email address	Janine.Ezendam@rivm.nl
23	Phone number	+31302743447
24	Fax number	+31302744446

16

Date:

Name of the method/project:	Toxicogenomics of hexachlorobenzene
Name of the contact person	Janine Ezendam
Organisation:	National Institute for Public Health and the Environment (RIVM)
Country:	The Netherlands

No	Question	Answer
Species		
1	Common name of the species	rat
2	Scientific name of the species	Rattus norvegicus (liver, kidney, blood, spleen, thymus, mesenteric lymph node)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished http://www.ncbi.nlm.nih.gov/genome/guide/rat/
4	Number of expression sequence tags (or genes sequenced)	Available at http://www.ncbi.nlm.nih.gov/genome/guide/rat/
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Commercial: Affymetrix RG U34A
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	8799 probe sets
14	Names and CAS numbers of the chemicals studied using the method	Hexachlorobenzene (118-74-1)
References		
15	Publications	Environmental Health Perspectives (2004) 112 (7): 782-91
16	Supplemental websites or database accession numbers	Available at ArrayExpress accession number E-TOXM-15
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Study on mechanisms of immunotoxicological effects of hexachlorobenzene
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Janine Ezendam[1], Jeroen Pennings[1]Raymond Pieters[2]
20	Affiliation	[1]National Institute for Public Health and the Environment; [2]Institute for Risk Assessment Sciences, University of Utrecht
21	Country	The Netherlands
22	Email address	Janine.Ezendam@rivm.nl
23	Phone number	+31302743447
24	Fax number	+31302744446

17

Date:

Name of the method/project:	Immunotoxicogenomics of TBTO in rat
Name of the contact person	Henk van Loveren
Organisation:	National Institute for Public Health and the Environment (RIVM)
Country:	The Netherlands

No	Question	Answer
Species		
1	Common name of the species	rat
2	Scientific name of the species	Rattus Norvegicus (liver, spleen, thymus)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished http://www.ncbi.nlm.nih.gov/genome/guide/rat/
4	Number of expression sequence tags (or genes sequenced)	Available at http://www.ncbi.nlm.nih.gov/genome/guide/rat/
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Custom: rat array ready oligo set v1.0 Operon Biotechnologies GmbH
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	Real time RT-PCR
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	5705 C6-amino-linked oligos
14	Names and CAS numbers of the chemicals studied using the method	bis(tri-n-butyltin)oxide (TBTO) (56-35-9)
References		
15	Publications	Journal of Immunotoxicology (submitted)
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Study on immunotoxicological effects
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Kirsten Baken, Jeroen Pennings, Henk van Loveren
20	Affiliation	National Institute for Public Health and the Environment
21	Country	The Netherlands
22	Email address	kirsten.baken@rivm.nl
23	Phone number	+31302743105
24	Fax number	+31302744446

18

Date:	4th of September, 2006
Name of the method/project:	Environmental effects of pharmaceuticals and mixtures
Name of the contact person	Joakim Larsson
Organisation:	the Sahlgrenska Academy of Göteborg University
Country:	Sweden

No	Question	Answer
Species		
1	Common name of the species	Rainbow trout
2	Scientific name of the species	Oncorhynchus mykiss
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	(>250,000 in total available at Genbank)
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	GRASP salmonid cDNA array and from sept 2006 "Geniom" (flexible oligo array - www.geniom.com)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE, Maldi-TOF, Q-TOF, FT-ICR
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR (up to 900 MHz available)
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	Analytical chemistry, various molecular biomarkers (RT-PCR, ELISA, Western blot, enzyme activity assays), histology, field work
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	16,000 spots on GRASP array, up to 150,000 spots on Geniom array
14	Names and CAS numbers of the chemicals studied using the method	Selected pharmaceuticals and complex sewage effluents
References		
15	Publications	Samuelsson L., Förlin L., Karlsson G., Adolfsson-Erici M. and Larsson D.G.J. 2006. Using NMR metabolomics to identify responses of an environmental estrogen in blood plasma of fish. Aquatic Toxicology, 78, 341-349.
16	Supplemental websites or database accession numbers	www.geniom.com; www.cgrasp.org; www.physiology.gu.se/endo/staff/JL.htm
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology research. Develop biomarkers in fish for exposure to pharmaceuticals.
18	Comments (as appropriate)	Work also initiated on zebrafish. Geniom platform allows flexibility in terms of species selection.
Contact Information		
19	Main researchers	Joakim Larsson and Lars Förlin
20	Affiliation	Göteborg University
21	Country	Sweden
22	Email address	joakim.larsson@fysiologi.gu.se
23	Phone number	+46-31-7733589
24	Fax number	+46-31-7733512

19

Date:	07 July, 2006
Name of the method/project:	Mouse Array
Name of the contact person	Hajime Watanabe
Organisation:	National Institute of Natural Sciences
Country:	Japan

No	Question	Answer
Species		
1	Common name of the species	House mouse
2	Scientific name of the species	Mus musculus (Liver, Uterus)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished http://www.ncbi.nlm.nih.gov/genome/seq/MmHome.html (NCBI)
4	Number of expression sequence tags (or genes sequenced)	availble in public http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?dbFrom=nucleotide&db=nucest&cmd=Search&cmd_current=Limits&orig_db=nucest&term=(txid10090%5Borgn%5D+AND+gbdiv_est%5Bprop%5D) (NCBI)
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affymetrix: mouse430A
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	NA
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA

Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	22600 genes
14	Names and CAS numbers of the chemicals studied using the method	β-Estradiol (50-28-2); Bisphenol A (80-05-7); Di-n-butyl phthalate (84-74-2)
References		
15	Publications	Genes Cells. (2002) 7:497-507.
16	Supplemental websites or database accession numbers	NA
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Study on estrogenic chemicals.
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Hajime Watanbe
20	Affiliation	National Institute of Natural Sciences
21	Country	Japan
22	Email address	watanabe@nibb.ac.jp
23	Phone number	81-(0)564-59-5237
24	Fax number	81-(0)564-59-5236

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Date:	07 July, 2006
Name of the method/project:	Mouse Proteome
Name of the contact person	Hajime Watanabe
Organisation:	National Institute of Natural Sciences
Country:	Japan

No	Question	Answer
Species		
1	Common name of the species	House mouse
2	Scientific name of the species	Mus musculus (Uterus)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	NA
Proteomics		
7	Does the method include proteomics? (Yes/No)	yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	NA
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	200 spots

14	Names and CAS numbers of the chemicals studied using the method	β-Estradiol (50-28-2)
References		
15	Publications	NA
16	Supplemental websites or database accession numbers	NA
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Study on estrogenic chemicals.
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Hajime Watanbe
20	Affiliation	National Institute of Natural Sciences
21	Country	Japan
22	Email address	watanabe@nibb.ac.jp
23	Phone number	81-(0)564-59-5237
24	Fax number	81-(0)564-59-5236

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Date:	August 30, 2006
Name of the method/project:	
Name of the contact person	Dr. David Rouquié Dr. Rémi Bars
Organisation:	BAYER CROPSCIENCE
Country:	France

No	Question	Answer
Species		
1	Common name of the species	Rat; Mouse
2	Scientific name of the species	Rattus norvegicus
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	Finished
4	Number of expression sequence tags (or genes sequenced)	Full genome
Microarray		
5	Does the method include a microarray? (Yes/No)	yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Agilent full genome gene chip
Proteomics		
7	Does the method include proteomics? (Yes/No)	yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2DE
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	yes
12	If yes, please provide information on the technology.	Quantitative PCR
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	41 000 trancripts and variants
14	Names and CAS numbers of the chemicals studied using the method	Flutamide; Finasteride; Clofibrate; Phenobarbital, Methyl testosterone; Estradiol benzoate; Ethinyl estradiol; Diethyl stilbestrol (DES); Genistein; Dinitrobenzene
References		
15	Publications	Cayatte, C., C. Pons, et al. (2006). "Protein profiling of rat ventral prostate following chronic finasteride administrationIdentification and localization of a novel putative androgen regulated protein." Mol Cell Proteomics. Friry-Santini, C., Rouquié, D., Kennel, P., Tinwell, H., Benahmed, M., and Bars, R. (2007). Correlation between protein accumulation profiles and conventional toxicological findings using a model antiandrogenic compound, flutamide. Toxicol Sci 97, 81-93. Tinwell, H., Friry-Santini, C., Rouquié, D., Belluco, S., Elies, L., Pallen, C., and Bars, R. (2007). Evaluation of the Antiandrogenic Effects of Flutamide, DDE, and Linuron in the Weanling Rat Assay Using Organ Weight, Histopathological, and Proteomic Approaches. Toxicol Sci 100, 54-65.
16	Supplemental websites or database accession numbers	http://www.ncbi.nlm.nih.gov/entrez/query.fcgi?cmd=Retrieve&db=PubMed&dopt=Citation&list_uids=16837577
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. David Rouquié Dr.Rémi Bars
20	Affiliation	Bayer Cropscience
21	Country	France
22	Email address	david.rouquie@bayercropscience.com remi.bars@bayercropscience.com
23	Phone number	33 492 94 34 00
24	Fax number	334 93 95 84 54

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Date:	8th August 2006
Name of the method/project:	Developmental toxicology of Japanese medaka embryos
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Japanese medaka
2	Scientific name of the species	Oryzias latipes (homogenates of whole embryos)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites

References		
15	Publications	M. R. Viant, C. A. Pincetich, D. E. Hinton and R. S. Tjeerdema, Toxic Actions of Dinoseb in Medaka (Oryzias latipes) Embryos as Determined by in vivo 31P NMR, HPLC-UV and 1H NMR Metabolomics. Aquat. Toxicol. 76, 329-342 (2006); M. R. Viant, J. G. Bundy, C. A. Pincetich, J. S. de Ropp and R. S. Tjeerdema, NMR-Derived Developmental Metabolic Trajectories: An Approach for Visualizing the Toxic Actions of Trichloroethylene during Embryogenesis, Metabolomics 1, 149-158 (2005); M. R. Viant, Improved Methods for the Acquisition and Interpretation of NMR Metabolomic Data, *Biochem. Biophys. Res. Comm*. 310, 943-948 (2003)
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Toxicology; chemical risk assessment
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

23

Date:	8th August 2006
Name of the method/project:	Developmental toxicology of Chinook salmon eggs and alevins
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Chinook salmon
2	Scientific name of the species	Oncorhynchus tshawytscha (homogenates of whole embryos)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites

References		
15	Publications	M. R. Viant, C. A. Pincetich and R. S. Tjeerdema, Metabolic effects of dinoseb, diazinon and esfenvalerate in eyed eggs and alevins of Chinook salmon (Oncorhynchus tshawytscha) determined by 1H NMR metabolomics. Aquat. Toxicol. 77, 359-371 (2006).
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

24

Date:	8th August 2006
Name of the method/project:	Metabolomics investigation of endocrine disruption in roach
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Roach
2	Scientific name of the species	Rutilus rutilus (plasma, gonad)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	MS (specifically FT-ICR MS)
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	MS estimated to detect ca. 1000 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		

15	Publications	None to date
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	8th August 2006
Name of the method/project:	Toxicity studies in European flounder
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	European flounder
2	Scientific name of the species	Platichthys flesus (liver)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		

15	Publications	None to date
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	8th August 2006
Name of the method/project:	Toxicity studies in 3-spined stickleback
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	3-spined stickleback
2	Scientific name of the species	Gasterosteus aculeatus (liver)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		
15	Publications	None to date

16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	8th August 2006
Name of the method/project:	Toxicity studies in Daphnia
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Water flea
2	Scientific name of the species	Daphnia magna (whole body homogenates)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	MS (specifically FT-ICR MS)
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	MS estimated to detect ca. 1000 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		
15	Publications	None to date

16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Chemical risk assessment; ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	8th August 2006
Name of the method/project:	Biomarker development in mussels
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Common mussel
2	Scientific name of the species	Mytilus edulis (adductor muscle, mantle)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		
15	Publications	In preparation

16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	8th August 2006
Name of the method/project:	Biomarker development in mussels
Name of the contact person	Dr Mark Viant
Organisation:	University of Birmingham
Country:	UK

No	Question	Answer
Species		
1	Common name of the species	Mediterranean mussel
2	Scientific name of the species	Mytilus galloprovincialis (adductor muscle, mantle)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	?
4	Number of expression sequence tags (or genes sequenced)	?
Microarray		
5	Does the method include a microarray? (Yes/No)	No
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	Yes
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NMR
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	NMR estimated to detect ca. 100 metabolites
14	Names and CAS numbers of the chemicals studied using the method	Low molecular weight endogenous metabolites
References		

15	Publications	In preparation
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Ecotoxicology
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Dr. Mark Viant
20	Affiliation	University of Birmingham
21	Country	UK
22	Email address	m.viant@bham.ac.uk
23	Phone number	44-(0)121-414-2219
24	Fax number	44-(0)121-414-5925

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Date:	Sep 20, 2006
Name of the method/project:	Mouse array
Name of the contact person	Dr. Seokjoo Yoon
Organisation:	Korea Institue of Toxicology
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Mouse
2	Scientific name of the species	Mus Musculus(Liver, Kidney))
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affymetrix system
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	Blood biochemical analysis, histopathology
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes

14	Names and CAS numbers of the chemicals studied using the method	CCl_4(56-23-5);ENU(759-73-9);Bromobenzene(108-86-1); Acetaminophen(103-90-2); ANIT(551-06-4);Thioacetamide(62-55-5);Gentamicin(1403-66-3);Cephalexin(15686-71-2);Puromycin(53-79-2);Metapyrilene(91-80-5);Phalloidin(17466-45-4)
References		
15	Publications	Mol. & Cell. Toxicol.(2005) 1(4), 275-280; Mol. & Cell. Toxicol. (2005)1(4), 268-274;Mol. & Cell. Toxicol.(2006) 2(1), 21-28;. Mol. & Cell. Toxicol.(2006) 2(1), 48-53;Mol. & Cell. Toxicol.(2006) 2(2), 126-133
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Ecotoxicology; Pharmacology; others)	Screening for Hepatotoxicity & Nephrotoxicity biomarker
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Seokjoo Yoon
20	Affiliation	Korea Institute of Toxicology
21	Country	Korea
22	Email address	sjyoon@kitox.re.kr
23	Phone number	82-42-860-7476
24	Fax number	82-42-860-7488

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person	Dr. Kui Lea Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Mouse
2	Scientific name of the species	Balb/c mouse (spleen, thymus)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	-
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Applied Biosystem(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	-
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	-
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	-
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	32,381 genes
14	Names and CAS numbers of the chemicals studied using the method	hexachlorobenzene; cyclosporine A; tacrolimus
References		
15	Publications	No
16	Supplemental websites or database accession numbers	-
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening of gene expression profile and biomakers for immunotoxicity prediction
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Kui Lea Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	parkkl@kfda.go.kr
23	Phone number	82-02-380-1797~8
24	Fax number	82-02-380-1799

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Date:	Sep 29, 2006
Name of the method/project:	mouse array
Name of the contact person	Dr. Cho, Dae Hyun
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Mouse
2	Scientific name of the species	C57BL/6J mouse(ovary, testis)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affymetrix (Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	-
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	-
Other technologies		
11	Does the method include other technologies? (Yes/No)	No
12	If yes, please provide information on the technology.	-
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes
14	Names and CAS numbers of the chemicals studied using the method	Cadmium(10108-64-2), 2-bromopropane(75-26-3)
References		
15	Publications	No
16	Supplemental websites or database accession numbers	-
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for reproductive and developmental toxicity prediction profiles and biomarkers
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Cho, Dae Hyun
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	dhcho@kfda.go.kr
23	Phone number	82-2-380-1804~805
24	Fax number	82-2-352-9446

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Date:	Oct 9, 2006
Name of the method/project:	Rat array
Name of the contact person	Dr. Young Na Yum
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	F344/N Rat
2	Scientific name of the species	
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Applied Biosystem(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	No
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	Blood biochemical and urine analysis, histopathology
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	
14	Names and CAS numbers of the chemicals studied using the method	HgCl2(7487-94-7)
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for nephrotoxicity profiles and biomarkers
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Young Na Yum
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	ynyum@kfda.go.kr
23	Phone number	82-02-380-1817~8
24	Fax number	82-02-380-1820

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person	Dr. Sue Nie Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Human
2	Scientific name of the species	TK6 cell line
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affimetrix(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE & MALDI/TOF
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes
14	Names and CAS numbers of the chemicals studied using the method	Mitomycin C, Methyl methanesulfonate, Doxorubicin, Wy-14643, Clofibrate, Methapyrilene
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for genotxicity prediction profiles and biomarkers, Prediction of carcinogenesis and prevention; human and mouse cell line comparison; In vivo-in vitro correlation studies
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Sue Nie Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	suenie@kfda.go.kr
23	Phone number	82-02-380-1792~4
24	Fax number	82-02-380-1795

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person	Dr. Sue Nie Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Human
2	Scientific name of the species	TK6 lymphoblast cell line
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Applied Biosystem(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE & MALD/TOF
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes
14	Names and CAS numbers of the chemicals studied using the method	MNNG, H2O2
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for genotxicity prediction profiles and biomarkers, Prediction of carcinogenesis and prevention
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Sue Nie Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	suenie@kfda.go.kr
23	Phone number	82-02-380-1792~4
24	Fax number	82-02-380-1795

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person	Dr. Sue Nie Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country:	Korea

No	Question	Answer
Species		
1	Common name of the species	Mouse
2	Scientific name of the species	Balb/c 3T3 A1 1-1 cell line
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affimetrix(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE & MALDI/TOF
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	
Scale and Chemicals		
13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes

14	Names and CAS numbers of the chemicals studied using the method	MMNG, TPA, H2O2, EGCG(food ingredient)
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for genotxicity prediction profiles and biomarkers, Prediction of carcinogenesis and prevention; human and mouse cell line comparison; In vivo-in vitro correlation studies
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Sue Nie Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	suenie@kfda.go.kr
23	Phone number	82-02-380-1792~4
24	Fax number	82-02-380-1795

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person:	Dr. Sue Nie Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country	Korea

No	Question	Answer
Species		
1	Common name of the species	Mouse
2	Scientific name of the species	Mus Musculus(Liver)
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Applied Biosystem(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE & MALDI/TOF
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	Blood biochemical analysis, histopathology
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes
14	Names and CAS numbers of the chemicals studied using the method	CCl_4(56-23-5);Acetaminophen(103-90-2); ANIT(551-06-4);Thioacetamide(62-55-5);
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Screening for Hepatotoxicity prediction profiles and biomarkers
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Sue Nie Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	suenie@kfda.go.kr
23	Phone number	82-02-380-1792~4
24	Fax number	82-02-380-1795

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Date:	Sep 29, 2006
Name of the method/project:	Mouse array
Name of the contact person:	Dr. Sue Nie Park
Organisation:	National Institute of Toxicological Research, Korea Food & Drug Administration
Country	Korea

No	Question	Answer
Species		
1	Common name of the species	Human
2	Scientific name of the species	K562
Genome Sequence		
3	Genome sequence been obtained? (Finished / In Progress / No)	No
4	Number of expression sequence tags (or genes sequenced)	NA
Microarray		
5	Does the method include a microarray? (Yes/No)	Yes
6	If yes, please provide information on the platform of the microarray (Custom /Commercial: Provide name of the company)	Affimetrix(Commercial)
Proteomics		
7	Does the method include proteomics? (Yes/No)	Yes
8	If yes, please provide information on the technology. (2D-PAGE or other methods)	2D-PAGE & MALDI/TOF
Metabolomics		
9	Does the method include metabolomics? (Yes/No)	No
10	If yes, please provide information on the technology. (MNR,LC-MS or other methods)	NA
Other technologies		
11	Does the method include other technologies? (Yes/No)	Yes
12	If yes, please provide information on the technology.	
Scale and Chemicals		

13	Scale (Number of genes, proteins or chemicals that can be analyzed)	>22,000 know genes
14	Names and CAS numbers of the chemicals studied using the method	1,2-dibromoethane Glycidol 8-OH-hydroxyquinoline Emodin Methylcarbamate o-nitrotoluene(D-mannitol 1,2-dichlorobenzene
References		
15	Publications	
16	Supplemental websites or database accession numbers	
Others		
17	Main purpose of the method and/or the project (Toxicology; Genotoxicology; Carcionogenicity; Pharmacology; others)	Molecular Screening forCharacterizing Genotoxic chemicals and chemical catergories; genotoxicity prediction profiles and biomarkers, Prediction of carcinogenesis and prevention;Comparison with Basic genotoxic test battery such as Ames; Comparison with Comet assay and in vitro MN test, too
18	Comments (as appropriate)	
Contact Information		
19	Main researchers	Sue Nie Park
20	Affiliation	NITR, KFDA
21	Country	Korea
22	Email address	suenie@kfda.go.kr
23	Phone number	82-02-380-1792~4
24	Fax number	82-02-380-1795

ANNEX 4: SUMMARY OF RESULT OF THE FORMER SURVEY (2004) (KYOTO SURVEY)

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
C. elegans	Completed	Available				metals, nonylphenol etc	Available	Arizono (Kumamoto Pref. U.)	Japan		
Ascidians	Completed	Available				TBT	Available	Azumi (Hokkaido U.)	Japan		
Daphnia magna	5000 EST clones	Available				Juvenile hormone agonists		Watanabe/Iguchi (Okazaki)	Japan	Included in OECD Test Guidelines	
Medaka	Completed	in progress						Nagahama (Okazaki)	Japan	Included in OECD Test Guidelines	targeted for sex determination
Medaka		in progress						Iguchi/Watanabe (Okazaki)	Japan	Included in OECD Test Guidelines	microarray for toxicology
Cormorant	3000 EST clones	Available	in progress			PCB		Iwata (Ehime U.)	Japan	Not included in Test Guidelines but relevant in RA	
Xenopus laevis	40000 EST clones	Available				BPA, nonylphenol, E2	submitted	Iguchi/Watanbe (Okazaki)	Japan		Affymetrix sells microarray
American alligator	5000 EST clones	in progress						Iguchi/Watanabe (Okazaki)	Japan		
Mouse	Completed	Available				estrogenic chemicals	Available	Watanbe/Iguchi (Okazaki)	Japan		Affymetrix

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Mouse	45,000 probe sets (Affymetrix MOE430 2.0)	Available		Planned (ciphergen protein chips)	Percellome system (absolute mRNA quantity data in copy number per one cell)	Toxic chemicals, drugs, hormones(database of 90 chemicals in 3 years)	Kanno J, Aisaki K, Igarashi K, Nakatsu N, Ono A, Kodama Y, et al. 2006. "Per cell" normalization method for mRNA measurement by quantitative PCR and microarrays. BMC genomics 7: 64. Shinya Matsumoto, Ken-ichi Aisaki, Jun Kanno, Mass Distributed Clustering: A New Algorithm for Repeated Measurements in Gene Expression Data. Genome Informatics (2005), 16, 183-194 Aisaki K, Aizawa S, Fujii H, Kanno J, Kanno H. 2007. Glycolytic inhibition by mutation of pyruvate kinase gene increases oxidative stress and causes apoptosis of a pyruvate kinase deficient cell line. Experimental hematology 35(8): 1190-1200.	Kanno, J (NIHS)	Japan		Ultimate goal: Signal cascade data for predictive, high-throughput toxicology
Rat	ca 8000 clones	customised	in progress			known carcinogens/non-carcinogens	not yet	"Yakabe, Y (CERI)			prediction of carcinogenicity based on gene/protein expression patterns after short term dosing (less than 4 weeks)

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
yakabe-yoshikuni@ceri.jp"	Japan		prediction of carcinogenicity based on gene/protein expression patterns after short term dosing (less than 4 weeks)								KISTCHIP-400 (Self-manufactured)
Homo Sapiens	416 Unigene Clones	Available				Sex hormones (estradiol, progesterone, testosterone) Alkylphenols (Bisphenol A, Nonylphenol), Phthalates (DEHP, DBP, BBP) Benzophenone-3	submitted	Jae-Chun Ryu (KIST)	Korea		Digital-Genomics
Homo Sapiens	8000 Unigene Clones	Available	in progress			Methylmercury	submitted	Jae-Chun Ryu (KIST)	Korea		
Mouse/Human	8000	available				hepatotoxicants	available	Duck-Young Ryu(Seoul National University)	Korea		
C. elegans	Completed	Available		Not available (Partially available, at Young-Ki Paik's lab)	RNAi (at Paik's lab)	metals, nonylphenol etc-caffein (Y. Shim's lab)	Available	Young-Ki Paik (Yonsei University), Arizono (Kumamoto Pref. U.)	Korea, Japan	It should be included.	Serum / Plasma (Human), Hepatocellular carcinoma tissue (Human), Lung canser tissue (Human), Cell cultures (Animal cell), etc

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Human, Mouse, Rat, C.elegans, C. albicans	None		2-DE, Depletions, Pre-fractionation, MALDI-TOF, LC-MS/MS,		Free Flow Electrophoresis, PF2D, GradiFlow, etc.	Hepatotoxicants	Hepatology 35, 1459-1466; Int J Cancer 97, 261-265; Proteomics 2, 1104-1113; Cancer Res. 2003 May 1;63(9):2188-2193; Proteomics 3, 569-79; Proteomics 3, 569-579l; Proteomics 3, 1883-1894; Proteomics, 3, 1955-1961; Proteomics, 4, 514-23; Molecular & Cellular Proteomics 2, 1086-1095;	Young-Ki Paik(Yonsei University) , Sang-Yeon Cho(Yonsei University)	Korea	None	Full cDNA chip, microarray for toxicogenimics
Medaka(Oryzias latipes)		120 stress respose gene cDNA chip available, in progress for hepatic cDNA chip (2000 genes)			Real-time PCR for quantification of RNA or DNA level	estrogenic chemicals, gamma ray, pharmaceutics, mant toxic chemicals	In preparation, presented already at SETAC (2003), realtime PCR publication available	Man-Bock Gu (Gwangju Institute of Science and Technology)	Korea	Included in OECD Test Guidelines	
Medaka	3,000 EST clones	Available				Nonylphenol	will be submitted	Jae-Seong Lee (Hanyang Univ)	Korea		
Rivulus marmoratus	1,577 EST clones	in progress	in progress				will be submitted	Jae-Seong Lee (Hanyang Univ)	Korea		

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Medaka		in progress	in progress			Bisphenol A, DEHP, Alachlor	in progress	Hyun-Mi Kim, Chulwoo Lee, Kwang-Soo Choi (National Institute of Environmental Res.)	Korea		Microarray for Intestinal toxicology
Mouse	Completed	in progress			LCM	Antibiotics	in progress	Sang-Hee Jeong (NVRQS)	Korea		
Human Mouse	10000 EST clones	Available	available	in plan	Nuclear Biochemistry	Radioisotope	Available	Eun-Il Lee(Korea University), Meyoung Kon Kim (Korea University), Donggeun Sul (Korea University)	Korea	Included in OECD Test Guidelines	
HumanNeuronal Cells			in progress			Cadmium, Mercury	Available	Dae-Kyung Kim(Jung-Ang University)	Korea		
Human Respiratory Epithelial Cells			im progress			Formaldehyde, Benzene	Available	Dae-Kyung Kim(Jung-Ang University)	Korea		Adaptation in Contaminated soil
Earth worm			in progress			soil contaminants		Jeong Han Kim(Seoul National Uni.)	Korea		biomarker for contamination

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Nematode			under plan			soil contaminants		Jeong Han Kim(Seoul National Uni.)	Korea		
Mouse, Rat, Zebrafish and Human	11,000, 5,000 500 and 16,000 EST clones	Available	available	available		EDS; nonylphenols, PAHs, tamoxiphen, Hepatotoxicants		Kong-Gu(Han-Yang University)	Korea		Affymetrix
mouse	14,000 genes	in progress				hepatotoxin	non-available	Hoil Kang, Ph.D. (NITR), (kanghi@kfda.go.kr)	Korea		Arrays through GRASP. Collaborations with SGP, GRYAAB, ITM, SWEGENE, Swedish NMR centre
Atlantic salmon/ rainbow trout	>75,000 EST clones	Yes. Available chip 16K.	Yes	Yes (bile fluid, blood plasma)	Analytical chemistry + a set of widely used biomarkers in fish ecotoxicology	Pharmaceuticals		J.Larsson/ L.Förlin Göteborg University (joakim.larsson@fysiologi.gu.se)	Sweden	Relevant in RA. Size good for metabonomics+ field studies.	Investigating community resilience to stress
nucella lapillus, mytilus edulis			yes		AFLP	petrol, cupper		T.Elwing, J. Gardeström	Sweden		Investigating effects on sexual differentiation of the brain in birds
coturnix coturnix, gallus domesticus		yes (g.domesticus)	yes			estrogenic compounds		B.Brunström, L Dencker	Sweden		investigating PICT caused by antifouling paints
microalgae communities					PCR-DGGE, PCR-TGGE	irgarol		H.Blanck, A.Clarke	Sweden		understand mechanisms of toxicity + develop biomarkers in fish

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Oncorhynchus mykiss, danio rerio, zoarces viviparus			yes			effluents + chemical mixtures (TBT, HBCDD, EE2, TBBPA etc)		L.Förlin	Sweden		
Chicken	????	Oligo						Affymetrix	USA		
Zebra Finch								Wade	USA		
Herring Gull								Grasman	USA		
Green Anole								Wade	USA		
Zebrafish	14,000 Oligo							Affymetrix	USA		
Zebrafish	14,000 Oligo							MWG	USA		
Zebrafish	22,000 Oligo							Agilent	USA		
Xenopus laevis	Oligo							Affyetrix	USA		
Xenopus laevis	40,000 EST							UENO-NIBB	Japan		
Xenopus laevis	400 cDNA							ViagenX Biotech	USA		
Fathead minnow	2,500 Oligo		in progress			EDCs		EcoArray	USA		
Fathead minnow	50,000 EST							Vulpe	USA		
Largemouth bass	500 cDNA							EcoArray	USA		
Sheepshead minnow	250 cDNA		in progress			EDCs		EcoArray	USA		
Mummichug	10,000 cDNA							Crawford	USA		arrays used as screening tool to identify target genes, rather than using arrays as routine detection system

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Danio rerio (zebrafish)		X	X			endocrine disrupting, mutagenic, reproduction		Rik Eggen, Jane Muncke, NN	Switzerland	ecotoxicological and vertebrate model system	arrays used as screening tool to identify target genes, rather than using arrays as routine detection system
Chlamydomonas reinhardtii	X					model compounds to cause various photoxidative stress	ES&T in press	Rik Eggen, Beat Fischer	Switzerland	algal model organism	arrays used as screening tool to identify target genes, rather than using arrays as routine detection system
S. cerevisae		X				oxidative stress compounds, reactive chemicals		Rik Eggen, Beate Escher, Barbara Luchsinger	Switzerland		arrays used as screening tool to identify target genes, rather than using arrays as routine detection system
E. coli		x				reactive chemicals		Rik Eggen, Beate Escher, Barbara Luchsinger	Switzerland		NA
Homo sapiens	NA	Affymetrix	NA	NA	NA	Xenoestrogens, Dioxins, PCBs, acrylamide	Buterin et al. (2004) Potential application of gene expression fingerprinting for food safety screening. Anal. Chim. Acta, in press	Dr. Tonko Buterin, Dr. Ramiro Dip, Prof. Dr. Hanspeter Naegeli	Switzerland	Determination of biological activity of residues in human breast milk	

Species	Genome or # of EST genes (Expression Sequence Tags)	Microarray	Proteomics	Metabolomics	Other technologies	Main chemicals studied	Availability of publication	Main researchers	Country	Ecotoxicological relevance of the species	Main purpose
Folsomia candida (Collembola)	no	no	yes	no	no	Insecticides (Insect growth regulators)	not yet	Sophie Campiche (EPFL), Prof. Emanuela Felley-Bosco (UNIL), Dr. Kristin Becker van Slooten (EPFL)	Switzerland	high	